

# STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number: 161552

TO: Louis V Wollenberger Location: rem/3861/2C18

Art Unit: 1635

Friday, August 19, 2005

Case Serial Number: 10/774721

From: Barb O'Bryen

**Location: Biotech-Chem Library** 

Remsen 1a69

Phone: 571-272-2518

Bolls

barbara.obryen@uspto.gov

Search Notes		
	o	



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GenCore version 5.1.6
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- nucleic search, using sw model OM nucleic

Run on:

August 18, 2005, 06:25:21 ; Search time 72.5 Seconds (without alignments) 473.956 Million cell updates/sec

US-10-774-721-37 21 Title: Perfect score:

1 gugccugucgggaacuggctt 21 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1202784 segs, 818138359 residues

Searched:

457068 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 21

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents NA:\*

(Ggn2\_6/ptodata/1/ina/5A\_COMB.seq:\*
(Ggn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
(Ggn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
(Ggn2\_6/ptodata/1/ina/BCTUS\_COMB.seq:\*
(Ggn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
(Ggn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		df			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
п	13.8	65.7	20	-	US-08-136-811-24	Sequence 24, Appl
7	13.8	65.7	20	-	US-08-835-770-24	24,
<u>س</u>	13.8	65.7	20	Н	US-08-628-731-24	24,
4	13.2	65.9	19	m	US-08-637-732A-26	26,
'n	13.2	62.9	21	Н	US-08-271-942A-57	57,
9	13.2	62.9	21	m	US-08-779-916A-57	57,
7	13.2	62.9	21	Ŋ	PCT-US95-08604-57	57,
80	12.8	61.0	19	Н	US-08-271-946A-13	13,
σ,	12.8	61.0	19	н	US-08-271-942A-13	13,
10	12.8	61.0	19	٣	US-08-779-916A-13	13,
11	12.8	61.0	19	m	US-08-750-232-13	13,
12	12.8	61.0	19	ហ	PCT-US95-08604-13	13
13	12.8	61.0	19	ß	PCT-US95-08606-13	13
14	12.4	59.0	20	4	US-09-657-346A-126	12
15	12.2	58.1	17	m	US-09-275-680-7	7
16	12.2	58.1	20	m	US-09-366-257-38	Sequence 38, Appl
11	12.2	58.1	20	m	US-09-844-634-62	62
c 18	12.2	58.1	21	4	US-09-762-195-8	8
19	12.2	58.1	21	4	US-09-762-195-17	17
20	11.8	56.2	17	٣	US-09-375-318-50	Sequence 50, Appl
2 21	11.8	56.2	20	4	US-10-177-573-15	15
25	11.6	55.2	18	7	US-08-897-340-26	26,
23	11.6	55.2	18	ო	US-08-757-024-823	823,
c 24	11.6	55.2	18	٣	US-09-252-329-26	
25	11.6	55.2	18	4	US-09-093-972C-823	823,
56	11.6	55.2	19	m	US-08-757-024-809	
27	11.6	55.2	19	m	US-08-757-024-822	822,

Sequence 809, App Sequence 822, App Sequence 50, Appl Sequence 50, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 50, Appl Sequence 794, Appl Sequence 81, Appl Sequence 81, Appl Sequence 821, Appl Sequence 821, Appl Sequence 50, Appl
US-09-093-972C-809 US-09-093-972C-822 US-08-286-889-50 US-08-485-618-50 US-08-640-672-19 US-08-640-672-19 US-08-640-672-19 US-08-640-672-19 US-08-943-363-50 US-08-77-888A-19 US-08-77-024-808 US-08-757-024-808 US-08-757-024-808 US-08-757-024-808 US-08-757-024-808 US-08-757-024-808 US-08-757-024-808 US-08-757-024-808 US-09-366-257-12 US-09-366-257-12 US-09-366-259-50 US-09-350-259-50
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2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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## ALIGNMENTS

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Query Match 65.7%; Score 13.8; DB 1; Length 20; Best Local Similarity 76.5%; Pred. No. 1.1e+03; Matches 13; Conservative 2; Mismatches 2; Indels
        Sequence 24, Application US/08136811
; Sequence 24, Application US/08136811
; Patent No. 5510239
; GENERAL INFORMATION:
APPLICANT: Baracchini, Jr., Edgardo and Bennett,
APPLICANT: Clarence Frank
TITLE OF INVENTION: Milidrug Resistance
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEB: Law Offices of Jane Massey Licata
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MD STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,811
PILING DATE: Herewith
CLASSIFICATION NUMBER: US/08/136,811
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SIA
PRIOR APPLICATION NUMBER: ATPORNEY AGENT INFORMATION:
NAME: Jane Massey Liceta
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                NJ
USA
US-08-136-811-24/c
                                                                                                                                                                                                                                                                                                                                                                                                 08002
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US-08-136-811-24
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4 CCUGUCGGGAACUGGCT 20

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Gaps

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
MAPPLICANT: Rudel, Thomas
APPLICANT: Rudel, Thomas
APPLICANT: Roles.
APPLICANT: Scheuerfleug, Ina B.
ITILE OF INVENTION: Recombinant PilC Proteins, Process for TITLE OF INVENTION: Recombinant PilC Proteins, Process for TITLE OF INVENTION: Recombinant PilC Proteins, Process for TITLE OF INVENTION: Recombinant Pilc B.
CORRESPONDENCE ADDRESS:
ADDRESSES: Birch, Stewart, Kolasch & Birch, LLP STREET: P.O. Box 747
CITY: Falls Church
STREET: P.O. Box 747
CITY: Falls Church
STREET: P.O. Box 747
CONDUTER: Plants Church
STREET: P.O. Box 747
CONDUTER READABLE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DEFAULT Release #1.0. Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13.8; DB 1; Length 20;
Pred. No. 1.1e+03;
                                       CITY: CALETY HILL
STATE: NJ
COUNTRY: USA
ZIP: 08002
ZIP: 08002
ZIP: 08002
COMPUTER READABLE FORM:
WEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: BM PS/2
COMPUTER: USA PSETTING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,731
FILING DATE:
TALGASIFTCATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION NUMBER: 08/136,811
FILING DATE:
ATTORNEY AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 32,257
REGISTRATION NUMBER: 32,257
REJERPANTION NUMBER: 32,257
REJERPANTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,732A FILING DATE: 28-UUN-1996
GLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
210 Lake Drive East, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-637-732A-26
; Sequence 26, Application US/08637732A
; Patent No. 6268171
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Best Local Similarity 76.5%;
Matches 13; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; STRANDEDNESS: Sir; TOPOLOGY: Linear; ANTI-SENSE: Yes
   STREET: ZIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
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                                                                                                                                                                                                                    Sequence 24, Application US/08835770

Sequence 24, Application US/08835770

Patent NO. 5801124:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Edgardo Baracchini, Jr., C. Frank Bennett
APPLICANT: Edgardo Baracchini, Jr., C. Frank Bennett
APPLICANT: Edgardo Baracchini, Jr., C. Frank Bennett
TITLE OF INVENTION: Oligomucleotide Modulation of Multidrug
TITLE OF INVENTION: Resistance-Associated Protein
TITLE OF INVENTION:
STATE: Jo Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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GREEAL INFORMATION:
GREEAL INFORMATION:
GREEAL INFORMATION:
APPLICANT: Baracchini, Jr., Edgardo and Bennett,
APPLICANT: Clarence Frank
APPLICANT: Clarence Frank
TITLE OF INVENTION: Multidrug Resistance
TITLE OF INVENTION: Multidrug Resistance
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM P6/2
COMPUTER: IBM P6/2
COMPUTER: IBM P6/2
COMPUTER: IBM P6/2
SOPTWARE: WORDPERFECT 5.1
CURRENT APPLICATION NUMBER: US/08/835,770
FILING DATE: Herewith
CLASSIFCATION NUMBER: 08/136,811
PRIOR APPLICATION NUMBER: 08/136,811
FILING DATE: 10/18/93
PRIOR APPLICATION NUMBER: 08/628,731
FILING DATE: 04/16/96
ATTORNEY/AGENT INFORMATION:
NAME: Anne Massey Licate
REGISTRATION NUMBER: 1SPH-0208
REGISTRATION NUMBER: 1SPH-0208
TELEPANICATION NUMBER: 132,257
REFRENCE/DOCKET NUMBER: 128-400
TELEPANICATION NUMBER: 128-400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-628-731-24/c
; Sequence 24, Application US/08628731
; Patent No. 5807838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 ccreccrecaacrect 4
                                                   20 CCTGCCTGGAACTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Linear
HANTI-SENSE: Yes
US-08-835-770-24
                                                                                                                                                                                                                                                       US-08-835-770-24/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
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Indels

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Query Match 62.9%; Score 13.2; DB 1; Length 21; Best Local Similarity 66.7%; Pred. No. 2.3e+03; Matches 12; Conservative 3; Mismatches 3; Indels
  ; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
US-08-271-942A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
COMPUTE 10598-4412
COMPUTE READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN.P-003-US2
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM COMPACTION
COMPUTER: IBM COMPACTION
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,916A
PILING DATE: 07-JAN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/271,942
PILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                     1 GUGCCUGUCGGGAACUGG 18
                                                                                                                                                                                                            21 GCGTCTGTGGGGAACTGG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (914) 245-3252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
FOOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHEFICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (914) 962-4330
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.73
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                     RESULT 6
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| Sequence 57, Application US/08271942A
| Patent No. 5550020
| GENERAL INFORMATION:
| GALLICANT: Gallie, Brenda L. APPLICANT: Gallie, Brenda L. APPLICANT: Dunn, James M. APPLICANT: Stevens, John K. TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis TITLE OF INVENTION: Method, Reagents and Stephania CORRESPONDENCE ADDRESS:
| ADDRESSEE: Oppedable & Larson STREET: 1992 COmmerce Street, Suite 309
                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                      Query Match 62.9%; Score 13.2; DB 3; Length 19; Best Local Similarity 72.2%; Pred. No. 2.2e+03; Matches 13; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10598-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGEN . P-003-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION UNMBRE: US/08/271,942A
FILING DATE: 08-7UL-1994
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
    147-155P (PCT)
                                                                                                                                                                                                                             MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "PCR primer T60"

US-08-637-732A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Marina T. Latson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 245-3252
                                                                                                                                                                                                                                                                                                                                                                                                               2 UGCCUGUCGGGAACUGGC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TGCCAGTCGGGAAACGGC 19
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
                                                          INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
LYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (914) 962-4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                 EXECUTE (No. 6053567).

Sequence 57, Application US/08779916A

Sequence 57, Application US/08779916A

Sequence 57, Application US/08779916A

Sequence 57, Application US/08779916A

APPLICANT: Gallie, Brenda L.

APPLICANT: Dunn, James M.

APPLICANT: Hui, May

TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis

TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis

TITLE OF INVENTION: Method, Reagents and Sequence of Title OF INVENTION: ADDRESSES: 123

CORRESPONDENCE ADDRESS:

ADDRESSEE: Oppedahl & Larson

STRRET: 1992 Commerce Street, Suite 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
US-08-779-916A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GUGCCUGUCGGGAACUGG 18
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TYPE: nucleic
STRANDEDNESS:
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                                                                                                                                                      GENERAL INTERPRETATION:
APPLICANT: Wisible Genetics Inc.
APPLICANT: Hosible Genetics Inc.
APPLICANT: Hosible Season and Development Limitied Partnership APPLICANT: Gallie, Brenda L.
APPLICANT: Gallie, Brenda L.
APPLICANT: Stevens, John K.
APPLICANT: Stevens, John K.
TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis TITLE OF INVENTION: and Targeted Screening for Retinoblastoma NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSE: Oppedable Larson
STREET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 13.2; DB 5;
Pred. No. 2.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , NAME/KEY: primer for exon 1 of human RB1 gene PCT-US95-08604-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFWARE: WORT PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08604
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US95/08604
FILING DATE: US 08/271,942
FILING DATE: US 08/271,942
ATTORNEY/AGENT INFORMATION:
NAME: MATINA T. LATSON
REGISTRATION NUMBER: 32,038
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN.P-003-WO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.00-08-271-946A-13/c
; Sequence 13, Application US/08271946A
Patent No. 5545527
; PENERAL INFORMATION:
                                                                                                  TT-US95-08604-57/c
Sequence 57, Application PC/TUS9508604
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 gugccugucgggAcugg 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 62.9%;
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (914) 245-3252
21 GCGTCTGTGGGGAACTGG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (914) 962-4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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Gaps
APPLICANT: Stevens, John K.
APPLICANT: Dunn, James M.
TITLE OF INVENTION: Method for Testing for Mutations in DNA
TITLE OF INVENTION: Method for Testing for Mutations in DNA
TITLE OF INVENTION: Errom a Patient Sample
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSE: Oppedabl & Larson
STREET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
CITY: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/08271942A

Sequence 13, Application US/08271942A

Patent No. 5550020

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gallie, Brenda L.
APPLICANT: Stevens John K.
TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
TITLE OF INVENTION: and Targeted Screening for Retinoblastoma TITLE OF INVENTION: and Targeted Screening for Retinoblastoma TITLE OF INVENTION: and Targeted Screening for Retinoblastoma NUMBER OF SEQUENCES: 123
CORRESPONDENCE ADDRESS:
ADDRESSES: Oppedahl & Larson
STREET: 1992 Commerce Street, Suite 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: primer for exon 1 of human RB1 gene US-08-271-946A-13
                                                                                                                                                                                                                                                                                          STATE: N1
COUNTRY: USA
ZIP: 10598-4412
ZIP: 10598-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: LBM Compatible
COMPUTER: LBM Compatible
COMPUTER: Word Perfect
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,946A
FILING DATE: 08-JUL-1994
FILING DATE: 08-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION ASSET OF JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNSY/AGENT INFORMATION:
NAME: MARINA T. LARSON
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN.P-002-US
TELEPHONE: (914) 245-2352
TELEPHONE: (914) 245-2352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GCCUGUCGGGAACUGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: genomic DNA HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yorktown Heights
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 68.8
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: no
FRAGMENT TYPE: in
ORIGINAL SOURCE:
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GENERAL INCORNATION:
APPLICANT: Visible Genetics Inc.
APPLICANT: Stevens, John K.
APPLICANT: Dunn, James M.
APPLICANT: Capatos, Denis
APPLICANT: Capatos, Denis
APPLICANT: Matthews, David E.
TITLE OF INVENTION: Method for Testing for Mutations in DNA
TITLE OF INVENTION: from a Patient Sample
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
61.0%; Score 12.8; DB 3;
Best Local Similarity 68.8%; Pred. No. 3.5e+03;
Matches 11; Conservative 3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: primer for exon 1 of human RB1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Disblacte, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
CURRENT APPLICATION DEFFECT
APPLICATION NUMBER: US/08/750,232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Oppedahl & Larson
STREET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
RIOR APPLICATION 1935
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,946
FILING DATE: 08-JUL-1994
ATTORNEY AGENT INFORMATION:
NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/21,942
FILING DATE: 08-JUL-1994
ATORNEY/AGENT INFORMATION:
NAME: MARINA T. LARSON
REGISTRATION NUMBER: 32.038
REFERENCE/DOCKET NUMBER: VGEN.P-CTELECPMONN: (914) 245-3252
TELEFRAX: (914) 962-4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 13, Application US/08750232
; Patent No. 6270963
                                                                                                                                                                                                                                                                                                   13:
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07-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: genomic DNA HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 GTCTGTGGGGAACTGG 4
                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              no
PE: internal
                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: no
FRAGMENT TYPE: i
ORIGINAL SOURCE:
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US-08-750-232-13/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-779-916A-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ద
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| Patent No. 6063567
| GENERAL INPORMATION:
| APPLICANT: Gallie, Brenda L. |
| APPLICANT: Dunn, James M. |
| APPLICANT: Stevens, John K. |
| APPLICANT: Hui, May |
| TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis |
| TITLE OF INVENTION: and Targeted Screening for Retinoblastoma |
| NUMBER OF SEQUENCES: 123 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Oppedahl & Larson |
| STREET: 1992 Commerce Street, Suite 309 |
| CITY: Yorktown Heights |
| STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 61.0%; Score 12.8; DB 1; Length 19; Best Local Similarity 68.8%; Pred. No. 3.5e+03; Matches 11; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) NAME/KEY: primer for exon 1 of human RB1 gene US-08-271-942A-13
           ZIP: 10598-4412
COMPUTER READABLE FORM:
WEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,942A
FILING DATE: O8-UUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA

ZIP: 10598-4412
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOPERATING SYSTEM: DOS 5.0
SOURCENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,916A
                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MAXING T. LATEON
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN
TELECOMUNICATION INFORMATION:
TELEPHONE: (914) 245-3352
TELEPHONE: (914) 962-4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GCCUGUCGGGAACUGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
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US-08-779-916A-13/c
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PCT-US95-08606-13/c
Sequence 13, Application PC/TUS9508606
Sequence 13, Application PC/TUS9508606
Sequence 13, Application PC/TUS9508606
Sequence 13, Application PC/TUS9508606
Sequence 13, Application
APPLICANT: Visible Genetics Inc.
APPLICANT: Stevens, John K.
APPLICANT: Captones Matchews, David E.
APPLICANT: Matchews, David E.
TITLE OF INVENTION: Method for Testing for Mutations in DNA TITLE OF INVENTION: from a Patient Sample NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                        Query Match 61.0%; Score 12.8; DB 5; Length 19; Best Local Similarity 68.8%; Pred. No. 3.5e+03; Matches 11; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                       NAME/KEY: primer for exon 1 of human RB1 gene pcr-US95-08604-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10598-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08606
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Oppedahl & Larson
STREET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/271,946
APPLICATION NUMBER: 08-JUL-1994
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 245-3252
TELEPHONE: (914) 962-4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
                    TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
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FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: human
FEATURE:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
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STRANDEDNESS: single
STRANDEDNESS: single
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FEGURE 13, Application PC/TUS9508604

Sequence 13, Application PC/TUS9508604

GENERAL INFORMATION:
APPLICANT: Visible Genetics Inc.
APPLICANT: Ballie, Brenda L.
APPLICANT: Gallie, Brenda L.
APPLICANT: Stevens, John K.
APPLICANT: Stevens, John K.
TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
TITLE OF INVENTION: and Targeted Screening for Retinoblastoma TITLE OF SEQUENCES: 125

CORRESPONDENCE ADDRESS:
ADDRESSER: Oppedable & Larson
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Best Local Similarity 68.8%; Pred. No. 3.5e+03;
Matches 11; Conservative 3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
US-08-750-232-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10598-4412
COMPUTER READBLE FORM:
COMPUTER: Diskette, 3.5 inch, 1.44 Mb
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: DWG SYSTEM: DOS 5.0
SOFTWARE: WOR'D PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,942
FTILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN.P-003-WO
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Oppedahl & Larson
STREET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
               REFERENCE/DOCKET NUMBER: VGEN.P-002-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
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SEQUENCE CHARACTERISTICS:
LENGTH: 19
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19:20.044
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19 GTCTGTGGGGAACTGG 4
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MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                              no
PE: internal
                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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RESULT 14

US-09-657-346A-126/c
; Sequence 126, Application US/09657346A
; Patent No. 6503754
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST
; TITLE OF INVENTION: EXPRESSION
; FILE REPERENCE: RTS-0135
; CURRENT APPLICATION NUMBER: US/09/657,346A
; CURRENT FILING DATE: 2000-09-07
; SEQ ID NO 126
; SEQ ID NO 126
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Patent No. 622630

GRNERAL INFORMATION:
APPLICANT: Hopper, James E
TITLE OF INVENTION: Regulated High-level Production of Polypeptides in
TITLE OF INVENTION: Yeast
FILE REFERENCE: 98428

CURRENT APPLICATION NUMBER: US/09/275,680

CURRENT FILING DATE: 1999-03-24

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 7
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                                                                Query Match 61.0%; Score 12.8; DB 5; Length 19; Best Local Similarity 68.8%; Pred. No. 3.5e+03; Matches 11; Conservative 3; Mismatches 2; Indels
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59.0%; Score 12.4; DB 4; Length 20;
Best Local Similarity 78.6%; Pred. No. 5.7e+03;
Matches 11; Conservative 2; Mismatches 1; Indels
; NAME/KEY: primer for exon 1 of human RB1 gene
PCT-US95-08606-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Antisense Oligonucleotide US-09-657-346A-126
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CRGANISM: Saccharomyces cerevisiae
US-09-275-680-7
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ORGANISM: Artificial Sequence
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                                                                                                                                                                            19 GTCTGTGGGGAACTGG 4
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US-09-275-680-7
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Scoring table:

Searched:

Minimum DB Maximum DB

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Perfect score:

Sequence:

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OM nucleic

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AX614231 Sequence
AX240883 Sequence
AX708916 Sequence
AX708918 Sequence
AX075066 Sequence
B15984 Oligonucleo
AR025500 Sequence
AR052377 Sequence
AR053273 Sequence
AR053273 Sequence
AR055175 Sequence
AR055175 Sequence
AR055175 Sequence
AX150046 Sequence
AX150046 Sequence
AX150046 Sequence
AX150047 Sequence
AX150047 Sequence
AX150047 Sequence
AX150045 Sequence
AX1509783 Sequence
AX168995 Sequence
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Patent: WO 2004072293-A 37 26-AUG-2004;
Patent: WO 2004072293-A 37 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERW) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jockers, R., Couturier, C. and Uhlmann, E. Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/mb_xref="taxon:32630"
/noce="Artificiel"
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synthetic construct
other sequences; artificial sequences.
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Sequence 38 from Patent WO2004072293.
CQ860126
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Sequence 37 from Patent WO2004072293.
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4; Mismatches
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AX095592
ZAMRRN04
ZAMRRNA03
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AR052377
AR053123
AR055175
AR158046
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CQ860125.1 GI:51982013
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Best Local Similarity 81.0%;
Matches 17; Conservative
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SOURCE
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AUTHORS
TITLE
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12526 Sequence 13
CQ848735 Sequence
AR21182 Sequence
AR215747 Sequence
BD190410 Phosphati
BD190410 Phosphati
BRR45253 Sequence
AR452572 Sequence
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CQ860126 Sequence
CQ860119 Sequence
AR037349 Sequence
AR040632 Sequence
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CQ858638 Sequence
AR163030 Sequence
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AX471987 Sequence
                                                                         Search time 842 Seconds
(without alignments)
1208.503 Million cell updates/sec
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                                                                                                                                                                                                                          892778
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                   4708233 seqs, 24227607955 residues
                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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                                                                           August 18, 2005, 05:29:57;
                                                     nucleic search, using sw model
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CQ860119
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Maximum Match
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Match 1
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VERSION
KEYWORDS
SOURCE
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AR040632/c
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AUTHORS
                                                            ORGANISM
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Patent: WO 2004072293-A 31 26-AUG-2004;
Patent: WO 2004072293-A 31 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSEM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
Location/Qualifiers
                                                                                                                                                              leptin receptor
Patent: WO 2004072293-A 38 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
Location/Qualifiers
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                                                                                            Jockers,R., Couturier,C. and Uhlmann,B.
Oligonuclectides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the
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90.5%; Score 19; DB 6; Length 21;
Best Local Similarity 78.9%; Pred. No. 2.46+02;
Matches 15; Conservative 4; Mismatches 0; Indels
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87.6%; Score 18.4; DB 6;
Best Local Similarity 75.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 4; Mismatches 1;
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/db_xref="taxon:32630"
/noTe="AS10"
                                                                                                                                                                                                                                                                 /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificiel"
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Sequence 31 from Patent WO2004072293.
CQ860119
                                                                   other sequences; artificial sequences.
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Sequence 24 from patent US 5801154.
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            SQ860126.1 GI:51982014
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synthetic construct
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CQ860119/c
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Unclassified.
1 (base 1 to 20)
Baracchini, E. Jr. and Bennett, C.F.
Oligonucleotide modulation of multidrug resistance-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 20)
Baracchini, E. Jr. and Bennett, C. Frank.
Oligonucleotide modulation of multidrug resistance-associated protein
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Wasses 1 to 20)

Baracchini,E., Bennett,C.Frank, and Dean,N.M.
Antisense oligonucleotide modulation of multidrug resistance-associated protein

Antisense Sisolista-A 24 01-SEP-1998;

Location/Qualifiers
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Best Local Similarity 76.5%; Pred. No. 9.8e+04;
Matches 13; Conservative 2; Mismatches 2; Indels
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1 Similarity 76.5%; Score 13.8; DB 6;
1 Similarity 76.5%; Pred: No. 9.8e+04;
13; Conservative 2; Mismatches 2;
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Patent: US 5510239-A 24 23-APR-1996;
Location/Qualifiers
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Sequence 24 from patent US 5510239.
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I19643.1 GI:1599998
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Location/Qualifiers
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Sequence 24 from patent US 5807838.
AR040632
AR040632.1 GI:5959995
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/mol_type="unassigned DNA"
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PAT 07-0CT-1996
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                               Oligomeric compounds for the modulation of survivin expression Patent: WO 2004069991-A 100 19-AUG-2004; Santaris Pharma A/S (DK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unclassified.

1 (bases 1 to 19)
Stevens, J.K., Dunn, J.M., Capatos, D. and Matthews, D.E.
Method for testing for mutations in DNA from a patient sample patent: US 6270963-A 13 07-AUG-2001;
Location/Qualifiers
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Wissenbach, M.
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61.0%; Score 12.8; DB 6;
Best Local Similarity 68.8%; Pred. No. 3.1e+05;
Matches 11; Conservative 3; Mismatches 2;
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Best Local Similarity 68.8%; Pred. No. 3.2e+05;
Matches 11; Conservative 3; Mismatches 2;
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Sequence 100 from Patent WO2004069991.
CQ858638
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Sequence 13 from patent US 554527.
124629 1 GI:1604499
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1 GUGCCUGUCGGGAACUGG 18
                                                                                                                                                                    CQ858638.1 GI:51852605
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                 21 GCGTCTGTGGGGAACTGG 4
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16 CTGTGGGGACTGGCT 1
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GTCTGTGGGGAACTGG 4
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AR163030/c
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124629/c
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Unclassified.

Unclassified.

(allie, B.L., Dunn, J.M. and Stevens, J.K.

Method, reagents and kit for diagnosis and targeted screening for retinoblastoma

retinoblastoma

Patent: US 5550020-A S7 27-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer,C., Goppelt,A. and Koegel,H.
Use of intermediate-conductance potassium channels and modulators
for the diagnosis and treatment of illnesses having disturbed
keratinocyte activity
                                                                                                  Gaps
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                                                               Query Match 65.7%; Score 13.8; DB 6; Length 20; Best Local Similarity 76.5%; Pred. No. 9.8e+04; Matches 13; Conservative 2; Mismatches 2; Indels
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LUDWIG MAXIMILIANS UNI (DE)
LOCATION/Qualifiers
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Sequence 57 from patent US 555020.
125270 GI:1605140
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                                                                                                                                                                                                                                                   AX471987 16 bp
Sequence 6 from Patent WO02053171.
AX471987.1 GI:22207038
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                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                  4 CCUGUCGGGAACUGGCT 20
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Best Local Similarity 80.01
Matches 12; Conservative
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125270/c
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PAT 10-APR-2003

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Gaps

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Unclassified.

1 (bases 1 to 20)

Bennett, C. F. and Watt, A. T.

Antisense modulation of tumor necrosis factor receptor 2 expression partients us 6410324-A 62 25-JUN-2002;

Location/Qualifiers
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Zhang, H. and Wyatt, J.
Antisense modulation of BH3 interacting domain death agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 58.1%; Score 12.2; DB 6; Length 20; Best Local Similarity 70.6%; Pred. No. 6.2e+05; Matches 12; Conservative 2; Mismatches 3; Indels
                                        Query Match 61.0%; Score 12.8; DB 6; Length 21; Best Local Similarity 68.8%; Pred. No. 3.1e+05; Matches 11; Conservative 3; Mismatches 2; Indels
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Patent: US 6503754-A 126 07-JAN-2003;
Location/Qualifiers
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Sequence 126 from patent US 6503754.
AR271882.1 GI:29703450
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/db_xref="taxon:9606"
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17 CCTGTAGGGAACGGGGT
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1 GCCTGTGGGTAACTGG 16
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Gallie, B.L., Dunn, J.M. and Stevens, J.K.
Gallie, B.L., Dunn, J.M. and Stevens, J.K.
Method, reagents and kit for diagnosis and targeted screening for retinoblastoma
retinoblastoma
Patent: US 5550020-A 13 27-AUG-1996;
Location/Qualifiers
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                                           Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 19)
2 (bases, J. K. and Dunn, J.M.
Method for testing for mutations in DNA from a patient sample Patent: US 5545527-A 13 13-AUG-1996;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                  linear
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Matches 11; Conservative 3; Mismatches 2;
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    19
    organism="unknown"
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Sequence 13 from patent US 5550020.
125226
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A2288957 Human MDR Aaf53027 IGF-1 Oli Aaf53027 IGF-1 Oli Aa632643 Wourine pr Ad32643 PCR prime Ad127267 Antisense Ad158620 Nucleic a Ad15386 Human GPC Ad12280 Human end Ad12280 Human end Ad12280 Human end Ad12281 Human end Ad12881 Human end

ADG32643 ADI27267 ADJ86220 ADJ53366 ADJ53437 ADJ22606 ADJ22882 ADJ22097

ADG72431 ADG72397 AAZ88957 AAZ88966 AAF53027 AAN80323 ADG32645

Adm57172 Murine mo Adm57173 Murine mo Adm70133 Plant gen

ADJ22833 ADJ23216 AAF96883 ABK65513 ABK65513 ADM57172 ADM57173 ADM70133

Nav11871 Mus muscu

ALIGNMENTS

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diabetes;

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Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antinflammatory; Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic; Leptin receptor related protein; OB-RGRP; leptin receptor; leptin receptor; leptin receptor; leptin receptor; alabete disorders; osteoporosis; calcification; obesity; diabete anorexia; sexual maturity disorder; haematopoiesis; angiogenesis; thrombus formation; immunity; inflammation; fetal development; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OB-RGRP antisense oligonucleotide, AS 10.
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Adr27688 OB-RGRP a
                                                                                                                   August 18, 2005, 04:18:21; Search time 229 Seconds (without alignments) 542.858 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                     2380332
               GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                4390206 seqs, 2959870667 residues
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Listing first 45 summaries
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triethyleneglycol spacer" /mod\_base= OTHER /note= "Optional thioester" OTHER O-methylation" O-methylation" Location/Qualifiers OTHER OTHER 10-FEB-2003; 2003FR-00001543 1. .5 /\*tag= a /mod\_base= C /note= "2' C /\*tag= d /mod\_base= C /note= "3' t /\*tag= c /mod\_base= ( /note= "2' ( 1. .20 /\*tag= b modified\_base modified base FR2850971-A1 13-AUG-2004 Adil532 Retinobla Adil532 Retinobla Add31737 Multiplex Ad31737 Multiplex Ad3828 Mouse BH3 Ad46888 Human c-C Ah524024 Yeast GAL Ab152426 Human RPI Ab152422 Human FLI Aaz95350 Human mtP Ab152426 Human FLI Ab152442 Human FLI Abq74812 Human TNF Abz86558 Human Oli Abd22788 Human myo Aaq86849 Antisense Aav53600 Wuclectid Abq78935 Mouse int Aaq88255 Neisseria Aat1420 Retinobla Adr70031 Human sur Adp66743 Mouse KIA

AAT11532 AAT12851 ADQ31737

AAL38283 ADP46888 AAH24024

ABQ74812 ABZ86558 ABD22788

AAZ95350 ABL52426 ABL52442

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The present invention relates to a leptin receptor related protein (OB-RGRP) antisense oligonuclectide (ON; ADR27653), that hybridises CC specifically with and inhibits the expression of ADR27652. The ON promotes expression of Leptin receptors on the cell surface and may promotes expression of Leptin receptors on the cell surface and may contain phosphorothicate bonds; 2'-onethyl nucleotides and/or a contain phosphorothicate bonds; 2'-onethyl nucleotides and/or a contain phosphorothicate bends; 2'-one Also claimed are interfering RNA triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA circussion of OB-RGRP. Also claimed are fusion proteins (FPS) and inhibit confing sequences comprising OB-RGRP or MY047 (thought to be a member of coding sequences comprising OB-RGRP or MY047 (thought to be a member of sa donor or acceptor of energy eq. luciferase or yellow fluorescent is a donor or acceptor of energy eq. luciferase or yellow fluorescent protein (YFP) for detecting compounds that modify the interaction between protein (YFP) for detecting compounds that modify the interaction between protein (YFP) for detecting compounds that modify the interaction between creat leptin-related disorders. Which can be used to prevent or the leptin receptor and OB-RGRP proteins, which can be used to prevent or creat leptin-related disorders. On seteoporosis (or other conditions involving reduced bone density); calcification; obseity, diabetes; anorexia, disorders of sexual maturity, can be interaction, ferminity mematopoliesis, angiogenesis, thrombus formation, resulted on fimmunity mematons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Untranslated region; coding sequence; chemotherapeutic drug treatment; antisense; modulation; multidrug resistance protein; drug; cancer; ss.
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1. .20
/*tag= a
/note= "contains phosphorothioate internucleotide
                                                                                                                                                                        New oligonuclectides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e\cdot g\cdot osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antisense oligonuclectide was used to illustrate the invention
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(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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4; Mismatches
                                                                                                          Uhlmann E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 UGCCUGUCGGGAACUGGCTT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4:
                                                                                                                                                                                                                                                                                     Example 6; Fig 1; 104pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ86849 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.6%;
nilarity 75.0%;
Conservative 4.
            10-FEB-2003; 2003FR-00001543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linkages"
                                                                                                            Couturier C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 15; Conserv
                                                                                                                                                    WPI; 2004-595751/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9510938-A1
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                                                                                                                                                                                                                                                        angiogenesis.
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                                                                                                                  Jockers R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ86849;
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Matches
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Gaps

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Indels

Length 20;

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                                                                                                                                                                            oligonucleotides AAQ86826-50 are antisense oligonucleotides used to modulate the expression of the multidrug resistance protein (MRP) by modulate the expression of the multidrug resistance (WDR) gene or tis RNA message. This sequence is targeted to the 3' untranslated region (3'UTR) of the MNR gene. The oligonucleotides can be used to improve the efficacy of chemocherapeutic drug treatment of a disease such as cancer or to prevent multidrug resistance developing during drug treatment of a disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorothioate oligonucleotide; antisense; inhibition; cancer; multidrug resistance; multiresistant protein; MRP; chemotherapy; human; leukotriene; inflammatory condition; ss.
                                                                                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                             New oligo:nucleotide cpds., esp. for cancer therapy - which are specifically hybridisable with nucleic acid encoding multi:drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of a phosphorothioate oligonucleotide 24.
                                                                                                                                                                                                                                                                                                 Score 13.8; DB 2; Length 20;
pred. No. 4.9e+03;
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/note= "phosphorothioate backbone"
                                                                                                                                                                                                                                                                            Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baracchini E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                 Claim 7; Page 11; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV53600 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-00136811.
96US-00628731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-00835770.
                                                                                                                                            resistance-associated protein.
                                                                                                                                                                                                                                                                                                                                                     20
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                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 76.5%;
Matches 13; Conservative
    94WO-US010827.
                           93US-00136811.
                                                                                                                                                                                                                                                                                                                                                                4 CCUGUCGGGAACUGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                         Bennett CF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...20
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                                                     PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-494825/42
                                                                                                WPI; 1995-169974/22.
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SISI (-SISI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-APR-1996;
                                                                            Baracchini E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-1998
         23-SEP-1994;
                                                      SISI (-SISI)
                                18-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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Best Local Similarity
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                                                                                     This is the nucleotide sequence of the phosphorothioate oligonucleotide used in the method of the invention, involving the used of antisense oligonucleotides are used for the antisense inhibit multidug resistance. The oligonucleotides are used for the antisense inhibition of multiresistant proteins (WRPS). These proteins are commonly found in some cancers which initially respond to chemotherapy, but overexpression of the protein leads to chemotherapy drug resistance. They are administered with the drugs to attempt to and as such, the oligonucleotides can be used to treat these conditions as well. The sequences are based on the human MRP and are used to treat conditions such as cancers, especially small-cell lung cancer, prevention of development of multidrug resistance during chemotherapy, and treatment of conditions characterised by leukotriene production, especially inflammatory conditions. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                 ö
            Anti:sense oligo:nucleotide(s) inhibiting multi:drug resistance protein expression - useful for increasing the efficacy of drugs that certain conditions have become resistant to e.g. small cell lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; intermediate-conductance potassium channel; dermatological; antiinflammatory; kerstolytic; vulnerary; antipsoriatic; atopic eczema; contact dermatitis; vitiligo; skin; hyperkeratosis; actinic keratose; hypertrophic scar; keloids; lentigo; aged skin; ulcer; psoriasis; mIKl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse intermediate-conductance potassium channel protein mIK1 primer 1.
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of intermediate-conductance potassium channel proteins for the diagnosis, prevention and treatment of disorders associated with disturbed keratinocyte activity, especially psoriasis.
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                                                                                                                                                                                                                                                                                                                      'Match 65.7%; Score 13.8; DB 2; Length 20; Local Similarity 76.5%; Pred. No. 4.9e+03; les 13; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                             Seguence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koegel H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 119; 121pp; German
                                                                 Claim 11; Col 12; 29pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABQ78935 standard; DNA; 16 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-2000; 2000DE-01065475.
20-MAR-2001; 2001US-0277453P.
                                                                                                                                                                                                                                                                                                                                                                                          20 CCTGCCTGGAACTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-643295/69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200253171-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABQ78935;
                                                                                                                                                                                                                                                                                                                       Query Match
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The invention relates to a novel use of intermediate-conductance potassium channel proteins. The proteins of the invention have dermatological, antiinflammatory, keratolytic, vulnerary, and antipsoriatic activity. The method is used especially in the field of damaged skin, e.g. contact dermatitis, atopic eczema, vitiligo, hyperkartosis, actinic keratosis, hypertrophic scars, keloids, lentigo, aged skin, ulcers and especially psoriasis. The sequence represents a PCR primer for the mouse potassium channel protein mIKI of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences coding for pilin PilC proteins from Neisseria spp. have been isolated (see AAQ88239-Q88241). The pilC1 and pilC2 genes from N.gonorrhoese have 84% identity. Probes were designed based on regions of shared homology (see AAQ88242-88261) and these constant region probes were used in Southern hybridisations to identify other pilC genes in N.gonorrhoeae strain MS11 and N.meningitidis strain A493. Also, the same probes were used to screen a Pseudomonas aeruginosa strain and identified a pilC-like sequence. Gene sequences which hybridise with any of the constant region probes are claimed. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant PilC-proteins derived from Neisseria gonorrhoeae - and their prodm. methods; useful for immunisation against pathogen type 4 pilus carrying bacteria or their detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PilC protein; pilin; pathogenic type 4 pilus bacteria; vaccine; detection; bacterial adhesin; phase variation; constant region; probe; Neisseria gonorrhoeae; Neisseria meningitidis; Pseudomonas aeruginosa;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                      63.8%; Score 13.4; DB 6; Length 16; 80.0%; Pred. No. 7.6e+03; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 19;
                                                                                                                                                                                                                                                                                                           Sequence 16 BP; 3 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 4 A; 6 C; 7 G; 2 T; 0 U; 0 Other;
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Pred. No. 9.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria pilC gene constant region probe TR60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rylf RR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
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72.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 CUGUCGGGAACUGGC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ88255 standard; DNA; 19
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07-DEC-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.0.
These 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-140328/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-OCT-1993;
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Matches

à 셤 AAT11420/c ID AAT114

RESULT 6

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The invention relates to an oligomeric compound (I) capable of modulating univity expression, having 8-50 nucleotides and/or nucleotide analogues, where the compound comprises a subsequence of at least 8 nucleotides or nucleotide analogues, where the subsequence is located within a sequence chosen from one of 143 sequences given in the specification. (I) is chosen from one of 143 sequences given in the specification. (I) is useful for treating a mammal suffering from or susceptible from a disease caused by abnormal anajogenesis, by administering (I) containing one or more LNA units that are targeted to survivin. (I) is useful as a more LNA units that are targeted to survivin. (I) is useful as a cancer, in combination with chemotherapeutic agent such as busulfan cancer, in combination with chemotherapeutic agent such as busulfan etc. (I) or a conjugate (II) containing (I) is useful in the preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New locked nucleic acid containing oligomeric compound capable of modulating survivin expression, useful for treating cancer such as breast
                                                        antiangiogenic; cytostatic; antiarteriosclerotic; antipsoriatic; antidabetic; ophthalmological; antiarthritic; antirheumatic; antiallergic; antiallarmatory; dermatological; anti-HIV; antiallergic; antiallarmatory; dermatological; anti-HIV; virucide; survivin antagonist; apoptosis inhibitor; callular proliferation inhibitor; survivin; gene expression; carboplatin; paraplatin; Taxol; doxorubicin; adramycin; atherosclerosis; psoriasis; diabetic retinopathy; rheumatoid arthritis; asthma; warts; psoriasis; diabetic retinopathy; rheumatoid arthritis; asthma; warts; melanoma; osteosarcoma; Ewing's sarcoma; chondrosarcoma; malignan; fibrosarcoma; Ewing's sarcoma; Kaposi's sarcoma; malignan; astroma; fibrosarcoma; Kaposi's sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mode="OTHER = phosphorothioate internucleotide for forther = phosphorothioate internucleotide s'-linkages, all locked nucleic acid (LNA) residues are 5'-methyl cytosine residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "OTHER = beta-D-oxy-locked nucleic acid but optionally DNA nucleotides, optionally phosphate internucleotide linkages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mod_base= OTHER
/note= "OTHER = beta-D-oxy-locked nucleic acid bu
optionally DNA nucleotides, optionally phosphate
internucleotide linkages"
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                          Human survivin gene modulatory oligonucleotide #99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 100; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Petersen KD,
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carcinoma, lung carcinoma, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-FEB-2004; 2004WO-DK00096.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-FEB-2003; 2003DK-00000183.
18-NOV-2003; 2003DK-00001708.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Д
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(first entry)
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                                                                                                                                                                                                                                                                                                            Paclītaxel; Docetaxel.
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modified_base
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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04-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of exons 1 to 27 and the promoter of the human retinoblastoma RB1 gene, of exons 1 to 27 and the promoter of the human retinoblastoma RB1 gene, used to amplify RB1 exons for use in a method of diagnosing mutations in the RB1 gene. By comparing the lengths of amplification products of RB exons from a suspected RB patient with those of RB wild-type DNA, patients can be diagnosed early which may avoid the need for radiotherapy. Any difference in length of exons between a suspected RB patient and those from wild-type RB1 indicates either a deletion or insertion mutation. Further sequencing of suspect exons can pinpoint the mutation. The method is directed to the diagnosis of and targeted genetic exception of the method is directed to the diagnosis of and targeted genetic exception.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying mutation(s) in RB1 exons by quantitative amplification - and by comparing length of amplification products and sequencing, for diagnosis and genetic screening of retinoblastoma.
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                                                                                                                                                                                                                                                                                                                                                     Retinoblastoma; RB; tumour suppressor gene; cancer; diagnosis; screening; mutation; polymerase chain reaction; PCR; ss.
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             Gaps
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               Indels
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                 3;
                                                                                                                                                                                                                                                                                                                       Retinoblastoma gene, RB1, exon 1 PCR 5' primer.
                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stevens JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 22; 48pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADR/10031 standard; DNA; 16 BP.
                       7
                                                            19
                                                                                       AAT11420 standard; DNA; 21 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-US008604.
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                                                            2 UGCCUGUCGGGAACUGGC
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                                                                                                                                                                                                                                                                                        (first entry)
                       13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-097637/10.
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12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADR70031
                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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Best Local
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RESULT 7 ADR70031/c

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Matches

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of a medicament for the treatment of atherosclerosis, psoriasis, diabetic retinopathy, rheumatoid arthritis, asthma, warts and allergic dermatitis.

(1), (11) or a pharmaceutical (III) containing (I) is useful for treating cancer in the form of a solid tumour, sarcoma, glioma or carcinoma chosen from malignant melanoma, basal cell carcinoma, ovarian carcinoma, breast carcinoma, non-small cell lung cancer, renal cell carcinoma, bladder carcinoma, ecurrical superficial bladder cancer, stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung carcinoma, cervical carcinoma and carcinoma, lung carcinoma, colorectal dysplasia, laryngeal papillomatosis, colon carcinoma, colorectal carcinoma and carcinoma melanoma, nodular melanoma, lentigo maligna melanoma, acral melagnoma, amelanotic melanoma, and desmoplastic
                                                                                                                                                                                                                                                                                                                                                                            melanoma. The sarcoma is chosen from osteosarcoma, Ewing's sarcoma, chondrosarcoma, malignant fibrous histiocytoma, fibrosarcoma and Kaposi's sarcoma. The treatment further involves administration of a chemotherapeutic agent such as taxanes, preferably Taxol, Paclitaxel or apoptosis. (I), (II) is also useful for preventing or limiting apoptosis or for preventing cellular proliferation. This sequence corresponds to an antisense oligonucleotide targeted to the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        survivin gene
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61.0%; Score 12.8; DB 13; Length 16; 68.8%; Pred. No. 1.5e+04; ive 3; Mismatches 2; Indels ( 

Sequence 16 BP; 4 A; 8 C; 3 G; 1 T; 0 U; 0 Other;

20 16 crerececeacrecer 1 5 CUGUCGGGAACUGGCT 셤 ઠે

ADP66743 standard; cDNA; 18 BP. ADP66743; RESULT 8 ADP66743 

Mouse KIAA0377 forward primer. 09-SEP-2004 (first entry)

ss; acid phosphatase; BT42-1; BT42; histidine acid phosphatase; hydrolysis; phosphate ester; BT42-II; deletion; fasting; genetically induced; obesity; isoform; metabolic disease; dysfunction; metabolic syndrome; obesity; diabetes; eating disorder; cachexia; hypertension; coronary heart disease; hypercholesterolaemia; dyslipidemia; osteoarthritis; gallstone; liver fibrosis; primer.

Mus sp.

WO2004050007-A2.

17-JUN-2004.

01-DEC-2003; 2003WO-EP013521.

29-NOV-2002; 2002EP-00026693.

(DEVE-) DEVELOGEN AG.

Schreiter K;

WPI; 2004-460971/43.

New pharmaceutical composition comprising a BT-42 homologous protein or nucleic acid, and carriers, diluents or/and additives, useful for treating obesity, hyperlipidemia, osteoarthritis, cell masses.

Example 4; Page 39; 79pp; English

This sequence is a primer which was used in the amplification of the mouse KIAA0377 coding sequence. KIAA0377 is homologous to human BT42.

CC which are known to hydrolyze phosphate ester at low pH and are able to use a wide spectrum of substrates. The two BT42 isoforms of the cinvention, BT42-1 hypercholesterolaemia of 40 amino acids compared to invention, BT42-1 hypercholesterolaemia of 40 amino acids compared to mouse BT42-1 Also BT42-11 contains an additional exon of 40 amino acids. BT42 is regulated by facting and by genetically induced obesity. BT42, and the disclosed isoforms, may be used for the manufacture of an agent for detecting or/and verifying, for the treatment, alleviation and/or prevention of metabolic diseases or dysfunctions, including metabolic syndrome, obesity or/and diabetes, as well as related disorders such as extinct disease, cachexia, hypertension, coronary heart disease, cypndrome, obesity or/and diabetes, as well as related disorders such as extinct disorder, cachexia, hypertension, coronary heart disease, cypndrome, obesity, orland and metabolic syndrome for controlling the function of a gene or/and a cyland metabolic syndrome for controlling the function of a gene or/and a cyland modified by a BT42 homologous cyland substances capable of interacting with a BT42 homologous polypeptide, and for the production of a non-human cylands and cylanses the BT42. Sequence 18 BP; 3 A; 5 C; 7 G; 3 T; 0 U; 0 Other; 

Gaps ö 61.0%; Score 12.8; DB 12; Length 18; 68.8%; Pred. No. 1.5e+04; ive 3; Mismatches 2; Indel8 ( 11; Conservative Sest Local Similarity Query Match Matches

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4 CCUGUCGGGAACUGGC 19 16 1 cererecacaacrece ð 셤

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Gaps

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AAT11532 standard; DNA; 19 BP RESULT 9
AAT11532/c

AAT11532; 

10-SEP-1996 (first entry)

Retinoblastoma gene, RB1, exon 1 PCR 5' primer.

Retinoblastoma; RB; tumour suppressor gene; cancer; diagnosis; screening; mutation; polymerase chain reaction; PCR; ss.

Synthetic.

WO9601908-A1

25-JAN-1996.

95WO-US008604. 07-JUL-1995; 94US-00271942 08-JUL-1994;

(VISI-) VISIBLE GENETICS INC. (HSCR-) HSC RES & DEV LP.

Hui M; Stevens JK, Dunn JM, Gallie BL,

WPI; 1996-097637/10.

Identifying mutation(s) in RB1 exons by quantitative amplification - and by comparing length of amplification products and sequencing, for diagnosis and genetic screening of retinoblastoma.

Claim 12; Page 14; 48pp; English.

AAT11532 is a PCR amplification primer used for the amplification of exon 1 of the human retinoblastoma RB1 gene. This primer and many other primers (see AAT11420-T11473) are used to amplify RB1 exons for use in a method of diagnosing mutations in the RB1 gene. By comparing the lengths of amplification products of RB exons from a suspected RB patient with

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AAT12839-T12899 (excluding AAT12878) are PCR primers used to amplify various regions of the RB-1 genome, including exons 1-27, the promoter region and a control sequence unrelated to RB-1 from chromosome 15. The primers are used in an example of a method for testing a disease-associated mutation in a gene, the gene may not necessarily be a tumour suppressor gene like the retinoblastoms gene another example is the partial transmembrane conductance regulator (CFTR) gene which may be analysed using the same method. The primers are used in various groupings to produce a hierarchical assay useful to test a group of patients angeleted to have a genetic mutation. The method allows the optimum (or near optimum) diagnostic algorithm by considering the cost and the sensitivity and specificity of each test
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those of RB wild-type DNA, patients can be diagnosed early which may avoid the need for radiotherapy. Any difference in length of exons between a suspected RB patient and those from wild-type RB1 indicates either a deletion or insertion mutation. Further sequencing of suspect exons can pinpoint the mutation. The method is directed to the diagnosis of and targeted genetic screening for retinoblastoma in family members of a retinoblastoma patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Testing for a disease-associated mutation in a gene - using a hierarchy of tests selected to optimise performance while minimising cost.
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR; polymerase chain reaction; retinoblastoma; tumour suppressor; cancer; mutation; identification; diagnosis; cystic fibrosis; hierarchy assay; method; specificity; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR 5' primer for exon 1 of human RB1 (retinoblastoma-1) gene.
                                                                                                                                                                                                   61.0%; Score 12.8; DB 2; Length 19; 68.8%; Pred. No. 1.5e+04; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19 BP; 4 A; 10 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                               Sequence 19 BP; 4 A; 10 C; 3 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT12851 standard; DNA; 19 BP.
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                                                                                                                                                                                                                                                                                            3 GCCUGUCGGGAACUGG 18
                                                                                                                                                                                                                                                                                                                 22-OCT-1996 (first entry)
                                                                                                                                                                                                                 Query Match
Best Local Similarity 68.8
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dunn JM, Stevens JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-171632/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-1996.
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The invention relates analysing multiple targets in polymucleotide, convolves providing a set or sets of multiple primers with target nucleic acids in separate reactions of primer extension or amplification, where acids in separate reactions of primer extension or amplification, where the reactions produce nucleic acid products in that each nucleic acid tragments comprise at least one restriction sites with cognate products of the separate reactions on the restriction sites with cognate products of the separate reactions on the restriction sites with cognate reactions together, where randomly joining nucleic acid fragments from the separated reactions are created, amplifying the joined products, and the separated reactions are reacted, amplifying the joined products, and detecting the amplified products. Also included are an oligonucleotide detecting target nucleic acid sequence (complementary portion and 5' non-complementary portion and 5' non-complementary portion and 5' non-complementary portion comprises a restriction enzyme site, where the complementary portion or complementary portion or restriction marker in the process of detecting target nucleic acid sequence, where the detection signal generated from target nucleic acid sequence, where the detection product is comprising a set or sets of multiple targets in a polymocleotide condition on restriction of multiple targets in a polymocleotide condition on restriction of multiple targets in a polymocleotide and for genotyping mutations, preferably single creatriction enzymes, DNA ligase, DNA polymerase, dNATP, buffers for all enzymes, and dNTPs). The method is useful for analysing differential gene conclete acids from any source. The method any speciation of multiple targets quantitatively. An experiment was performed, using the method of the invention, where SNPs were detected in 70 human genomic DNA in the fragets quantitatively. The present sequence is a primer used in the engance of targets quantitatively. The present sequence is a primer used in the en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Analyzing multiple targets in polymucleotide, by providing multiple primers with target nucleic acids, digesting nucleic acid products with cognate restriction enzymes, amplifying digested products, and detecting
                                                                                                                                                                                                                                                                                                            Human; Multiplex nucleic acid detection; ss; PCR; primer; SNP; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                     Multiplex amplification of human SNP fragments, primer #153.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; SEQ ID NO 195; 65pp; English.
                                                                                                                                              ADQ31737 standard; DNA; 21 BP
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18
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3 GCCUGUCGGGAACUGG
                      | |:|: ||||||:
19 GTCTGTGGGGAACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amplified products.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2004146866-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FUGG/) FU G.
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                          21-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                ADQ31737;
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                                                                                                                RESULT 11
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61.0%; Score 12.8; DB 2; Length 19; 68.8%; Pred. No. 1.5e+04; ive 3; Mismatches 2; Indels

Local Similarity 68.8 nes 11; Conservative

Best Loc Matches

Query Match

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Sequence 20 BP; 5 A; 8 C; 5 G; 2 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reagents and kits. This polymoracy is propriate an antisense oligonucleotide inhibitor of the DNA from mouse BH3 interacting domain oligonucleotide inhibitor of the DNA from mouse BH3 interacting domain oligonucleotide inhibitor of the DNA from mouse BH3 interacting domain oligonucleotide 20 nucleotides in length, which is flanked on both sides by five-nucleotide 'wings'. The wings are composed of 2'-methoxyethyl (2'-MOB) nucleotides. The internucleoside (backbone) linkages are phosphorothicate (P=S) throughout the oligonucleotide. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatotrophic; immunomodulatory; cytostatic; antiinflammatory; hepatitis; haemostatic; BH3 interacting domain death agonist; liver disease; haematopoietic disorder; developmental disorder; immunological disorder; hyperproliferative disorder; apoptosis; mouse; chimeric; 2'-methoxyethyl; 2'-MOE; phosphorothioate backbone; murine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel antisense compound targeted to nucleic acid molecule encoding the BH3 interacting domain death agonist, useful for treating animals with diseases associated with BH3 interacting domain death agonist, e.g.
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse BH3 interacting domain death mRNA agonist inhibitor SEQ ID 126
                                                                               ;
0
   Length 21;
                                                                           Indels
Score 12.8; DB 13;
Pred. No. 1.6e+04;
3; Mismatches 2;
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61.0%; Scc
68.8%; Pre
tive 3;
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07-MAR-2001; 2001US-00800631.
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GCCTGTGGGTAACTGG 16
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AAL38283 standard; DNA; 20
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                                                                           11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised
Query Match
Best Local Similarity
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15-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying compounds capable of modulating feeding behavior, fat deposition, metabolic rate, or the ratio of lean muscle mass to body fat by detecting a proto-oncogene Cbl in disorders such as diabetes, obesity and hypolipidemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as diabetes, obesity and hyperlipidaemia. The present sequence is the antisense strand for a human c-Cbl siRNA. The siRNA is useful in modulating a metabolism-associated phenotype in a cell, tissue or animal
                                                                                                                                                                                                                                                                                                                                                   Antidiabetic, Anorectic, Bating-Disorder, feeding behaviour, fat deposition, metabolic rate, lean muscle mass; body fat, Cbl; multi-adaptor protein, feeding disorder, glucose uptake disorder; metabolism disorder; diabetes; obesity; hyperlipidaemia; human; c-Cbl; siRNA; short interfering RNA; ds; RNA interference; gene silencing.
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 Length 20;
                                      Indels
Score 12.4; DB 6;
Pred. No. 2.5e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 12.4; DB 12
Pred. No. 2.5e+04;
                                                                                                                                                                                                                                                                                                                  Human c-Cbl siRNA antisense strand, SEQ ID 224.
                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 86; SEQ ID NO 224; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GARV-) GARVAN INST MEDICAL RES.
                                                                                                                                                                                                       ADP46888 standard; DNA; 21 BP.
 59.0%;
78.6%;
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71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-DEC-2002; 2002AU-00953393.
14-NOV-2003; 2003AU-00906285.
                                                                         7 GUCGGGAACUGGCT 20
                                                                                                                                                                                                                                                                               23-SEP-2004 (first entry)
                                                                                                        16 GTCGGGAACTGCCT 3
                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    James D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-488065/46.
                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2004055181-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molero JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                          ADP46888;
Query Match
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                                      Matches
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                                                                                                                                                                   RESULT 13
                                                                                                                                                                                      ADP46888
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Length 17;

4 ;

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The invention relates to high copy number expression constructs for high comprise a nucleic acid sequence encoding a set of trans-acting comprise a nucleic acid sequence encoding a set of trans-acting comprise a nucleic acid encoding a yeast selectable marker transcription factors, a nucleic acid encoding a yeast selectable marker convoluting an inefficiently or efficiently selected phenotype, a nucleic acid encoding a yeast or bacterial origin of replication (ori), and a cuique restriction site downstream of a promocer containing a cis-acting cunique restriction site downstream of a promocer containing a cis-acting caracterist in the interest that the expression construct. In a specific embodiment of the invention, the expression construct contain DNA cacting control element within the promoter which drives expression of acting control element within the promoter which drives expression of the invention actors and a dala, when constructs of the invention express to fall and dal80, and a UASgal cis are expressed in stoichiometrically-balanced amounts, which is particularly important for a galactose-inducible system, as Gal4, when constructs of the invention express the transcription factors at levels constructs of the invention express the transcription factor, and can become toxic to the cell. The expression of the gene of interest. The expression constructs provide expression of the gene of interest. The expression constructs provide constructs of the expression of a gene of interest. The expression constructs provide constructs of the synession of a gene of interest (which can encode an robust, high level expression of a gene of interest (which can encode an construct of expression constructs of the expression of a gene of interest (which can encode an encode constructs yeast galactose-inducible synession construct of extince in a galactose-inducible expression construct of expression construct of extince the expression of expression construct of extince the expression of expression constructs of extince the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expression construct for inducing and sustaining high level recombinant polypeptide production in yeast, comprises nucleic acids encoding a trans-acting transcription factor, selectable marker and yeast origin of
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                                                                                                                                                                                                                                                                                                                                                                          UASGal site; cis-acting transcription control element; Gal4; Gal3; Gal80; stoichiometrically balanced expression; yeast; truct; promoter; GAL7; ds. galactose-inducible expression; expression construct; promoter; GAL7; ds.
Gaps
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Indels
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  1;
    Mismatches
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                                                                                                                                                                                                          AAH24024 standard; DNA; 17
                                               3 GCCUGUCGGGAACU 16
                                                                           |||::||||||:
7 GCCTCTCGGGAACT 20
                                                                                                                                                                                                                                                                                                 (first entry)
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       10; Conservative
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Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

invention

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ95320 to AAZ95359 represent antisense oligomucleotides targeted to a nucleic acid molecule encoding human mitochondrial phosphoenolpyruvate carboxykinase (also known as PEPCK-mitochondrial; PEPCK-M; PCK2 and with the expression of pland especifically hybridise with and inhibit the expression of human mtPEPCK. The antisense oligonucleotides can be used for inhibiting the expression of mtPEPCK in human cells or tissues in vitro and can also be used for treating an animal, particularly a human suspected of having or being prone to a condition of disease associated with expression of mtPEPCK. They can also be used in disease associated with expression of mtPEPCK. They can also be used in disease associated with expression of mtPEPCK. They can also be used in disease associated with expression of mtPEPCK.
                                                                                                                                                                                                                                                                                  Human, mitochondrial phosphoenolpyruvate carboxykinase; PEPCK-M, PCK2;
PEPCK-mitochondrial; mtPEPCK, antisense oligonucleotide; modulation;
phosphorothioate; inhibition; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                     Human mtPBPCK phosphorothioate antisense oligonucleotide SEQ ID NO:38.
                           Gaps
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                            3; Indels

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    *tag= a
    /note= "phosphorothioate linkages"

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Score 12.2; DB 4 Pred. No. 3e+04; 3; Mismatches
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                                3,
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4 GTGTCTCTCGGGCACTG 20
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 Query Match 58.1%;
Best Local Similarity 64.7%;
Matches 11; Conservative
                                                                                           1 GCCTGTTGACAACTGGC
                                                                                                                                                                       AAZ95350 standard; DNA; 20
                                                              3 GCCUGUCGGGAACUGGC
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modified base
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Best Local Simi
Matches 10;
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                                                                                                                                                                                                                                                                                                                                                            sapiens
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Search completed: August 18, 2005, 06:25:06 Job time: 238 secs

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DKFZp434D DKFZp434F DKFZp434D DKFZp434L DKFZp434L

nx24h11.8 ub33a03.r 1M0446L13

1M0145C08 2M0097A22 DKF2p434L 1M0233F03

Pan trogl Arabidops 5009-0-62 1M0016N09 2M0063L17 E012766-0

OM nucleic

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Run

Sequence:

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GSS 16-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                             Mis musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Musi
1 (2019)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                                                                                   AZ763411
1M0558B24R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0558B24 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_llb="Mouse lokb plasmid UGC2M lbrary."
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
        AZ309156
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AL043263
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Insert Length: 10000 Std Error: 0.00
Plate: 0558 row: B column: 24
Seg primer: CACACAGGAAACAGCTATGACC
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC1M0558B24"
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Location/Qualifiers
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AZ823352
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AA876113
AI049374
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BM399863
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AZ803105
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Fax: 801 585 7177
 USA
Rm. 308,
84112, US
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RESULT 1
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LOCUS
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KEYWORDS
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                                                                      August 18, 2005, 06:17:36 ; Search time 1765 Seconds (without alignments) 452.889 Million cell updates/sec
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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/note="T-DNA flanking sequence
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Burget Submission

Direct Submission

Direct Submission

Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Submitted (23-OCT-2003) For the Direct Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Submitted Cremitary, 91075 Evry cedex, FRANCE

Gaston Tremitary For The DNA fragment(s) resulting from plants from INRA (Versailles). The DNA fragment(s) resulting from plants from INRA (Versailles). The DNA fragment or order the Porder the PCR were directly sequenced flanking the insertion. T-DNA to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the derived sequences were removed. Information site are available at graphical display of the insertion site are available at graphical display of the insertion site are available at graphical display of the insertion site are available at program 'Genoplante' (http://www.genoplante.com and program 'Genoplante' (http://www.genoplante.com and Location/Qualifiers
                              was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 was blunt location with T4 DNA polymerase and T4 polymerase and T4 inches with the mass. Adaptor oligomucleotides were polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The ligated bnA was purified and size-selected for a 9.5 to adaptored bnA was purified and size-selected for a 9.5 to electrophoresis. Vector DNA was prepared from a derivative of pwn92 (gi|4732114|gp|AR129072.1), a copy-number of pwn92 (gi|4732114|gp|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated inthe adaptors complementary to the insert adaptors and with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XIJO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AJS89126 17-JAN-2004 AAS89126 SS 15-JAN-2004 Arabidopsis thaliana T-DNA flanking sequence, left border, clone
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GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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T-DNA integration into the Arabidopsis genome depends on sequences
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/mol_type="genomic DNA"
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/clone="545A02"
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EMBO Rep. 3 (12), 1152-1157 (2002)
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Balzergue, S.
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musculus CJ/DL/OU NUMBLE DNA RESOURCE LICHEL LICENTIFICATION CHARLES AND RESOURCE ASSOURCE S/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/). The DNA orgonization of the organization of the searced bna was blunt ends in high molar excess. The ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to adaptored DNA was preparative agarose gel 10.5 kb range using preparative agarose gel crophoresis. Vector DNA was prepared from a derivative electrophoresis. Vector DNA was prepared from a derivative of pWN42 (gil473214) [gb/Hz129072.1], a copy-number of pWn42 (gil473214) [gb/Hz129072.1], a copy-number of pWn42 (gil473214) [gb/Hz129072.1], a copy-number of pwn41 (gil473214) [gb/Hz129072.1], a copy-num
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Palam, M., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                               Gaps
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0
    Length 17;
                                                                                    Indels
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Score 9.8; DB 9; I
pred. No. 3.8e+06;
2; Mismatches 2;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Flate: 0314 row: E column: 21
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/organism="Mus musculus"
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/clone="UUGC1M0314E21"
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                      46.7%;
milarity 69.2%;
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Unpublished (2000)
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EST (Duesterhoeft, et al.)
Unpublished (1999)
Contact: MIPS
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1 GTACCGGTCCGGAATT 16
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
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E | Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unipublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                           20 bp DNA linear GSS 13-DEC-2000 1M0405C21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0405C21 F, genomic survey sequence.
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chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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69.2%; Pred. No. 3.8e+06;
tive 2; Mismatches 2; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0405 row: C column: 21
Seq primer: CGTTGTAAAACGACGCCAGT
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/mol type="genomic DNA"
/strain="C57BL/6J"
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4 TGCCTGATGGGAA 16
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Best Local Similarity 69.2
Matches 9; Conservative
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16 bp mRNA linear EST 06-JUL-2004
DKF2p434B1612 r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434B1612, mRNA sequence.
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chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 18)
Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
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Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
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                                                                                                     Score 9.8; DB 8; Length 20; Pred. No. 3.9e+06; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="testis"
dev stage="adult"
/lab_host="DH108"
/clone_lib="434 (synonym: htes3)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp434B1612"
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Unpublished (1999)
Contact: MIPS
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Caramania, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Rammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rally, M., Rose, M., Mahmoud, M., Meenen, E., Pedersen, T., Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Thngey, A., von Diasmid inserte to Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University Of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ466725 19 bp DNA linear GSS 04-OCT-2000 1M0277C09R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0277C09 R, genomic survey sequence.
                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 19)
Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
BST (Blum, et al.)
Unpublished (1999)
Contact: MIPS
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7. crganism="Homo sapiens"

/mol type="mRNA"

/db_xref="taxon:9666"

/clone="DRFXP4943C1822"

/tissue type="testis"

/dev_stage="adult"

/dev_stage="adult"

/clone lib="434 (synonym: htes3)"

/note="vector: pSport1; Site_1: Sall"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0277 row: C column: 09
Seq primer: CACACAGGAAACAGCTATGACC
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/db_xref="taxon:10090"
/clone="UUGC1M0277C09"
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High quality sequence stop: 19.
Location/Qualifiers
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Mus musculus
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Homo sapiens (human)
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18 bp mRNA linear BST 06-JUL-2004
DKF2p434B1823_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434B1823, mRNA sequence.
AL043072
AL043072.1 GI:49682480
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Bukaryota, Metazoa, Chordata, Craniata; Vertebrata; Buteleostomi;
Bukaryota, Metazoa, Chordata; Catarrhini; Hominidae; Homo.
I (bases I to 18)
Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Blum, et al.)
Contact: MIPS
MIPS
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/note="Vector: pSport1; Site_1: Not1; Site_2: Sall"
                                                                                                    1..18
// organism="Homo sapiens"
// organism="Homo sapiens"
// organism="Homo sapiens"
// clone="Dyre2p434G1212"
// tissue type="testis"
// dev_stage="adult"
// lab host="P0H108"
// clone lib="434 (synonym: htes3)"
// note="Vector: pSport1; Site_1: Sall"
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Location/Qualifiers
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                                           Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          Length 18;
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Similarity 56.2%; Pred. No. 4.8e+06;
9; Conservative 3; Mismatches 4;
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AL042746.1 GI:49682451
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Matches 9; Conserv
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AL042746
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AL043072
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AL039677.1 GI:49682316
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MIPS
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                                                                                                                               Laboratory Mouse DNR Resources (documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwMp42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ858446 19 bp DNA linear GSS 21-FEB-2001 2M0163D08R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0163D08 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Ros
                             /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Insert Length: 10000 Std Brzor: 0.(
Plate: 0163 row: D column: 08
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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2 CTGTGGGGAACCTACT 17
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Fax: 801 585 7177
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Best Local
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g 8

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(http://www.jax.org/resources (http://www.jax.org/resources documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWn2 (gil 4772114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_llb="Mouse_lokb plasmid UGCIM library"
/note="Vector: PWD47" purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/note="Vector: pSport1; Site_1: Not1; Site_2: Sall"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 56.2%; Pred. No. 4.8e+06; 9; Conservative 3; Mismatches 4; Indels
                                                                                                                                            Laboratory Mouse DNA Resource
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/db_xref="taxon:9606"
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/dev_stage="adult"
/lab_host="DH10B"
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Unpublished (1999)
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Gaps

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AZ794033

21 bp DNA linear GSS 16-FEB-2001
2M0047D12R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0047D12 R, genomic survey sequence.
AZ794033
AZ794033.1 GI:12939589
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Mesen, E., Pedersen, T.,
Islam, M., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Islam, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Nouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                      AL045408 20 bp mRNA linear EST 06-JUL-2004 DKFZp434E105 rl 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E105, mRNA sequence.
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1 (bases 1 to 20)

Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
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/note="Wector: pSport1; Site_1: Not1; Site_2: Sal1"
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Location/Qualifiers
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Best Local Similarity 56.2%; Pred. No. 4.9e+06;
Matches 9; Conservative 3; Mismatches 4; Indels
                           Length 20;
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                           45.7%; Score 9.6; DB 1;
56.2%; Pred. No. 4.9e+06;
tive 3; Mismatches 4;
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/mol_type="mRNA"
/db xref="taxon:9606"
/clone="DKFZp434E165"
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/dev stage="adult"
/lab_host="DH10B"
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EST (Duesterhoeft, et al.)
Unpublished (1999)
Contact: MIPS
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DKFZp444P1923 rl 434 (synonym: htes3) Homo sapiens cDNA clone
AL043349
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1. (bases 1 to 20)

                                                                                20 bp mRNA linear EST 06-JUL-2004
DKFZp43402323 r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp43402323, mRNA sequence.
                                                                                                                                                                                                                                                                                                         Homo sapiens
Buckaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 20)
Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S. BST (Blum, et al.)
Unpublished (1999)
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/dev_stage="adult"
/dev_stage="adult"
/lab_host="bulos"
/clone lib="444 (synonym: htes3)"
/note="vector: pSport1; Site_1: Not1; Site_2: Sall"
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Location/Qualifiers
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Location/Qualifiers
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Best Local Similarity 56.2%; Pred. No. 4.9e+06;
Matches 9; Conservative 3; Mismatches 4; Indels
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/db_xref="taxon:9606"
/clone="DKFZp434P1923"
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Homo sapiens
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Gaps

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University of Utah Genome Center

University of Utah Genome Center

Em. 101.58 5 200.

Fax: 801 585 7177

Email: ddinmagenetics. utah. edu

Insert Length: 10000 Std Error: 0.00

Plate: 0047 row: D column: 12

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Anol. Pape="genomic DNA"

Anol. Pape="genomic D
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Query Match
45.7%; Score 9.6; DB 8; Length 21;
Best Local Similarity 62.5%; Pred. No. 4.9e+06;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps

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3 GCCUGUCGGGAACUGG 18 | | : | | | | | : | | 4 GGCTGGAGGAGGTGG 19

8 8

Search completed: August 18, 2005, 07:56:22 Job time : 1773 secs

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Sequence 37093, A Sequence 195, App Sequence 1, Appli Sequence 126, App

Sequence

Sequence 778,

Sequence

Run on:

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APPLICANT: JOCKERS, Ralf
APPLICANT: COUTURIER, Cyril
APPLICANT: CUTHARANN, Eugen
TITLE OF INVENTION: Disproclectides Which inhibit Expression of the OB-RGRP Protein
TITLE OF INVENTION: Detween Proteins Of the OB-RGRP Family And The Leptin Receptor
TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
TITLE REPERENCE: FRAV2003/0005 US NP
FILE REPERENCE: FRAV2003/0005 US NP
CURRENT APPLICATION NUMBER: US/10/774,721
CURRENT FILING DATE: 2004-02-09
PRIOR PRIOR APPLICATION NUMBER: 60/461,005
PRIOR PRILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-02-10
1 US-10-776-934-541

1 US-10-776-934-542

1 US-10-756-934-542

1 US-10-756-934-542

1 US-10-751-736-36589

0 US-10-751-736-36589

2 US-10-736-980-195

2 US-10-736-980-195

2 US-10-736-980-126

1 US-10-739-788-126

2 US-10-739-788-126

1 US-10-739-788-104

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1 US-10-738-788-106

1 US-10-738-788-108

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1 US-10-738-788-108

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1 US-10-847-948-3427

1 US-10-847-948-3427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 37, Application US/10774721; Publication No. US20050009042A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin version 3.1
SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                   RESULT 1
US-10-774-721-37
                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                              August 18, 2005, 06:53:53 ; Search time 1790 Seconds (without alignments) 76.221 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pu
                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-10-774-721-31
US-10-774-721-31
US-10-451-805-6
US-10-776-934-100
US-10-776-934-100
US-10-776-934-540
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                                                                                                                                                                                                                                                                                             7316285 segs, 3248459403 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                  nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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87.6
63.8
61.9
61.0
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18.4
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Database

Sequence 823, App Sequence 823, App Sequence 27, Appl Sequence 809, App

Seguence 822

Sequence

21;

Length

Score 21; DB 21; Pred. No. 1.3;

100.0%;

Query Match Best Local Similarity

281, App 100, App 540, App

Sequence Sequence Sequence Sequence Sequence Sequence Sequence 1

1264597

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Result

; OTHER INFORMATION: Artificial US-10-774-721-37

Sequence 36, Appl Sequence 62, Appl Sequence 104, Appl Sequence 120, Appl Sequence 279, Appl Sequence 279, Appl Sequence 1359, Appl Sequence 1360, Appl Sequence 1361, Appl Sequence 1361, Appl Sequence 161, Appl Sequence 161, Appl Sequence 161, Appl Sequence 17, Appl Sequence 17, Appl Sequence 188, Appl Sequence 17, Appl Sequence 188, Appl Sequence 188, Appl Sequence 188, Appl Sequence 37, Appl Sequence 188, Appl Sequence 1128, Appl Sequence 1128, Appl Sequence 37, Appl Sequence 37, Appl

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APPLICANT: Wyeth
APPLICANT: Bowman, Michael
APPLICANT: Bowman, Michael
APPLICANT: Chen, Heng
APPLICANT: Chen, Heng
APPLICANT: Chen, Heng
APPLICANT: Williams, Cara
APPLICANT: Liu, Wei
APPLICANT: Minkler, Aaron
APPLICANT: Minkler, Aaron
APPLICANT: Williams, ComPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING ASTHMA OR
ITILE OF INVENTION: OTHER ALLERGIC OR INFLAMMATORY DISEASES
FILE REFERENCE: AM101023-2
CURRENT APPLICATION WUMBER: US/10/792,280
CURRENT FILING DATE: 2004-03-04
NUMBER OF SEQ ID NOS: 1535
SOFTWARE: Patentin version 3.2
SEQ ID NO 281
LENGTH: 21
                                                                                                                                                                                                                                                                         GENERAL INFORMATION

GODPELL, Andreas

APPLICANT: Adopell, Andreas

APPLICANT: Adopell, Andreas

APPLICANT: Adopell, Andreas

APPLICANT: Adopell, Heidi

TITLE OF INVENTION: Use of Intermediate-Conductance

TITLE OF INVENTION: Decasium Channels and Modulators For Diagnosing and

TITLE OF INVENTION: Treating Diseases Having Disturbed Keratinocyte Activity

TITLE OF INVENTION: Treating Diseases Having Disturbed Keratinocyte Activity

TITLE OF INVENTION: Treating Diseases Having Disturbed Keratinocyte Activity

TITLE OF INVENTION: Treating Diseases Having Disturbed Keratinocyte Activity

TITLE OF INVENTION: Treating Diseases Having Disturbed Keratinocyte Activity

FURRENT FILING DATE: 2003-06-25

PRIOR FILING DATE: 2001-12-27

PRIOR PILING DATE: 2000-12-28

PRIOR PILING DATE: 2000-12-28

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6

LENGTH: 16
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                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.8%; Score 13.4; DB 20;
Best Local Similarity 80.0%; Pred. No. 8.5e+03;
Matches 12; Conservative 2; Mismatches 1;
1 Similarity 75.0%; Pred. No. 26; 15; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 281, Application US/10792280; Publication No. US20040234517A1; GENERAL INFORMATION:
                                                                                                                                                                                                              Sequence 6, Application US/10451805; Publication No. US20040248099A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: RNA
; ORGANISM: RNAi-antisense strand
US-10-792-280-281
                                                                                               61.9%;
66.7%;
                                                                    2 UGCCUGUCGGGAACUGGCTT
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; ORGANISM: Mus musculus
US-10-451-805-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
           Best Local Similarity
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US-10-792-280-281
                                                                                                                                                                                   RESULT 4
US-10-451-805-6
                                  Matches
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Sequence 31, Application No. US2005009042A1

PUBLICATION.

PUBLICATION.

APPLICANT: OCCURRIER, Ralf

APPLICANT: OCCURRIER, Cyril

APPLICANT: UNIVENTION: And Method For Detecting Compounds Which Modify The Interaction

TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction

TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor

TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor

TITLE OF INVENTION NUMBER: US/10/774,721

CURRENT APPLICATION NUMBER: 0301543

PRIOR FILING DATE: 2003-02-10

NUMBER PRIOR FILING DATE: 2003-02-10

NUMBER PRIOR FILING DATE: 2003-02-10

NUMBER PRIOR FILING DATE: 2003-02-10

SOFTWARE: Patentin Version 3.1

SEQ ID NO 31

LENGTH: 20
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Pred. No. 13;
4; Mismatches 0; Indels
                      0; Indels
                         0; Mismatches
                                                                    1 GUGCCUGUCGGGAACUGGCTT 21
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ORGANISM: Artificial Sequence
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Best Local Similarity 78.9%;
Matches 15; Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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                               21; Conservative
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US-10-774-721-38/c
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APPLICANT: WESTERGAARD, MAJKEN
APPLICANT: WESTERGAARD, MAJKEN
APPLICANT: WESTERGAARD, MAJKEN
APPLICANT: WISSENBAARD, MAGNET
TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
FILE REFERENCE: 58610(71432)
CURRENT APPLICATION NUMBER: 00/446,372
PRIOR PELING DATE: 2003-02-10
PRIOR PELING DATE: 2003-11-19
NUMBER OF SEQ ID NOS: 741
SOFTWARE: PAGNETIN OF SEQ ID NOS: 741
LENGTHARE: PAGNETIN OF SEQ ID NOS: 741
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                                                                                                                                                                                                                                                                                  Length 16;
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Best Local Similarity 68.8%; Pred. No. 1.7e+04;
Matches 11; Conservative 3; Mismatches 2;
                                                                                                                                                                                                                                                                             61.0%; Score 12.8; DB 21;
68.8%; Pred. No. 1.7e+04;
tive 3; Mismatches 2;
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LOCATION: (1)..(4)
OTHER INFORMATION: beta-D-oxy-LNA modified base
                                                                          LOCATION: (13)..(15)
OTHER INFORMATION: beta-D-oxy-LNA modified base
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (13)..(1\overline{5})
OTHER INFORMATION: beta-D-oxy-LNA modified base
OTHER INFORMATION: beta-D-oxy-LNA modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (1)._(16)
OTHER INFORMATION: phosphorthioate linkage
                                                                                                                                                  NAME/KEY: misc_feature

// LOCATION: (1)..(16)

// OTHER INFORMATION: phosphorthioate linkage

US-10-776-934-540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 541, Application US/10776934
Publication No. US20050014712A1
GENERAL INFORMATION:
APPLICANT: HANSEN, BO
APPLICANT: THRUE, CHARLOTTE ALBAEK
APPLICANT: WESTERGAARD, MAJKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/10776934
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16 CTGTGGGGGACTGGCT 1
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Best Local Similarity 68.0.
Best Local 11, Conservative
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                          FEATURE:
NAME/KEY: modified_base
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US-10-776-934-542/c
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| Sequence 540, Application No. US20050014712A1
| Publication No. US20050014712A1
| GENERAL INFORMATION:
| APPLICANT: HANSEN, BO
| APPLICANT: WISSENGARD, MAJKEN
| APPLICANT: WISSENBACH, MAJKEN
| APPLICANT: WISSENBACH, MARGIT
| FILE REFERENCE: 58610(71432)
| CURRENT FILING DATE: 2004-02-10
| PRIOR APPLICATION NUMBER: 60/446,372
| PRIOR APPLICATION NUMBER: 60/446,372
| PRIOR APLICATION NUMBER: 60/523,591
| PRIOR FILING DATE: 2003-11-19
| NUMBER OF SEQ ID NOS: 741
| SOFTWARE: PatentIn version 3.2
| SEQ ID NO 540
                                                                                                                                                                                                                                                                                                  APPLICANT: HANSEN, BO

APPLICANT: HANSEN, BO

APPLICANT: HANSEN, CHARCOTTE ALBAEK
APPLICANT: WESTERGARD, MAJKEN
APPLICANT: WESTERGARD, MAJKEN
APPLICANT: WESTERRANG, KAMILLE DUMONG
APPLICANT: WISSENBACH, WARGIT
TILLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
FILE REPERENCE: 586.10 (714.3.2)
CURRENT PILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: 60/46,372
PRIOR APPLICATION NUMBER: 60/523,591
PRIOR PEPLICATION NUMBER: 60/523,591
PRIOR PEPLING DATE: 2003-11-19
NUMBER OF SEQ ID NOS: 741
SSQ ID NO 100
LENGTH: 16
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  Gaps
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     5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Synthetic oligonucleotide
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  2; Mismatches
                                                                                                                                                                                                                             Sequence 100, Application US/10776934 Publication No. US20050014712A1
                                                                               1 GUGGCUCUCUGGCACUUGCUU 21
                                                  1 GUGCCUGUCGGGAACUGGCTT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial sequence
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ORGANISM: Artificial sequence
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16 CTGTGGGGACTGGCT 1
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  14; Conservative
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LOCATION: (1)..(4)
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                                                                                                                                                                                                                                                       Publication No. US2
GENERAL INFORMATION
                                                                                                                                                                             RESULT 6
US-10-776-934-100/c
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APPLICANT: Martinez, Robert
APPLICANT: Martinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM100927 (031896-002000)
CURRENT PALLICATION NUMBER: US/10/751,736
CURRENT FILING DATE: 2003-01-06
PRIOR PRICK APPLICATION NUMBER: US Provisional Application 60/438,000
NUMBER OF SEQ ID NOS: 54873
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wheth
APPLICANT: Martinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
TITLE OF INVENTION: COMPOSITIONS TITLE OF INVENTION: COMPOSITION COMPOSITION COURTER AMIOO927 (031896-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
CURRENT FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
SOFTWARE PATENT OF VERSION 3.2
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61.0%; Score 12.8; DB 20;
Best Local Similarity 68.8%; Pred. No. 1.7e+04;
Matches 11; Conservative 3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 61.0%; Score 12.8; DB 20; Best Local Similarity 68.8%; Pred. No. 1.7e+04; Matches 11; Conservative 3; Mismatches 2;
                                                                                          Query Match 61.0%; Score 12.8; DB 21;
Best Local Similarity 68.8%; Pred. No. 1.7e+04;
Matches 11; Conservative 3; Mismatches 2;
             , OTHER INFORMATION: phosphorthicate linkage US-10-776-934-543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 37093, Application US/10751736; Publication No. US20040265230A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           Sequence 36589, Application US/10751736; Publication No. US20040265230A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 UGUCGGGAACUGGCTT 21
                                                                                                                                                                                                   5 CUGUCGGGAACUGGCT 20
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16 TGTCGTGAAGTGGCTT 1
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CRGANISM: homo sapiens
US-10-751-736-37093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: homo sapiens
US-10-751-736-36589
; LOCATION: (1)..(16)
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US-10-751-736-37093/c
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US-10-751-736-36589/c
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LENGTH: 21
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LENGTH: 21
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## Sequence 543, Application US/10776934

## Sequence 543, Application US US2055014712A1

## Sequence 543, Application No. US2055014712A1

## Septicant: Hornarion:

## APPLICANT: HANEE, CHARLOTTE ALBAEK

## APPLICANT: PETERSEN, MAJKEN

## APPLICANT: US1071422)

## CURRENT PILING DATE: 2004-02-10

## PRIOR APPLICATION NUMBER: 60/446,372

## PRIOR APPLICATION NUMBER: 60/523,591

## PRIOR PILING DATE: 2003-11-19

## NUMBER OF SEQ ID NOS: 741

## SEQ ID NO 543

## LENGTH: 16

## LENGTH: 16

## LENGTH: 16
                             APPLICANT: HANSEN, BO
APPLICANT: THRUE, CHARLOTTE ALBAEK
APPLICANT: THRUE, CHARLOTTE ALBAEK
APPLICANT: WESTERGAARD, MAJKEN
APPLICANT: WESTERGAARD, MAJKEN
APPLICANT: WISSENBACH, MARGIT
TILE, OF INVENTION: OLICAMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
FILE REPERENCE: 566.0 (71432)
CURRENT APPLICATION NUMBER: US/10/776,934
CURRENT APPLICATION NUMBER: 60/446,372
PRIOR APPLICATION NUMBER: 60/446,372
PRIOR APPLICATION NUMBER: 60/523,591
PRIOR FILING DATE: 2003-01-09
PRIOR FILING DATE: 2003-11-19
NUMBER OF SEQ ID NOS: 741
SEQ ID NO 542
LENGTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)..(4) OTHER INFORMATION: beta-D-oxy-LNA modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Synthetic oligonucleotide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetic oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
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LOCATION: (5). (13)
OTHER INFORMATION: phosphorthioate linkage
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16 CTGTGGGGGACTGGCT 1
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Best Local Similarity 68.84
Matches 11; Conservative
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US-10-776-934-543/c
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APPLICANT: J1, Tai
APPLICANT: J1, Tai
APPLICANT: J1, Inha
APPLICANT: J1, Inha
APPLICANT: J1, Inha
TITLE OF INVENTION: GENES AND AGENTS TO REGULATE FOLLICULAR DEVELOPMENT, OVULATION
TITLE OF INVENTION: CYCLE AND STERIODOGENESIS
FILE REPERENCE: 050229-043 48/10/736,892
CURRENT APPLICATION NUMBER: 06/10/736,892
PRIOR PELICATION NUMBER: 60/437,729
PRIOR PILLING DATE: 2003-01-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VERSION 3.3
SEG ID NO 1
LENGTH: 21
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                                                                                                                       Sequence 195, 0000-195

Sequence 195, Mpglication US/10349780A

Publication No. US20040146866A1

GENERAL INFORMATION:

APPLICANT: FW. GUOJIANG

TITLE OF INVENTION:

CURRENT APPLICATION UNMBER: US/10/349, 780A

CURRENT FILING DATE: 2003-01-24

NUMBER OF SEQ ID NOS: 284

SOFTWARE: Patentin version 3.2

SEQ ID NO 195

LENGTH: 21
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GOTHER INFORMATION: Chemically synthesized
US-10-736-892-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-09-800-631-126/c.
; Sequence 126, Application US/09800631
; Partent No. US20020082228A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10736892
Publication No. US20050148505A1
GENERAL INFORMATION:
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GCCTGTGGGTAACTGG 16
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6 UGUCGGGAACUGGCTT 21
                     :|:|| ||| :|||||
17 TGTCGTGAAGTGGCTT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 61.0
Best Local Similarity 68.8
Matches 11; Conservative
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Best Local Similarity
Matches 12; Conserval
                                                                                                    RESULT 13
US-10-349-780A-195
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## APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST EXPR
FITLE REFERENCE: 1284-0544
CURRENT APPLICATION NUMBER: US/09/0657,346
FRIOR PLING DATE: 2001-03-07
FRIOR PLING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 175
SEQ ID NO 126
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Antisense Oligonucleotide
FRATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-0800-631-126

Query Match
Best Local Similarity 78.6%; Pred: No. 2.76+04;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy
7 GUCGGAACUGGCT 20
| | | | | | | | | | | | |
Db 16 GTCGGGAACUGGCT 3
Search completed: August 18, 2005, 08:58:46
JOB time: 1797 secs
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                August 18, 2005, 06:53:53; Search time 1790 Seconds (without alignments) 76.221 Million cell updates/sec
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11. (cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*

12. (cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*

13. (cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*

14. (cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*

15. (cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*

15. (cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*

16. (cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*

17. (cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*

18. (cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*

18. (cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*

18. (cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*

18. (cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*

19. (cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*

10. (cgn2_6/ptodata/2/pubpna/USO9_PUBCOM
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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I US-10-774-721-31

I US-10-774-721-31

I US-10-74-721-31

I US-10-731-805-6

I US-10-349-780A-195

US-09-986-632-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7316285 seqs, 3248459403 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 21
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Sequence 31, Appl Sequence 6, Appli Sequence 280, App Sequence 195, App Sequence 27, Appl

920221

100.0 90.5 85.7 63.8 61.9 61.0

21 19 18 13.4 13.4 12.8

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Sequence 38, App.

Sequence

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Sequence 38, Application US/10774721

Sequence 38, Application US/10774721

Publication No. US2005000942A1

Sequence 38, Application No. US2005000942A1

Sequence 38, Application No. US2005000942A1

SEQUENCE 38, APPLICANT: OCCERSE, Ralf

APPLICANT: OCCERSE, Cyril

APPLICANT: OLIGNOCIDE CONTROL OF THE OF TH
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542, App
543, App
50, Appl
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1360, Ap
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14876, A
25591, A
39050, A
39053, A
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540, App
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26, Appl
97, Appl
1288, Ap
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Sequence 3427, A
Sequence 46, Apl
Sequence 189, Ap
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US-10-189-359-16

US-10-688-706-1896

US-10-688-706-1896

US-10-499-544-15

US-10-173-240-36

US-10-173-240-36

US-10-671-395-455

US-10-671-395-455

US-10-671-395-455

US-10-671-395-455

US-10-671-395-537

US-10-671-395-537

US-10-71-36-30050

US-10-751-736-1876

US-10-751-736-1876

US-10-776-934-541

US-10-776-934
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Pred. No. 1.2;
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US-10-251-117-46
US-10-251-117-189
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         Query Match
Best Local Similarity
      TYPE: DNA
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GENERAL IN COMENT.

GENERAL IN COMENT.

APPLICANT: Worth

APPLICANT: Bowman, Michael

APPLICANT: Chen, Heng

APPLICANT: Chen, Heng

APPLICANT: Williams, Cara

APPLICANT: Minkler, Aaron

APPLICANT: Liu, Wei

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING ASTHMA OR

TITLE OF INVENTION: OTHER ALLERGIC OR INFLAMMATORY DISEASES

FILE REFERENCE: AM101023-2

CURRENT APPLICATION NUMBER: US/10/792,280

CURRENT PILING DATE: 2004-03-04

NUMBER OF SEQ ID NOS: 1535

SOGTWARE: Patentin version 3.2

SEQ ID NO 280

LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/10451805

Sequence 6, Application US/10451805

publication No. US2004024809341

GENERAL INFORMATION:
APPLICANT: Goppelt, Andreas
APPLICANT: Alzheimer, Christian
APPLICANT: Ascall, Heidi
ITILE OF INVENTION: Decassium Channels and Modulators For Diagnosing and
ITILE OF INVENTION: Treating Diseases Having Disturbed Keratinocyte Activity
FILE REFERENCE: 50125/080001
CURRENT FILING DATE: 2003-06-25
PRIOR APPLICATION NUMBER: DFT/FP01/15317
PRIOR APPLICATION NUMBER: DFT/FP01/15317
PRIOR APPLICATION NUMBER: DE 10065475.4
PRIOR FILING DATE: 2000-12-28
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LEAST AND ACTIVE OF MINIOR ACTIVE O
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Pred. No. 8.3e+03;
2; Mismatches 1; Indels (
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                                               Mismatches
Pred. No. 39;
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US-10-792-280-280
S-10-792-280-280, Application US/10792280
; Publication No. US20040234517A1
; GENERAL INFORMATION:
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CRGANISM: RNAi-sense strand
US-10-792-280-280
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    Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 80.0°
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Best Local Similarity
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Sequence 31, Application US/10774721

Sequence 31, Application No. US20050009042A1

Publication No. US20050009042A1

GENERAL INFORMATION:

APPLICANT: COUTURIER, CYTI

APPLICANT: COUTURIER, CYTI

APPLICANT: UNIVANNI, Eugen

TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction

TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction

TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor

TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor

TITLE OF INVENTION NUMBER: US/10/774,721

CURRENT FILING DATE: 2004-02-09

PRIOR FILING DATE: 2003-04-07

PRIOR FILING DATE: 2003-04-07

PRIOR FILING DATE: 2003-02-10

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 31

LENGTH: 20

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; Sequence 37, Application US/10774721
; Sequence 37, Application US/10774721
; Publication No. US20050009042A1
; CENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: COUTUNIER, CYII

APPLICANT: UNIMANN, Eugen
: ITILE OF INVENTION: Olignocleotides Which inhibit Expression of the OB-RGRP Protein
: ITILE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
: ITILE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
: ITILE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
: ITILE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
: TILE REPERENCE: FRAV2003/0005 US NP
: TILE OF INVENTION NUMBER: 0204-02
: PRIOR APPLICATION NUMBER: 0301543
: PRIOR APPLICATION NUMBER: 0301543
: PRIOR APPLICATION NUMBER: 0301543
: SEQUENCE: PRIVING DATE: 2003-04-07
: RUMBER OF SEQ ID NOS: 47
: SOFTWARE: PatentIn version 3.1
: SEQUENCE: PRIVING DATE: PRIVING DATE: 2003-04-07
: PRIOR APPLICATION NUMBER: 0301543
: SEQUENCE: PRIVING DATE: 2003-04-07
: PRIOR APPLICATION NUMBER: 0301543
: SEQUENCE: PRIVING DATE: 2003-04-07
: PRIVING APPLICATION NUMBER: 0301543
: SEQUENCE: PRIVING DATE: 2003-04-07
: PRIVING APPLICATION NUMBER: 0301543
: SEQUENCE: PRIVING DATE: 2003-04-07
: PRIVING DATE: 200
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Pred. No. 12;
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90.5%; Score 19; DB
Best Local Similarity 89.5%; Pred. No. 12;
Matches 17; Conservative 2; Mismatches
                                               0, Mismatches
                                                                                                                                         1 GCCAGUUCCCGACAGGCACTT 21
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ORGANISM: Artificial Sequence
PEATURE:
COTHER INFORMATION: AS10
US-10-774-721-31
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, OTHER INFORMATION: Artificial
US-10-774-721-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                             21; Conservative
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US-10-774-721-37/C
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US-10-774-721-31
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Patent No. US20020119944A1
GENERAL INFORMATION:
APPLICANT: AGUERA, Michelle
TITLE OF INVENTION: Modulation of Ulip/CRMP activity for the prevention or TITLE OF INVENTION: treatment of myelin disorders
FILE REPERENCE: P069740301/Bas
CURRENT APPLICATION NUMBER: US/09/986,632
CURRENT PILING DATE: 2001-11-09
PRIOR FILING DATE: 2000-11-09
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                         Sequence 195, Application US/10349780A
Publication No. US20040146866A1
GENERAL INFORMATION:
TITLE OF INVENTION: QUANTITATIVE MULTIPLEX DETECTION OF NUCLEIC ACIDS
TITLE REPERENCE: patent1
CURRENT APPLICATION NUMBER: US/10/349, 780A
CURRENT PILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 195
LENGTH: 21
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US-09-986-632-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.0%; Score 12.8; DB 22;
75.0%; Pred. No. 1.6e+04;
tive 2; Mismatches 2;
2; Mismatches
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; Sequence 16, Application US/10189359
; Publication No. US20040039187A1
; GENERAL INFORMATION:
                                      1 GCCAGUUCCCGACAGGCACTT 21
                                                          1 GCAAGUGCCAGAGAGCCACUU 21
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SOFTWARE: PatentIn Ver. 2.1
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; APPLICANT: SANGAR, DAVID V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 75.0°
Matches 12; Conservative
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-10-349-780A-195
                                                                                                                              RESULT 6
US-10-349-780A-195/c
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LENGTH: 19
Matches
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US-10-189-359-16
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Publication No. US20040102412A1

GENERAL INPORMATION:

APPLICANT: Pharmacia Corp.

APPLICANT: Broschat, Kay

TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION

FILE REFERENCE: 01393/1

CURRENT APPLICATION NUMBER: US/10/688,706

CURRENT APPLICATION NUMBER: 60/419,268

PRIOR APPLICATION NUMBER: 60/419,268

PRIOR PILING DATE: 2002-10-17

NUMBER OF SEQ ID NOS: 3071

SOFTWARE: Patentin version 3.2

FENDING 1996
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; Publication No. US20040102412A1
; GENERAL INPORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; TILE REFERENCE: 01393/11
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 12.6; DB 18;
Pred. No. 2.1e+04;
2; Mismatches 4;
APPLICANT: LEMON, STANLEY M.
TITLE OF INVENTION: Chimeric GB Virus B (GBV-B)
FILE REFERENCE: UTSG:258US
CURRENT APPLICATION NUMBER: US/10/189,359
FRIOR APPLICATION NUMBER: .10/189,359
PRIOR APPLICATION NUMBER: .10/189,359
FRIOR FILING DATE: 2002-07-03
NUMBER OF SEQ ID NOS: 16
SEQ ID NOS: 16
SEQ ID NO 16
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: human GPAT antisense US-10-688-706-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCAGTTCCGGGCAAGAACT 19
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68.4%;
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Best Local Similarity 68.44
Matches 13; Conservative
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Best Local Similarity 73.7
Matches 14; Conservative
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RESULT 14

US-10-671-395-382

Sequence 382, Application US/10671395

Sequence 382, Application No. US20040132063A1

Sequence 382, Application No. US20040132063A1

GENERAL INFORMATION:
APPLICANT: PHARMACIA COPP.
APPLICANT: GIEFE, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: APPLICATION NUMBER: US/10/671,395

CURRENT APPLICATION NUMBER: 0/413,549

PRIOR APPLICATION NUMBER: 6/413,549

PRIOR APPLICATION NUMBER: 6/413,549

PRIOR APPLICATION NUMBER: 6/413,549

SEQ ID NOS: 1809

SEQ ID NO 382

LENGTH: 20
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US-10-173-240-70/C
Sequence 70, Application US/10173240
Sequence 70, Application US/10173240
Sequence 70, Splication No. US20030232436A1
DEDICATION NO. US2003023436A1
APPLICANT: Brett P. W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF E2-EPF EXPRESSION
TITLE OF INVENTION: ANTISENSE WS/10/173,240
CURRENT FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 70
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 12.2; DB 17; Length 20;
Pred. No. 3.3e+04;
0; Mismatches 3; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-10-671-395-455
Sequence 455, Application US/10671395
Publication No. US20040132063A1
PUBLICATION:
PAPLICANT: Pharmacia Corp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 GUUCCCGACAGGCACTT 21
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1 GTTCCCATCAGCCACTT 17
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                                                          3 ecchegaccccarcage 19
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Best Local Similarity 70.6
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: H. sapiens
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Sequence 15, Application US/10499544

Sequence 15, Application No. US20050130155A1

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICATION New primers for the detection and identification of bacterial trip. EPIER REFERENCE: P16814USPC

CURRENT APPLICATION NUMBER: US/10/499,544

CURRENT APPLICATION NUMBER: PC7/NO02/00490

PRIOR FILING DATE: 2002-12-19

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2011-12-19

NUMBER OF SEQ ID NOS: 32

SOFTWARE PATENTING DATE: PATENTING DATE
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Sequence 36, Application US/10173240

Publication No. US20030232436A1

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

TITLE OF INVENTION: ANTISENSE MODULATION OF E2-EPF EXPRESSION

TITLE OF INVENTION: ANTISENSE WS/10/173,240

CURRENT FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 80

LENGTH: 20
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                                                                                                                                                                                                                                                                     Length 20;
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                           Query Match
60.0%; Score 12.6; DB 19;
Best Local Similarity 73.7%; Pred. No. 2.1e+04;
Matches 14; Conservative 1; Mismatches 4;
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                                                                                                                                                                         , OTHER INFORMATION: human GFAT antisense US-10-688-706-2734
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SOFTWARE: Patentin version 3.2
SEQ ID NO 2734
LENGTH: 20
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Best Local Similarity
Matches 14; Conserv
                                                                                                 TYPE: DNA ORGANISM: artificial
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US-10-173-240-36
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LENGTH: 18
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## APPLICANT: Gierse, James K

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

TITLE OF INVENTION: EXPRESSION

FILE REPERENCE: 1179/1/US

CURRENT APPLICATION NUMBER: US/10/671,395

CURRENT PILING DATE: 2003-09-25

PRIOR FILING DATE: 2002-09-25

NUMBER OF SEQ ID NOS: 1809

SOFTWARE: Patentin version 3.2

LENGTH: 20

TYPE: DNA

ORGANISM: artificial

FRANCE: PROSMATION: Human PGE2 antisense

US-10-671-395-455
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3 GTTCCCATCAGCCACTT 19
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1M0361H08 1M0016N09 1M0047M08

AZ309156 AZ386570 AZ043263 AL043263 AZ048903 AZ168903 AZ168903

2M0038F15

E012766-0 1M0233F03 1M0434016 1M0546E01

DKFZp434F DKFZp434D DKFZp434L DKFZp434M

DKFZp434D

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Sequence:

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AZ486389
1M0314E21F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0314E21 F, genomic survey sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
1 (Base 1 to 19)
Bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Son, M., Meight, D., Weise, R., Tingey, A., von
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone_lib="Mouse_lokb_plasmid UUGCNM library."
/note="Vector: PWDATN; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
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Seg primer: CGTTGTAAAACGACGCCCAGT
Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0314E21"
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AZ318416
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AL043298
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AL045408 DKFZp434E
AZ393800 1M0157H04
AJ589126 Arabidops
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AL039794
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AL039409
BX315383
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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gb_est2:;
gb_htc:;
gb_est4:;
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seg length: 21
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Minimum DB Maximum DB

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Searched:

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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerase of polymerase and T6 polymerase preparative agarche gel of 5 to adaptoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored weeter DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus (bordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Lo 19)

E 1 (Dases 1 to 19)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Rolam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T., Rolam,H., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von Muse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
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Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Insert Length: 10000 Std Error: 0.00
Plate: 0558 row: B column: 24
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0558B24"
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Fax: 801 585 7177
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 BNA polymerase and T4 polymerase and T6 polymerase and T7 polymerase polymerase polymerase polymerase polymerase polymerase with preparative agarose gel polymerase vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AR12972.1), a copy-number of pwD42 (gi|4732114|gb|AR12972.1), a copy-number with adaptors complementary to the insert adaptors and with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored wector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol Lype="mRNA"
/mol Lype="mRNA"
/db xref="teaxon:9606"
/db xref="teaxon:9606"
/clone="DyPe="teatis"
/dev stage="adult"
/lab_lost="DH10B"
/clone lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: Sall"
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Location/Qualifiers
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                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
Desterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
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dev stage="adult"
/lab_host="bH108"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sal1"
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Insert Length: 10000 Std Error: 0.00
Plate: 0157 row: H column: 04
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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High quality sequence stop: 21.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="DKFZp434E105"
                                                                                                                                                                                                                                                               Wiemann, S.
BST (Duesterhoeft, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
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AL045408
AL045408.1 GI:49682595
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AZ393800.1 GI:10508872
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                                                                                      Homo sapiens (human)
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Pax: 801 585 7177
                                                                                                                       Homo sapiens
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinae. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwM92 (gilfa732114 gpl AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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T_DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from the Jackson
                                                                                                                                                                                                                                 /sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                                                              /clone_lib="Mouse 10kb plasmid UUGCiM library"
horte="Vector: PWNsZarv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jack
Laboratory Mouse DNA Resource
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47.6%; Score 10; DB 8; Length 21;
Best Local Similarity 61.1%; Pred. No. 3e+06;
Matches 11; Conservative 2; Mismatches 5; Indels
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GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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EMBO Rep. 3 (12), 1152-1157 (2002)
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                   /db_xref="taxon:10090"
/clone="UUGC1M0157H04"
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was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of puncible derivative of plasmid R1. The vector was ligated inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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DKFZp434G1212_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKRZp434G1212, mRNA sequence.
ALO39892.1 GI:49682352
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DKFZp44B1612 r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434B1612, mRNA sequence.
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1 (bases 1 to 16)
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="DkF2p434B1612"
/tissue_type="test1s"
/dev_stage="adult"
/lab_host==Bh1108"
/clone lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: Sall"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                             h similarity 69.2%; Pred. No. 3.7e+06; Predings 9; Conservative 2; Mismatches 2; Indels
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EST (Duesterhoeft, et al.)
Unpublished (1999)
Contact: MIPS
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16 AATTCCGGACCGGTAC 1
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17 CAGTTACCAACAG 5
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AL039794/c
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Unpublished (2000)
Conteact: Robert B. Weiss
Conteact: Robert B. Weiss
Conteact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., Cur
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Rm. 308, Biomedical Polymers Research 
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Eukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
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                                                      Length 17;
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Similarity 69.2%; Pred. No. 3.7e+06;
9; Conservative 2; Mismatches 2;
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/note="T-DNA flanking sequence
left border"
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/mol type="genomic DNA"
/grain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC1M0405C21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 20.
Location/Qualifiers
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AZS93689.1 GI:11715879
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ENGANCE ENCACE STATES OF CRANIAGES, Vertebrata; Enteleostomi; Musmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

3. 1 (bases 1 to 19)

3. Islam, Hamil, C., Rambor, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarce, S., Nahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Nose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Diasmid inserts

All Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                  ALU42746
DKFZp434C1822 r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434C1822, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A2858446 19 bp DNA linear GSS 21-FBB-2001 2M0163D08R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0163D08 R, genomic survey sequence.
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1. to 19)

Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S. EST (Blum, et al.)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol type="mRNA"
/db xref="taxon:9666"
/db xref="taxon:9666"
/clone="DkF2434Cl822"
/tissue type="restis"
/dev stage="adult"
/dev stage="bh108"
/clone lbs="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: Sall"
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Location/Qualifiers
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llarity 62.5%; Pred. No. 4.7e+06;
Conservative 2; Mismatches 4;
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Insert Length: 10000 Std Error: 0.00
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  AATTCCGGACCGGTAC 3
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Homo sapiens
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Fax: 801 585 7177
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hes 10; Conserv
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AUTHORS
TITLE
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DKF2p434B1823 r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKF2p434B1823, mRNA sequence.
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                                                Eukaryorania, Euteazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 18)

Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and Wiemann, S.

EST (Duesterhoeft, et al.)

Unpublished (1999)

Ontact: MIPS

MIPS
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 18)
11 (bases 1 to 18)
12 (blum, Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Blum, et al.)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                          /dev stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sal1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sal1"
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Location/Qualifiers
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Location/Qualifiers
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62.5%; Pred. No. 4.7e+06;
iive 2; Mismatches 4;
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|ab_host="DH10B"
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AG204980 20 bp DNA linear GSS 06-MAR-2004
Pan troglodytes DNA, clone: RP43-090P12.TJ, genomic survey
                                                                                                                                                                                                                                                                                        20 bp mRNA linear EST 06-JUL-2004 DKFZ0434P1923 r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZ043449 AL043349
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Blum, et al.) Unpublished (1999)
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Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
                                                                                                                Gaps
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Location/Qualifiers
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                                                                        Length 20;
                                                                                                                  4; Indels
                                                                      Query Match
Best Local Similarity 62.5%; Pred. No. 4.7e+06;
Matches 10; Conservative 2; Mismatches 4;
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Pan troglodytes
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AG204980.1 GI:45237155
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Homo sapiens
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                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarcse gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XLIO-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 bp mRNA linear BST 06-JUL-2004 DKFZp43402323 rl 434 (synonym: htes3) Homo sapiens cDNA clone AL063317 mRNA sequence.
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Homo sapiens
Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummania; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
Bummania; Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
BST (Blum, et al.)
Unpublished (1999)
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Location/Qualifiers
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Location/Qualifiers

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TITLE Direct Submission

JOURNAL Submitseion

JOURNAL Submitted (107-JAN4-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yusnong-gu, Daedleon 305-333, Korea

(E-mail:redetone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-409)

Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.

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R.Site 1: EcoRI

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AR075066 Sequence
EL5884 Oligonucleo
M81174 Zamia ofton
M8205 Zamia ofton
AR176696 Sequence
BD560047 Hybridiza
AR111342 Sequence
BD25242 Pyrazolo (
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AX292210 Sequence
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135557 Sequence
13554 Sequence
AX59445 Sequence
AX696470 Sequence
AX791415 Sequence
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Patent: WO 2004072293-A 38 26-AUG-2004;
Patent: WO 2004072293-A 38 26-AUG-2004;
Patent: WO 2004072293-A 38 26-AUG-2004;
RECHERCHE Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE Pharma S.A. (FR); Centre National de la Recherche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jockers, R., Couturier, C. and Uhlmann, E. Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the
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Pred. No. 9.3;
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Sequence 37 from Patent WO2004072293.
CQ860125
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Sequence 38 from Patent WO2004072293.
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ZAMRRNA03
AR176696
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90.5%; I
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Best Local Similarity 90.5'
Matches 19; Conservative
    RESULT 2
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125246 Sequence 13
AR037349 Sequence
AR040632 Sequence
119643 Sequence
24 C084873 Sequence
AX797219 Sequence
AX797219 Sequence
AX29883 Sequence
AR24088 Sequence
AR240883 Sequence
AR240883 Sequence
AX298581 Sequence
AX208916 Sequence
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CQ860125 Sequence
CQ860119 Sequence
AX411987 Sequence
I25270 Sequence
AR163030 Sequence
                                                                                 August 18, 2005, 05:29:57; Search time 842 Seconds (without alignments) 1208:503 Million cell updates/sec
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                5.1.6
Compugen Ltd.
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Copyright (c) 1993 - 2005
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(allie, B.L., Dunn, J.M. and Stevens, J.K.

Gallie, B.L., Dunn, J.M. and Stevens, J.K.

Method, reagents and kit for diagnosis and targeted screening for retinoblastoma retinoblastoma respect to 57 27-AUG-1996;

Patent: US 5550020-A 57 27-AUG-1996;

Location/Qualifiers
                                                                                                                                  Alzheimer,C., Goppelt,A. and Koegel,H.

Use of intermediate-conductance potassium channels and modulators
for the diagnosis and treatment of illnesses having disturbed
keratinocyte activity
Patent: WO 0205171-A 6 11-UUL-2002;
LUDWIG MAXIMILIANS UNI (DE)
LOCATION/Qualifiers
                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Unclassified.
1 (bases 1 to 19)
Stevens,J.K., Dunn,J.M., Capatos,D. and Matthews,D.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 21;
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80.0%; Pred. No. 8.4e+04;
tive 2; Mismatches 1;
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Sequence 13 from patent US 6270963.
AR163030
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 57 from patent US 5550020.
125270
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// Organism="Mus musculus"
// mol type="unassigned DNA"
// db_xref="taxon:10090"
// nofe="mIK1 Primer 1"
                                               Mus musculus (house mouse)
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nes 12; Conservative
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Patent: WO 2004072293-A 31 26-AUG-2004;
Patent: WO 2004072293-A 11 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
                                                                                                                      Jockers, R., Couturier, C. and Unlmann, E.
Oligonuclectides which inhibit the expression of the ob-rgrp
protein and method for detection of compounds modifying the
protein and method for detection of the ob-rgrp family and the
interaction between the proteins of the ob-rgrp family and the
leptin receptor
Patent: WO 2004072293-A 37 26-AUG-2004;
Patent: WO 2004072293-A 37 26-AUG-2004;
PANTICH PATENT OF THE LASANTE ET DE LA
AVENTIS PHARME S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
SCIENTIFIQUE (CNRS) (FR)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="AS10"
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/mol type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="Artificiel"
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synthetic construct
other sequences; artificial sequences.
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Sequence 31 from Patent WO2004072293.
CQ860119
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other sequences; artificial sequences.
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Sequence 6 from Patent WO02053171.
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Baracchini, E. Jr. and Bennett, C. Frank.
Oligonucleotide modulation of multidrug resistance-associated
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                                                                             linear
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Baracchini, B., Bennett, C.Frank. and Dean, N.M.
Antisense oligonucleotide modulation of multidrug
resistance-associated protein
Patent: US 5801154-A 24 01-SEP-1998;
Location/Qualifiers
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Patent: US 5807838-A 24 15-SEP-1998;
Location/Qualifiers
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                                                                                        Sequence 24 from patent US 5801154.
AR037349
AR037349.1 GI:5955205
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Sequence 24 from patent US 5510239.
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Gallie, B.L., Dunn, J.M. and Stevens, J.K.
Herbod, reagents and kit for diagnosis and targeted screening for retinoblastoma
Patent: US 5550020-A 13 27-AUG-1996;
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Stevens,J.K. and Dunn,J.M.
Method for testing for mutations in DNA from a patient sample Patent: US 5545527-A 13 13-AUG-1996;
Location/Qualifiers
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Method for testing for mutations in DNA from a patient sample Patent: US 6270963-A 13 07-AUG-2001; Location/Qualifiers
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                                                                                                                      Query Match 61.0%; Score 12.8; DB 6; Length 19; Best Local Similarity 75.0%; Pred. No. 1.7e+05; Matches 12; Conservative 2; Mismatches 2; Indels
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Sequence 13 from patent US 5550020.
125226
125226.1 GI:1605096
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/organism="unknown"
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Sequence 13 from patent US 5545527.
124629
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/organism="unknown"
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                                                             /organism="unknown"
/mol_type="unassigned DNA"
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125226
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PAT 31-AUG-2004
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Oligomeric compounds for the modulation of survivin expression Patent: WO 2004069991-A 100 19-AUG-2004;
Santaris Pharma A/S (DK)
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                                                 Length 18;
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     /note="Enterobacteriaceae family"
                                                 Query Match
Best Local Similarity 68.8%; Pred. No. 2.8e+05;
Matches 11; Conservative 3; Mismatches 2;
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Sequence 100 from Patent WO2004069991.
CQ858638.1 GI:51852605
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Patent: WO 02072882-A 5256 19-SEP-2002;
OGHAM GmbH (DE)
                                                                                                                                                                                                                  AX614231 21 bp DNA
Sequence 5256 from Patent WO02072882.
AX614231

    .16
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/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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New primers for the detection and identification of bacterial indicator groups and virulence factors
Patent: WO 030513-A 15-G-UUN-2003;
Angles D'Auriac, Marc B. (NO)
Location/Qualifiers
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1 (bases 1 to 20)
Baracchini, B. Jr. and Bennett, C.F.
Oligonucleotide modulation of multidrug resistance-associated
protein
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61.0%; Score 12.8; DB 6; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 12; Conservative 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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                                                                                Patent: US 5510239-A 24 23-APR-1996;
Location/Qualifiers
1 .20
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CQ848735.1 GI:51470163
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5 GCCAGTTCCAGGCAGG 20
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FR2850971-A1

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ADH09468 ADP46888 AAH24024

ADK94393 ADP78935 ADP78097

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                                                                                                                                                                                                                                                The present invention relates to a leptin receptor related protein (OB-RGRP) antisense oligonucleotide (ON; ADB27653), that hybridises CC specifically with and inhibits the expression of ADB27652. The ON promotes expression of leptin receptors on the cell surface and may contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a manager of triethylemeglycol residue at the 3'-end. Also claimed are interfering RNA triethylemeglycol residue at the 3'-end. Also claimed are interfering RNA cryptesion of 15-2s nt that hybridize specifically with ADB27672, and inhibit (RNA) of 15-2s nt that hybridize specifically with ADB27672, and inhibit (RNB) of 18-2s nt that hybridize specifically with ADB27672, and inhibit coding sequences comprising OB-RGRP or NYO47 (thought to be a member of the OB-RGRP family, shares 68% homology with OB-RGRP); and a protein that the OB-RGRP family, shares 68% homology with OB-RGRP, and a protein that protein (RTP) for detecting compounds that modify the interfering RNA, are the leptin receptor and OB-RGRP proteins, which can be used to prevent or the leptin and/or treatment of leptin-related disorders, e.g. cused for prevention and/or treatment of leptin-related disorders, e.g. calcification; obseity; diabetes; anorexia; disorders of sexual maturity, calcification; obseity; diabetes; anorexia; disorders of sexual maturity, and inflammation, fetal development and cancer. The present OB-RGRP and inflammation, fetal development and cancer. The present of immunity antisense oligonucleotide was used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                 New oligonucleotides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, ancrexia, hematopoiesis, and
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                                                       (AVET ) AVENTIS PHARMA SA.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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ID ABQ78935 standard; DNA; 16
                            10-FEB-2003; 2003FR-00001543
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                     Couturier C,
                                                                                                                                 WPI; 2004-595751/58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-NOV-2002
                                                                                                                                                                                                               angiogenesis.
                                                                                                        Jockers R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABQ78935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel use of intermediate-conductance obcassium channel proteins. The proteins of the invention have decreated, antiinflammatory, keratelytic, vulnerary, and antipsoriatic activity. The method is used especially in the field of damaged skin, e.g. contact dermatitis, atopic eczema, vitiligo, hyperkeratosis, actinic keratosis, hypertrophic scars, keloids, lentigo, aged skin, ulcers and especially psoriasis. The sequence represents a PCR primer for the mouse potassium channel protein mIXI of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pilC protein; pilin; pathogenic type 4 pilus bacteria; vaccine; detection; bacterial adhesin; phase variation; constant region; probe; Neisseria gonorrhoeae; Neisseria meningitidis; Pseudomonas aeruginosa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                    use of intermediate-conductance potassium channel proteins for th diagnosis, prevention and treatment of disorders associated with disturbed keratinocyte activity, especially psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.8%; Score 13.4; DB 6; Length 16; 80.0%; Pred. No. 6.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scheuerpflug IB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16 BP; 3 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria pilC gene constant region probe TR60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                   Ξ
                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 119; 121pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rylf RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 12; 29pp; German
                                                                                                                                                   Koegel
                                                                           SWITCH BIOTECH AG.
UNIV LUDWIG MAXIMILIANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93DE-04336530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ88255 standard; DNA; 19 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93DE-04336530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GCCAGUUCCCGACAG 15
28-DEC-2000; 2000DE-01065475.
20-MAR-2001; 2001US-0277453P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 GCCAGTTCCCGCCAG 1
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07-DEC-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.8
Query Match
Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                 Goppelt A, Alzheimer C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Meyer TFF, Rudel T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-140328/19.
                                                                                                                                                                                                         WPI; 2002-643295/69.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-OCT-1993;
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                                                                                   (-LIMS)
                                                                                                              (AXTO-)
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of exons 1 to 27 and the promoter of the human retinoblastoms RB1 gene, used to amplify RB1 exons for use in a method of diagnosing mutations in the RB1 gene. By comparing the lengths of amplification products of RB exons from a suspected RB patient with those of RB wild-type DNA, patients can be diagnosed early which may avoid the need for radiotherapy. Any difference in length of exons between a suspected RB patient and those from wild-type RB1 indicates either a deletion or insertion mutation. Further sequencing of suspect exons can pinpoint the mutation. The method is directed to the diagnosis of and targeted genetic screening for retinoblastoma in family members of a retinoblastoma
             Sequences coding for pilin PilC proteins from Neisseria spp. have been isolated (see AAQ88239-Q88241). The pilC1 and pilC2 genes from N. gonorrhoeae have 84% identity. Probes were designed based on regions of shared homology (see AAQ88242-88261) and these constant region probes were used in Southern hybridisations to identify other pilC genes in N. gonorrhoeae strain MS11 and N. meningitidis strain A493. Also, the same probes were used to screen a Pseudomonas aeruginosa strain and identified a pilC-like sequence. Gene sequences which hybridise with any of the constant region probes are claimed. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Retinoblastoma; RB; tumour suppressor gene; cancer; diagnosis; screening; mutation; polymerase chain reaction; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying mutation(s) in RB1 exons by quantitative amplification - and by comparing length of amplification products and sequencing, for diagnosis and genetic screening of retinoblastoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT11420-T11473 are PCR amplification primers used for the amplification
                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                       Score 13.2; DB 2; Length 19;
Pred. No. 8.3e+03;
2; Mismatches 3; Indels
                                                                                                                                                                                                                     Sequence 19 BP; 4 A; 6 C; 7 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Retinoblastoma gene, RB1, exon 1 PCR 5' primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hui M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stevens JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 22; 48pp; English
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                                                                                                                                                                                                                                                                                                                                GCCAGUUCCCGACAGGCA 18
                                                                                                                                                                                                                                                                                                                                                     GCCGTTTCCCGACTGGCA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95WO-US008604.
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                                                                                                                                                                                                                                                       62.9%;
72.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-097637/10.
                                                                                                                                                                                                                                                                         Local Similarity
ses 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                    field.)
                                                                                                                                                                                                                                                                                              Matches
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This sequence is a primer which was used in the amplification of the mouse KIAA0377 coding sequence. KIAA0377 is homologous to human BT42.

End contains the central signature of a histidine acid phosphatase, which are known to hydrolyze phosphate ester at low pH and are able to use a wide spectrum of substrates. The two BT42 isoforms of the customer of the mouse BT42. I hypercholesterolaemia of 40 amino acids compared to mouse BT42. Also BT42-II contains an additional exon of 40 amino acids.

ENT42 is regulated by fasting and by genetically induced obesity. BT42.

ENT42 is regulated by fasting and by genetically induced obesity. BT42.

ENT42 is regulated by fasting in any be used for the manufacture of an agent for detecting or/and verifying, for the treatment, alleviation and/or prevention of metabolic diseases or dysfunctions, including metabolic syndrome, obesity or/and diabetes, as well as related disorders such as caing disorder, cachexia, hypertension, coronary heart disease.

Compared to colling and phypeptical are useful for the hypercholesterolaemia, dyslipidemia, osteoarthritis, gallstones, or liver fibrosis, in cells, cell masses, organs and/or subjects in vivo or in control and metabolic syndrome for controlling the function of a gene or/and a medicament for the treatment of obesity, diabetes.

Cor/and metabolic syndrome for controlling the function of a gene or/and a gene product, which is influenced or/and modified by a BT42 homologous polypeptide, and for the production of a non-human correspond and any and any and any and and any an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New pharmaceutical composition comprising a BT-42 homologous protein or nucleic acid, and carriers, diluents or/and additives, useful for treating obesity, hyperlipidemia, osteoarthritis, cell masses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  se; acid phosphatase; BT42-1; BT42; histidine acid phosphatase; hydrolysis; phosphate ester; BT42-II; deletion; fasting; genetically induced; obesity; isoform; metabolic disease; dysfunction; metabolic syndrome; obesity; diabetes; eating disorder; cachexia; hypertension; coronary heart disease; hypercholesterolaemia; dyslipidemia; osteoarthritis; gallstone; liver fibrosis; primer.
                                                Gaps
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                                                Indels
Score 13.2; DB 2;
Pred. No. 8.4e+03;
                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Page 39; 79pp; English
                                                                                                                                            21
                                                                                                                                                                                                                                                                     ADP66743 standard; cDNA; 18 BP.
                                                                                                 2 CCAGUUCCCGACAGGCAC 19
                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse KIAA0377 forward primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-NOV-2002; 2002EP-00026693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2003; 2003WO-EP013521
                                                                                                                                  CCAGTTCCCCACAGACGC
                                                                                                                                                                                                                                                                                                                                                                      09-SEP-2004 (first entry)
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DEVE-) DEVELOGEN AG
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  Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                        ADP66743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp.
                       Best Lock
                                                                                                                                                                                                                         RESULT 5
ADP66743/c
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Sequence 18 BP; 3 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Sequence 21 BP; 4 A; 11 C; 4 G; 2 T; 0 U; 0 Other;

RESULT 6 AAT11532 ID AAT1:

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NATI2839-T12899 (excluding AAT12878) are PCR primers used to amplify various regions of the RB-1 genome, including exons 1-27, the promoter region and a control sequence unrelated to RB-1 from chromosome 15. The primers are used in an example of a method for testing a disease-sascitated mutation in a gene, the gene may not necessarily be a tumour suppressor gene like the retinoblastoms gene another example is the expressor gene like the retinoblastoms gene another example is the be analysed using the same method. The primers are used in various groupings to produce a hierarchical assay useful to test a group of patients uspected to have a genetic mutation. The method allows the optimum (or near optimum) diagnostic algorithm by considering the cost and the sensitivity and specificity of each test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Untranslated region; coding sequence; chemotherapeutic drug treatment; antisense; modulation; multidrug resistance protein; drug; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Testing for a disease-associated mutation in a gene - using a hierarchy of tests selected to optimise performance while minimising cost.
                                                                                                           PCR; polymerase chain reaction; retinoblastoma; tumour suppressor; cancer; mutation; identification; diagnosis; cystic fibrosis; hierarchy assay; method; specificity; ss.
                                                                         PCR 5' primer for exon 1 of human RB1 (retinoblastoma-1) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 12.8; DB 2; Length 19; Pred. No. 1.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense oligonucleotide ISIS 8363 hybridises to MRP gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19 BP; 4 A; 10 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                        Matthews DE;
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1. .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 32; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            Capatos D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ86849 standard; DNA; 20 BP.
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75.0%;
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                                                                                                                                                                                                                                                                                                            95WO-US008606.
                                                                                                                                                                                                                                                                                                                                                  94US-00271946
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                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              Stevens JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-171632/17.
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                                                                                                                                                                                                                                                                                                                                                      08-JUL-1994;
                                                                                                                                                                                                                                        WO9607761-A2.
                                                                                                                                                                                                                                                                                                                    07-JUL-1995;
                                                                                                                                                                                                     Homo sapiens
                                                 22-OCT-1996
                                                                                                                                                                                                                                                                              14-MAR-1996
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               AAT12851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                              Retinoblastoma; RB; tumour suppressor gene; cancer; diagnosis; screening; mutation; polymerase chain reaction; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying mutation(s) in RB1 exons by quantitative amplification - and by comparing length of amplification products and sequencing, for diagnosis and genetic screening of retinoblastoma.
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                                                           Gaps
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                       Length 18;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19 BP; 4 A; 10 C; 3 G; 2 T; 0 U; 0 Other;
                       61.0%; Score 12.8; DB 12;
75.0%; Pred. No. 1.38+04;
iive 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                Retinoblastoma gene, RB1, exon 1 PCR 5' primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hui M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stevens JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 14; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT12851 standard; DNA; 19 BP.
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                                                                                                                                                                                                                                        ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-00271942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (VISI-) VISIBLE GENETICS INC (HSCR-) HSC RES & DEV LP.
                                                                                                       1 GCCAGUUCCCGACAGG 16
                                                                                                                           16 GCCAGTTCTCCACAGG 1
                                                                                                                                                                                                                                      AAT11532 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Conservative
                                                                                                                                                                                                                                                                                                                (first entry)
                                                                 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dunn JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-097637/10.
                                 Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9601908-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUL-1995;
                                                                                                                                                                                                                                                                                                                  10-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallie BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local 9
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Matches

RESULT 7 AAT12851

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This is the nucleotide sequence of the phosphorothioate oligonucleotide used in the method of the invention, involving the used of antisense oligonucleotides to inhibit multidung resistance. The oligonucleotides are used for the antisense inhibition of multiresistant proteins (RRPB). These proteins are commonly found in some cancers which initially respond to chemcherapy, but overexpression of the protein leads to chemcherapy drug resistance. They are administered with the drugs to attempt to and as such, the oligonucleotides can be used to treat these conditions as well. The sequences are based on the human MRP and are used to treat conditions such as cancers, especially small-cell lung cancer, prevention of development of multidrug resistance during chemotherapy, and treatment of conditions characterised by leukotriene production, especially inflammatory conditions. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Analyzing multiple targets in polynucleotide, by providing multiple primers with target nucleic acids, digesting nucleic acid products with cognate restriction enzymes, amplifying digested products, and detecting
                                                                                                                                                            Anti:sense oligo:nucleotide(s) inhibiting multi:drug resistance protein expression - useful for increasing the efficacy of drugs that certain conditions have become resistant to e.g. small cell lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; Multiplex nucleic acid detection; ss; PCR; primer; SNP; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multiplex amplification of human SNP fragments, primer #153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.0%; Score 12.8; DB 2; Length 20; 75.0%; Pred. No. 1.3e+04; ive 2; Mismatches 2; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                  ä
                                                                                  Baracchini
                                                                                                                                                                                                                                              Claim 11; Col 12; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADQ31737 standard; DNA; 21 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JAN-2003; 2003US-00349780.
  96US-00628731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCCAGUUCCCGACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 75.0
Les 12; Conservative
                                          (ISIS-) ISIS PHARM INC
                                                                                  Dean NM,
                                                                                                                        WPI; 1998-494825/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-552653/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
Synthetic.
    16-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FUGG/) FU G.
                                                                                  Bennett CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADQ31737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotides AAQ86826-50 are antisense oligonucleotides used to modulate the expression of the multidrug resistance protein (MRP) by hybridising with the multidrug resistance (MDR) gene or its RNA message. This sequence is targeted to the 3' untranslated region (3'UTR) of the MDR gene. The oligonucleotides can be used to improve the efficacy of chemotherapeutic drug treatment of a disease such as cancer or to prevent multidrug resistance developing during drug treatment of a disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphorothioate oligonucleotide; antisense; inhibition; cancer; multidrug resistance; multiresistant protein; MRP; chemotherapy; human; leukotriene; inflammatory condition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
/*tag= a
/note= "contains phosphorothioate internucleotide
linkages"
                                                                                                                                                                                                                                                                                                                                                            New oligo:nucleotide cpds., esp. for cancer therapy - which are specifically hybridisable with nucleic acid encoding multi:drug resistance-associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of a phosphorothicate oligonucleotide 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.0%; Score 12.8; DB 2; Length 20; 75.0%; Pred. No. 1.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/note= "phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 11; 36pp; English.
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                                                                                                                                                                                                      93US-00136811
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                                                                                                                                                              94WO-US010827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCCAGUUCCCGACAGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCAGITCCAGGCAGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV53600 standard; DNA; 20
                                                                                                                                                                                                                                                                                      Bennett CF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Conservative
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/*tag=
                                                                                                                                                                                                                                            (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
                                                                                                                                                                                                                                                                                                                            WPI; 1995-169974/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
modified_base
                                                                                                                                                                                                                                                                                      Baracchini E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
Homo sapiens
                                                                                  WO9510938-A1
                                                                                                                                                            23-SEP-1994;
                                                                                                                                                                                                      18-OCT-1993;
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20-NOV-1998
                                                                                                                      27-APR-1995.
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Query Match Best Loc Matches

AAV53600;

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BELIN M. CHARRIER E. HONORAT J.

> HONO/ CHAR/)

AGUERA M.

AGUE/)

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The invention relates analysing multiple targets in polymucleotide, convolves providing a set or sets of multiple primers with target nucleic acids in separate reactions of primer extension or amplification, where the reactions produce nucleic acid products in that each nucleic acid tragments comprise at least one restriction sites with cognate products of the separate reactions on the restriction sites with cognate creations together, where randomly joining nucleic acid fragments from the separated reactions are created, amplifying the joined products, and the separated reactions are created, amplifying the joined products, and creations together, where randomly joining nucleic acid fragments from the separated reactions are created, amplifying the joined products, and complementary portion and 5' non-complementary portion, where the fromplementary portion and 5' non-complementary portion, where the complementary portion comprises a restriction enzyme site, where the complementary portion or comprises a restriction site, where the compression site acts as detection marker in the process of detecting target nucleic acid sequence, where the detection product is capter nucleic acid sequence, where the detection product is nated to the presence of target nucleic acid sequence, as as eat or sets of multiple targets in a polymucleotide and detection of multiple targets in a polymucleotide and for genoryping mutations, preferably single creaticition enzymes, DNA ligase, DNA polymerase, ddArrp, buffers for all enzymes, and dNTP9). The method is useful for analysing multiple expectation cargets from any source. The method is useful for analysing multiple expectation cargets guantitatively. An experiment was performed, using the method of the invention, where SNPs were detected in 70 human genomic DNA cargets and the invention, where SNPs were detected in 70 human genomic in the present sequence is a primer used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; 88; Ulip; CRMP; collapsin response mediator protein; PCR; Unc.13-like protein; neurodegenerative disease; Alzheimer's disease; paraneoplastic neurodegenerative disease; PND; myellination; demyellination; myelin disorder; multiple sclerosis; autoimmune neurodegenerative disorder; HTLV-1 associated myelopathy; human T lymphocyte virus 1; reverse transcriptase PCR; primer; glial fibrillary associated protein; GFAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human glial fibrillary associated protein, GFAP, RT-PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch
1 Similarity 75.0%; Pred. No. 1.3e+04;
12; Conservative 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 4 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
                                         Example 2; SEQ ID NO 195; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK91203 standard; DNA; 19 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-NOV-2000; 2000US-0246751P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CCAGUUCCCGACAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
amplified products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2002119944-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               above experiment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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The invention relates to a new method for prevention or treatment of myelin disorders, comprises administering to a patient an effective myelin disorders, comprises administering to a patient an effective amount of an agent selected from a Ulip (Unc-33-1ke protein/CRMP) can administering a nucleic acid, an antisense sequence capable of specifically hybridising with Ulip/CRMP, and antisense tup/CRMP, or an aptamer cologically acceptable carrier. C capable of binding ULIP/CRMP, and a pharmacologically acceptable carrier. Also included are methods of diagnosing a myelin disorder in a subject, disorders, using the Ulip/CRMP proteins/nucleic acids, agents capable of disorders, using the Ulip/CRMP proteins/nucleic acids, agents capable of c disorders, using the Ulip/CRMP proteins or the reatment of myelin decreasing), and a method for identifying an endogenous agent as a cofisorders. The agents are useful for preventing or treatment of myelin colisorder such as multiple sclerosis or HTLV-1 (human T lymphocyte virus is secondated myelopathy and neurodegenerative diseases (PND), autoimmune c diseases parametollastic neurodegenerative diseases (PND), autoimmune c unip/CRMP proteins are involved in neurodegenerative diseases (PND), autoimmune c ulip/CRMP proteins are involved in neurodegenerative diseases (PND), autoimmune c ulip/CRMP proteins are involved in neurodegenerative diseases (PND), autoimmune c to a ulip/CRMP protein are useful for diagnosing a myelin disorder. The present sequence is a reverse transcriptase (RT)-PCR primer for glial c present sequence is a reverse transcriptase (RT)-PCR primer for glial
                                                                                                                                                                                                         Prevention or treatment of myelin disorders, such as multiple sclerosis, by administering an agent selected from a Ulip/CRMP protein, a nucleic acid coding for the protein, or an antibody directed against protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ss; GB virus B; GBV-B; HCV; flavivirus; hepatitis C virus; antiviral; vaccine; virucidal; antiinflammatory; PCR; primer; NS5A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                              Rogemond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 60.0%; Score 12.6; DB 6; Length 19; Best Local Similarity 68.4%; Pred. No. 1.7e+04; Indels Matches 13; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primer used to amplify the GBV-B NS5A gene SeqID 16.
                                                                                                                              Honorat J, Ricard D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 BP; 3 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                     Charrier E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ccaguucccaacagcacr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 CCAGTTACCAGGAGGCACT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВЪ.
                                                                                                                                                                                                                                                                                                       Example, Page 8; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-2003; 2003WO-US021002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis GB virus B.
                                                                                                                                                                              WPI; 2002-627172/67.
                                                                                                                                       Aguera M, Belin M,
                                                                                                ROGEMOND V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004005498-A1.
                                                                          RICARD D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-2004
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                                                                              (RICA/)
(ROGE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
ADJ56746
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Length 21;

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The invention describes a new isolated polynucleotide (I) encoding a 3' sequence of the GB virus B (GBV-B) genome, or which comprises a chimeric GBV-B genome, where at least part, but not all of a 5' nontranslated region (NTR) sequence is derived from a hepatitis C virus (HCV) 5' NTR. (I) is a GB virus B and/or hepatitis C virus polynucleotide comprising a fully defined of 260 or 9199 bp (SEQ ID NOS: 1 or 2). The polynucleotides or chimaeras are useful diagnosing or treating hepatitis C virus (HCV) and in investigating the mechanisms for the different biological and in investigating the viruses. This sequence represents a primer used to detect a chimeric virus comprising domain III of the 5'NTR of HCV (IRES) within a genetic background of GBV-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a polynucleotide isolated from a human gene and is useful for detecting a single nucleotide polymorphism in a human gene or for diagnosing of disease. The invention enables the detection of a single nucleotide polymorphism in a human gene. The present sequence represents a primer of the invention.
                                            New GB virus B and/or hepatitis C virus (HCV) sequences, useful in diagnosing and in treating HCV and in investigating the mechanisms for the different biological properties of the viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotide useful for PCR amplification along with two DNA fragment from another set of sequences, or for detecting single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; single nucleotide polymorphism; SNP; ss; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 12.6; DB 12;
Pred. No. 1.7e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19 BP; 5 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
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Pred. No. 1.7e+04;
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                                                                                                                                              Example 24; SEQ ID NO 16; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fragment from another set of sequences nucleotide polymorphism in human gene.
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68.4%;
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les 13; Conservative
WPI; 2004-203294/19.
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                                                                                                                                                                                                                                                                                                                                                   This invention relates to novel isolated chimeric GB virus B (GBV-B)/HCV polynucleotides. Specifically, it refers to using the hepatotropic flavivius GBV-B that has a unique phylogenetic relationship to the human hepatitis C virus (HCV) and can serve as a surrogate virus in drug discovery efforts related to antiviral drug development. The present is using the newly determined 3' terminal sequence of GBV-B. Furthermore, the GBV-B/HCV chimeras exhibit liver-specific expression and express HCV envelope proteins such that they can have utility as a vaccine immunogen for the ABV-B/HCV chimeras exhibit liver-specific expression and express HCV envelope proteins such that they can have utility as a vaccine immunogen of for hepatitis C. In addition, they can be used for screening compounds active against viral infection, as well as for developing HCV preventative and therapeutic treatments. Accordingly, these compositions exhibit virucidal, antiinflammatory and hepatotropic activities. This coligonucleotide sequence is a PCR primer used to amplify the GBV-B NSSA gene sequence of the invention. NOTE: This sequence is given as SeqID 16 in the sequence listing but is referred to as SeqID 15 in example 24.
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                                                                                                                                                                                                            New chimeric GBV-B polynucleotide, useful as a model for hepatitis C virus, for identifying compounds active against a viral infection, or developing hepatitis C virus preventive and therapeutic treatments.
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                                                                                                                  Lemon SM, Rijnbrand R;
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03-JUL-2002; 2002US-00189359.
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(INSP ) INST PASTEUR.
                                            (TEXA ) UNIV TEXAS SYSTEM (INSP ) INST PASTEUR.
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                                                                                                                  Martin A,
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ADJ64258
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DB 12; Length 20;

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Indels

Length 19;

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The present invention relates to a compound which specifically hybridizes with a nucleic acid molecule encoding GFAT, and inhibits the expression of GFAT. Specifically claimed are antisense oligonucleotides capable of modulating the expression of GFAT, and which comprise any of the 3063 sequences of 20 base pairs, given in the specification. The compound, sequences of 20 base pairs, given in the specification. The compound composition and methods are useful for treating a disease or condition associated with GFAT, such as a disease or condition, e.g. diabetes, a cardiovascular or neurological disporder, is chemia/reperfusion injury. They are also useful in research and diagnostics for modulating the expression of GFAT. The present sequence represents a chimeric phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these oligonucleotides inhibit human GFAT expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase (GFAI), for treating diabetes, a cardiovascular or neurologic disorder, ischemia/reperfusion injury.
 Gaps
                                                                                                                                                                                                                                                                  GFAT; Antidiabetic; Cardiant;
Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 60.0%; Score 12.6; DB 12; Length 20; Best Local Similarity 73.7%; Pred. No. 1.7e+04; Matches 14; Conservative 1; Mismatches 4; Indels (
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   4; Indels
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                                                                                                                                                                                                                                    Chimeric phosphorothioate oligonucleotide #2734.
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/note= "2-methoxyethyl wing"
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                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                             20 CGAGGTCCAGACAAGCACT 2
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                                    2 CCAGUUCCCGACAGGCACT
                                                                                                                                                ADP78935 standard; DNA; 20
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    14; Conservative
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                                                                                                                                                                                                                                                                                                      reperfusion; ss.
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5.1.6
Compugen Ltd.
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US-08-771-946A-13

US-08-271-946A-13

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US-08-136-13-14

US-09-275-680-7

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GenCore version
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200 200 201 201 201 200 200 200		nce 26, Application US/086 nce 26, Application US/086 RAL INFORMATION: PLICANT: Rudel, Thomas F. PLICANT: Rudel, Thomas PLICANT: Rudel, Thomas PLICANT: Rudel, Thomas PLICANT: Scheuerfleug, III TLE OF INVENTION: Recombine OF EXCHENCES: 40 RRESPONDENCES: 40 RRESPONDENCES: 40 RRESPONDENCES: 40 RRESPONDENCES: 40 RRESPONDENCES: Birch, Stewart STREET: P.O. Box 74 CCITY: Falls Church STARET: Virginia CCOMPTRY: USA MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: 1BM PC Compatin FILING SYSTEM: PC-DOS, SOFFWARE: PAPPLICATION NUMBER: 18-COMMUNICATION FOR SEQ ID NO: 20 CUENCE CHARACTERISTICS: 18-COMMUNICATION FOR SEQ ID NO: 20 COMMUNICATION FOR SEQ ID NO: 20 COMUNICATION FOR SEQ ID NO: 20 COMUNICATION FOR SEQ ID NO: 20 COMUNICATION FOR SEQ ID NO: 2	72.2 ive
		137-732A-26/c nce 26, Application US t No. 6268 71 PLICANT: Meyer, Thoma PLICANT: Rudel, Thoma PLICANT: Radel, Thoma PLICANT: Redel, Thoma PLICANT: Redel, Thoma PLICANT: Rolen TIES OF INVENTION: Rec THE OF INVENTION: PO STREET: P.O. Box 747 CITY: Falls Church STREET: Virginia COMPUTER: USA TOWN THE IBM PC COMP OPERATING SYSTEM: PC COMPUTER: BARENCE DOCKET UNDREE TILING DATE: 28-UM-1 TELEPHONE: 703-205-80 THE SERENCE DOCKET UNDREE TECOMMUNICATION INFORMATI NAME: SVENDED NOT SEQUENCE THE OF THE	vat
		nce 26, Application nce 26, Application the No. 6268171 the No. 6268171 the No. 6268171 the Dilcant: Meyer, The PLICANT: Rudel, The PLICANT: Rudel, The PLICANT: Rudel, The PLICANT: Readel, The PLICANT: READERS STREET: D. O. BOX THE STREET: D. O. BOX THE STREET: D. BOX THE STATE: Wirginia COUNTRY: USA THE 22440-074 MEDIUGATION IN STATE: USA MEDIUGATION SYSTEM: SOFTWARE: PALENTION DAPPLICATION DAPPLICATION DAPPLICATION DAPPLICATION INFORM TELEPAN: TO3-205- READING DATE: 28-JU CLASSIFICATION NUMBER: PLING DATE: 28-JU CLASSIFICATION INFORM NAME: Svensson, Lee REGISTRATION NUMBER: TELEPHONE: 703-205 TRANDEDNESS: SING STRANDEDNESS: SING STRANDENESS: SING STRANDEDNESS:	Similarity 3, Conser
~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~		7-732A-26/c ce 26, Applic dL CANT: Mey LICANT: Mey LICANT: Ryll LICANT: Ryll LICANT: Ryll LICANT: Ryll LICANT: Ryll LICANT: Ryll RESPONDENCE BER OF INVENT RESPONDENCE BERSPONDENCE DDRESSES: 0.0 FREET VITGIS UNTAY: USA DDRESSES: 0.0 FREET VITGIS UNTAY: USA DDRESSES: 0.0 FREET VITGIS UNTAY: USA DDRESSES: 0.0 FREET RADABS RESPONDENCE DDRESSES: 0.0 FREET VITGIS UNTAY: 0.0 FREET RADABS FREET CATION ILLING DATE: 1 FREAT APPLICA FREET APPL	Con
4 4 4 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6		137-732A-26/ nce 26, App Rt Ino. 62681 Rt Ino. 62681 Rt Ino. 62681 PLICANT: R PR PLICANT: R P P P P P P P P P P P P P P P P P P P	Sim:
444444444460000000		137-732A-2 nce 26, A nce 2	al 1
		SGULT 1 SGULT 1 SGULCA Application US/08637732A SGGUGNECA Application US/08637732A SAPPLICANT: RADGL, Thomas APPLICANT: SCHOUENTION: Recombinant PTITLE OF INVENTION: Producing The NUMBER OF SEQUENCES: 40 CORRESPONDENCE ADDRESS: ADDRESSEE: Birch, Stewart, KolasTREET: P.O. Box 747 CITY: Falls Church STREET: Virginia COUNTRY: USA ZIP: 22040-0747 COMPUTER: RADDABLE FORM: WEDIUM TYPE: Floppy disk COMPUTER: READABLE FORM: WEDIUM TYPE: Floppy disk COMPUTER: READABLE FORM: WEDIUM TYPE: Floppy disk COMPUTER: BATCH ON AGRACH COMPUTER: SPATENTION DATA: APPLICATION NUMBER: US/08/637,77 FILING DATE: 28-UTN-1996 CLASSIFICATION NUMBER: 30330 REFERENCE/DOCKET NUMBER: 30330 REFERENCE/DOC	Local
00000000000000000000000000000000000000		SULT. Seque	Best Lo Matches
υ υυυ υ		RESULT 1  US-08-637-732A-26/c  Sequence 26, Application US/08637732A  Patent No. 6288171  APPLICANT: Rudel, Thomas  APPLICANT: Rudel, Tha B.  TITLE OF INVENTION: Recombinant P  TITLE OF INVENTION: Stewart, Kola  STREET: Po. Box 747  CONFUTER: Palls Church  STREET: Po. Box 747  COMPUTER: Readballs FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: READBALE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: READBALE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: READBALE FORM:  MEDIUM TYPE: Batentin Release H1.  COMPUTER: Batentin Release H1.  COMPUTER: Batentin Release H1.  COMPUTER: SPENSON: 435  ATTONNEY/AGENT INPORMATION:  NAME: Svensson, Leonard R.  REGISTRATION NUMBER: 30330  REFERENCE/COMPUTER: 109 base pairs  TELEPANDENCE/COSTEN NUMBER: 147-15  TELEPHONE: 703-205-8000  TELERANTION FOR SEQ 100  TELEFANTION FOR SEQ 100  TELERANTION FOR SEQ 100  TELERANTION: 435  INFORMATION FOR SEQ 100  TELERANTION: 435  ATTONEY/AGENT INPORMATION:  TELERANTENCE/CHARACTERISTICS:  LENGTH: 19 base pairs  TERERANTION: 46sc = "PCR PTIME  US-08-637-732A-26  GOER	ďΣ̈́

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                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brenda L.
APPLICANT: Stevens M.
APPLICANT: Stevens John K.
TITLE OF INVENTION: and Targeted Screening for Retinoblastoma TITLE OF INVENTION: and Targeted Screening for Retinoblastoma NUMBER OF SEQUENCES: 123
CORRESPONDENCE ADDRESS:
ADDRESSE: Oppedahl & Larson
STRET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
STATE: NY
COUNTRY: USA
ZIP: 10588-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: Word Perfect
CHARRING SYSTEM: US/08/271,942A
FILING DATE: 08-UUL-1994
CLASSIFICATION NUMBER:
BRIOR APPLICATION DATA:
APPLICATION NUMBER:
BRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: primer for exon 1 of human RB1 gene US-08-271-942A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN.P-003-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-779-916A-57
US-08-779-916A-57
; Sequence 57, Application US/08779916A
; Patent No. 6063567
; GENERAL INFORMATION:
                                                                                                      US-08-271-942A-57
; Sequence 57, Application US/08271942A
; Patent No. 5550020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CCAGUUCCCGACAGGCAC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nuclear con-
STRANDENDESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57:
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 13; Conservē
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Gaps
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Sequence 57, Application PC/TUS9508604
Sequence 57, Application PC/TUS9508604
APPLICANT: Visible Genetics Inc.
APPLICANT: Sequence and Development Limitied Partnership APPLICANT: Brenda L.
APPLICANT: Dunn, James M.
APPLICANT: Stevens, John K.
TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis TITLE OF INVENTION: Method Argered Screening for Retinoblastoma Manner C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
APPLICANT: Dunn, James M.
APPLICANT: Stevens, John K.
APPLICANT: Stevens, John K.
APPLICANT: Hui, May
TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
ADDRESSEE: Oppodabl & Larson
STREET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 62.9%; Score 13.2; DB 3; Length 21; Best Local Similarity 72.2%; Pred. No. 1.7e+03; Matches 13; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: primer for exon 1 of human RB1 gene US-08-779-916A-57
                                                                                                                                                                                                                                                                                                                                                         COMDITY: USA

ZIP: 10598-4412

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,916A
FILING DATE: 07-JAM-1997
CLASSIFICATION NUMBER: 08/271,942
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: MAINE INFORMATION:
NAME: MAINE INFORMATION:
TELEFRENCE/DOCKET NUMBER: 32,038
RESTERRENCE/DOCKET NUMBER: 32,038
TELEFRENCE/DOCKET NUMBER: 32,038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Oppedahl & Larson
1992 Commerce Street, Suite 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CCAGUUCCCGACAGGCAC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDONAL Linear TOPOLOGY: Linear MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: no
FRAGMENT TYPE: inte
ORIGINAL SOURCE:
ORGANISM: human
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PCT-US95-08604-57
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Gallie, Brenda L.

APPLICANT:

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APPLICANT: Gallie, Brenda L.
APPLICANT: Gallie, Brenda L.
APPLICANT: Dunn, James M.
APPLICANT: Stevens, John K.
TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
TITLE OF INVENTION: and Targeted Screening for Retinoblastoma NUMBER OF SEQUENCES: 123
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
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Pred. No. 2.7e+03;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: primer for exon 1 of human RB1 gene US-08-271-946A-13
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ZIP: 10598-4412

COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,942A
FILING DATE: 08-UU1-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MAINA T. LATSON
REGISTATION NUMBER: 32,038
REGISTATION NUMBER: 32,038
REGISTATION NUMBER: 32,038
REGISTATION NUMBER: 32,038
REGISTATION NUMBER: YOUNGEN TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                               VGEN. P-002-US
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Sequence 13, Application US/08271942A
Patent No. 5550020
                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Marina T Larson
REGISTRATION NUMBER: 32,038
REFRENCE/DOCKET NUMBER: VGEN
TELECOMMUNICATION:
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Oppedahl & Larson
STREET: 1992 Commerce Street,
CITY: Yorktown Heights
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 61.0%;
Best Local Similarity 75.0%;
Matches 12; Conservative ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
FOOLGGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
   08-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     no
PE: internal
FILING DATE: 08-JUL-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
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i Sequence 13, Application US/08271946A
j Fatent No. 254527
j GENERAL INFORMATION:
    APPLICANT: Stevens, John K.
    APPLICANT: Durn, James M.
    TITLE OF INVENTION: Method for Testing for Mutations in DNA
    TITLE OF INVENTION: Method for Testing for Mutations in DNA
    TITLE OF INVENTION: Method for Testing for Mutations in DNA
    TITLE OF INVENTION: Method for Testing for Mutations in DNA
    TITLE OF INVENTION: Method for Testing for Mutations in DNA
    TITLE OF INVENTION: Method for Testing for Mutations in DNA
    TITLE OF INVENTION: Method for Testing for Mutations in DNA
    TITLE OF INVENTION: Method for Testing for Mutations in DNA
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    TITLE OF INVENTION: Method for Testing for Mutations in DNA
    TITLE OF INVENTION: Method for Testing for Mutations in DNA
    TITLE OF INVENTION: Method for Testing for Mutations in DNA
    TITLE OF INVENTION: Method for Testing for Mutations in DNA
    TITLE OF INVENTION: Method for Testing for Mutations in DNA
    TITLE OF INVENTION: Method for Testing for Method for Testing for Method for Testing for Testing for Method for Testing for Method for Testing for Test
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: primer for exon 1 of human RB1 gene PCT-US95-08604-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

INF. 10598-4412
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: WOR'D PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,946A
                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb COMPUTER: Diskette, 3.5 inch, 1.44 Mb COMPUTER: IBM Compatible OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08604
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,942
FILING DATE: 08-UL-1994
ATTORNEY/AGENT INFORMATION:
NAME: MAITIN T. LAISON
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN.P-003-WO
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CCAGUUCCCGACAGGCAC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: genomic DNA HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21
Yorktown Heights
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           no
PR: internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: no
FRAGMENT TYPE: i
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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Gape

Gaps

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GENERAL INFORMATION:
APPLICANT: Visible Genetics Inc.
APPLICANT: Visible Genetics Inc.
APPLICANT: Stevens, John K.
APPLICANT: Dance M.
APPLICANT: Matthews, David E.
TITLE OF INVENTION: Method for Testing for Mutations in DNA TITLE OF INVENTION: Method for Patient Sample NUMBER OF SQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSE: Oppedahl & Larson STREET: 1992 Commerce Street, Suite 309
CITY: Vorktown Heights
                                                                                                                                                                                                                         Ouery Match 61.0%; Score 12.8; DB 3; Length 19; Best Local Similarity 75.0%; Pred. No. 2.7e+03; Anatches 12; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: primer for exon 1 of human RB1 gene
                                                                                                                                                        NAME/KEY: primer for exon 1 of human RB1 gene US-08-779-916A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10598-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/FORT NUMBER: VGEN.P-002-WO
RELECOMMUNICATION INFORMATION:
TELECHONE: (914) 245-3252
TELEFROX: (914) 962-4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,946
FILING DATE: 08-UUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,232
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-08-750-232-13
Sequence 13, Application US/08750232
Sequence 13, Application US/08750232
Patent No. 6270963
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                            4 ccacrcccacacac 19
                                                                                                                                                                                                                                                                                                                                 2 CCAGUUCCCGACAGGC 17
MOLECULE TYPE: genomic DNA HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: no FRAGMENT TYPE: internal ORIGINAL SOURCE: ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                           HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: human
FRATURE:
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19. 916A-13

19. 5equence 13. Application US/08779916A

19. Sequence 13. Application US/08779916A

19. Patent No. 6063567.

10. GENERAL INFORMATION:

APPLICANT: Gallie, Brenda L.

APPLICANT: Gallie, Brenda L.

APPLICANT: Hui, May

TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis

TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis

TITLE OF INVENTION: and Targeted Screening for Retinoblastoma

NUMBER OF SEQUENCES: 123

CORRESPONDENCE ADDRESS:

ADDRESSEE: Oppedable & Larson

STREET: 1992 Commerce Street, Suite 309

CITY: Yorktown Heights
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Best Local Similarity 75.0%; Pred. No. 2.7e+03; Indels
Matches 12; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: primer for exon 1 of human RB1 gene US-08-271-942A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
COMPUTER: IBM COMPACE:
COMPUTER: OF DESS.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,916A
FILING DATE: 07-JAN-1997
CLASSIFICATION NUMBER: 08/21,942
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INPOMBER: 08-JUL-1994
ATTORNEY/AGENT INPOMBER: 32,038
REGISTRATION NUMBER: 32,038
REGISTRATION NUMBER: 32,038
REGISTRATION NUMBER: 32,038
REGISTRATION NUMBER: 32,038
RELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13:
                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ccaguucccaacaggc 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 CCAGTTCCCCACAGAC 19
                        TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (914) 962-4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
                                                                                                                                                                                                                                                                                            ANTI-SENSE: no
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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US-08-750-232-13

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FRAGMENT TYPE: internal ORIGINAL SOURCE:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                         PCT-US95-08606-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-136-811-24
                                                                                                                                                                                                                                                                                                                           STATE:
    RESULT 10
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                                           Gaps
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                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Visible Genetics Inc.
APPLICANT: HSC Reasearch and Development Limitied Partnership
APPLICANT: Gallie, Brenda L.
APPLICANT: Gallie, Brenda L.
APPLICANT: Stevens, John K.
TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedabl & Larson
STREET: 1992 Commerce Street, Suite 309
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61.0%; Score 12.8; DB 3; Length 19; 75.0%; Pred. No. 2.7e+03; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAWE/KEY: primer for exon 1 of human RB1 gene PCT-US95-08604-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTAI: USA
ZIP: 10598-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VGBN . P-003-WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13:
                                                                               2 CCAGUUCCCGACAGGC 17
                                                                                                    4 CCAGTTCCCCACAGAC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: genomic DNA HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yorktown Heights
Query Match
Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                  PCT-US95-08604-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Yor)
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                               RESULT 9
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Sequence 13, Application PC/TUS9508606
GENERAL INFORMATION:
APPLICANT: Visible Genetics Inc.
APPLICANT: Stevens, John K.
APPLICANT: Dunn, James M.
APPLICANT: Capatos, Denis
APPLICANT: Matthews, Denis
APPLICANT: Matthews, David E.
TITLE OF INVENTION: Method for Testing for Mutations in DNA
TITLE OF INVENTION: from a Patient Sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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; Patent No. 5510239
; GENERAL INFORMATION: Baracchini, Jr., Edgardo and Bennett,
APPLICANT: Clarence Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.0%; Score 12.8; DB 5; 75.0%; Pred. No. 2.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KBY: primer for exon 1 of human RB1 gene PCT-US95-08606-13
                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
CONPUTER 10598-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSES: Oppedanl & Larson
STREET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/271,946
APPLICATION NUMBER: 08-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MATINE T. LATEON
RECISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ccagrrccccacagac 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (914) 245-3252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: genomic DNA HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible OPERATING SYSTEM: DOS 5.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (914) 245-329
TELEFAX: (914) 962-4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.0° Matches 12; Conservative
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Gaps
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61.0%; Score 12.8; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 2; Mismatches 2; Indel8
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US-08-628-731-24

Sequence 24, Application US/08628731

Sequence 24, Application US/08628731

Setent No. 5807838

GENERAL INFORMATION:

APPLICANT: Garence Frank

TITLE OF INVENTION: Oligonucleotide Interference with

TITLE OF INVENTION: Multidrug Resistance

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Jane Massey Licata

STREET: 210 Lake Diive East, Suite 201

CITY: Cherry Hill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 08002
COMPUTER READBLE FORM:
COMPUTER: BADDELE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: NORDERRECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,731
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/136,811
FILLING DATE: 10/18/93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/628,731
FILLING DATE: 04/16/96
ATTORNEY/AGENT INFORMATION:
NAME: JAHE MASSEY LICEAT
REFERENCE/DOCKET NUMBER: 1SPH-0208
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEPHONE: (609) 779-2400
TELEPHONE: (609) 779-2400
TELEPAX: (60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
FILING APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/136,811
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licate
NAME: Jane Massey Licate
NAME: Jane Massey Licate
NEGISTRATION NUMBER: 32,257
REFRENCE/DOCKET NUMBER: 1SPH-
TELECOMMUNICATION INFORMATION:
TELEFAX: (609) 779-2400
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5 GCCAGTTCCAGGCAGG 20
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STRANDEDNESS: Single
TOPOLOGY: Linear
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US-08-835-770-24

Sequence 24, Application US/08835770

Sequence 24, Application US/08835770

Sequence 24, Application US/08835770

SEQUENCE 26 SEQUENCE

APPLICANT: Edgardo Baracchini, Jr., C. Frank Bennett

APPLICANT: and Nicholas M. Dean

TITLE OF INVENTION: Resistance-Associated Protein

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIE: 08002
COMPUTER READLES FORM:
COMPUTER: DISKETTE, 3.5 INCH, 1.44 MD STORAGE
COMPUTER: IBM PS/2
COMPUTER: IBM PS/3
CURRENT APPLICATION DATA:
FILING DATE: Herewith
CLASSIFICATION SATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
COMPUTER: OSYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
PTILING DATE: Herewith
CLASSIFICATION: 514
                                                                                                      Oligonucleotide Interference with Multidrug Resistance
                                                                                        TITLE OF INVENTION: Oligonuclectide Interference TITLE OF INVENTION: Miltidrug Resistance NUMBER OF SEQUENCES: 25 CORRESPONDENE ADDRESS: ADDRESSEE: Law Offices of Jane Massey Licata STRET: 210 Lake Drive East, Suite 201 CITY: Cherry Hill STATE: USA COUNTRY: USA ZIP: 08002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORWATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REPERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEPHONE: (609) 779-2400
TELEPAK: (609) 779-2400
TELEPAK: 200 10 No: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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RESULT 14

US-09-275-680-7/c

i Sequence 7, Application US/09275680

patent No. 6221630

GENERAL INFORMATION:

APPLICANT: HOpper, James E

TITLE OF INVENTION: Regulated High-level Production of Polypeptides in

TITLE OF INVENTION: Yeast

PITLE OF INVENTION: Yeast

TITLE OF INVENTION: Yeast

PITLE OF INVENTION: US/09/275,680

CURRENT APPLICATION UNMER: US/09/275,680

CURRENT PAPLICATION UNMER: 1999-03-24

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.0

LENGTH: 17
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Patent No. 6030837

GENERAL INFORMATION:

APPLICANT: Robert McKay

APPLICANT: Lex M. Cowsert

TITLE OF INVENTION: ANTIENSE MODULATION OF PEPCK-MITOCHONDRIAL EXPRESSION

TITLE OF INVENTION: ANTIENSE MODULATION OF PEPCK-MITOCHONDRIAL EXPRESSION

TURENT APPLICATION NUMBER: US/09/366,257

CURRENT PILING DATE: 1999-08-03

NUMBER OF SEQ ID NOS: 47

LENGTH: 20
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                                                             Query Match 61.0%; Score 12.8; DB 1; Length 20; Best Local Similarity 75.0%; Pred. No. 2.8e+03; Matches 12; Conservative 2; Mismatches 2; Indels
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Best Local Similarity 76.5%; Pred. No. 5.6e+03;
Matches 13; Conservative 1; Mismatches 3; Indels
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; ORGANISM: Saccharomyces cerevisiae
US-09-275-680-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CAGUUCCCGACAGGCAC 19
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5 GCCAGTTCCAGGCAGG 20
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  Yes
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US-09-366-257-38/c
; ANTI-SENSE:
US-08-628-731-24
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August 18, 2005, 00:02:48; Search time 852 Seconds (without alignments) 8494.798 Million cell updates/sec
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| cgn2 6/ptodata/1/pubpna/USO7 PUBCOMB.seq:*
| cgn2 6/ptodata/1/pubpna/DCT_NEW_PUB.seq:*
| cgn2 6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| cgn2 6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| cgn2 6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| cgn2 6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## CTIMMADIES

			Description	Seguence 21, Appl	Sequence 2162, Ap	Sequence 178, App	Sequence 178, App	Sequence 161, App	Sequence 2, Appli	Sequence 148, App
SUMMARIES			ID	US-10-774-721-21	21 US-10-956-157-2162	US-09-925-302-178	US-09-925-302-178	US-10-115-831-161	US-09-993-756A-2	US-10-893-315-148
			 BB	21	21	ο.	10	11	10	22
			Match Length DB ID	:	1114					207542
	ф	Query	Match	100.0	100.0	99.8	8.66	96.7	78.1	69.0
			Score	1114	1114	1111.6	1111.6	1077	9.698	768.4
		Result	No.		8	٣	4	'n	9	7

Sequence 134, App Sequence 1, Appli Sequence 7397 Ap	73.5	46	Sequence 23, Appl Sequence 3. Appli	7	'n	41	41.	e 56,	82,	e 82,	82	8	82	55.	85	275	275	275	275	275	275	equence 275	equence 275,	equence 275,	275	275	275	275	275	275	275	275	275	Sequence 275, App
22 US-10-893-315-134 21 US-10-774-721-1 21 US-10-956-157-7397	2 US-10-893-315-733	9 US-10-283-975A	14 US-10-038-010-23 21 US-10-774-721-3	1 US-10-774	1 US-10	7 US-10-242-535A	8 US-10-085-783A-412	0 US-10-842-740-	US-09-984-245-	0 US-09-966-262	996-883-969	4 US-10-059-395	4 US-10-143-090	7 US-10-264-237	1 US-10-960-251	US-09-989-725-	US-09-989-723-	6-60-SD	US-09-989-727-	US-09-989-731-	US-09-989-732-	US-09-991-073-	US-09-990-442-	US-09-991-163-	-60-SD	-60-SN	-60-SD .	-60-SD	-60-SD	-60-SD	US-09-990-444-27	US-09-991-181-27	US-09-989-73	9 US-09-990-436-275
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## ALIGNMENTS

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RESULT 1
US-10-74-721-21
Sequence 21, Application US/10774721
Sequence 21, Application No. US2005009042A1
Sequence 21, Mapplication No. US2005009042A1
Sequence 21, Application No. US20050009042A1
SEQUENCE CONTRORMATION
SEQUENCE CONTROLLING NAME
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SEQUENCE CONTROLLING NAME
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SEQUENCE FRAV2003/0005 NO NO
TITLE OF INVENTION NAMES: US-10/774,721
CURRENT FILING DATE: 2004-02-04-07
SPRIOR APPLICATION NUMBER: 00/461,005
SPRIOR PILING DATE: 2003-04-07
SPRIOR FILING DATE: 2003-04-07
SPRIOR PILING DATE: 2003-04-07
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RESULT 2
US-10-956-157-2162
US-10-956-157-2162
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Patent No. US20020044941A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 178
LENGTH: 2732
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Pred. No. 2.2e-308;
2; Mismatches 1;
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NAME/KEY: misc feature

LOCATION: (1653)

OTHER INFORMATION: n equals a,t,g, or

NAME/KEY: misc feature

LOCATION: (2664)

OTHER INFORMATION: n equals a,t,g, or

NAME/KEY: misc feature

LOCATION: (2699)

COTHER INFORMATION: n equals a,t,g, or

US-09-925-302-178
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Best Local Similarity 99.7%;
Matches 1111; Conservative
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ORGANISM: Homo sapiens
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US-09-925-302-178
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98.4%; Pred. No. 1.2e-298;
:ive 0; Mismatches 0;
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Best Local Similarity 98.4
Matches 1105; Conservative
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ORGANISM: Homo sapiens
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, LOCATION: (95)
US-10-115-831-161
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             US-09-925-302-178
; Sequence 178, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REPERBNCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR PILING DATE: 2000-03-08
; PRIOR PILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOGTWARE: Patentin Ver. 2.0
; SEQ ID NO 1732
                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                           LOCATION: (2664)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (2699)
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NAME/KEY: misc feature
LOCATION: (1653)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (2664)
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Sequence 161, Application US/10115831

Publication No. US20030219743A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Branac, Radoje T.
TITLE OF INVENTION: No. US20030219743A1e1 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 792CTE2ADIV
CURRENT APPLICATION NUMBER: US/10/115,831
CURRENT FILING DATE: 2002-04-02
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 178

SOFFWARE: PL-Legenes Version 2.0

LENGTH: 1156
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1114 TAAACCACTTAACCTCTCTGGGTGTTACCTGCTCATTTGTTTA 1156
                                                                                          Sequence 2, Application US/09993756A
Publication No. US20030166847A1
GENERAL INFORMATION:
APPLICANT: Akerblom, Ingrid E.
TITLE OF INVENTION: A NOVEL HUMAN LEPTIN RECEPTOR
GENE-RELATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/993,756A
FILING DATE: 05-No. US20030166847A1-2001
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/212,153
FILING DATE: CURROWN>
APPLICATION NUMBER: US/08/843,370
FILING DATE: CURROWN>
APPLICATION NUMBER: US/08/843,370
FILING DATE: AUGUST 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0111-1 US
                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 874 base pairs
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STRANDEDNESS: single
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CLONE: 492703
                                                                                                                                                                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                 CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
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Best Local Similarity 99.4
Matches 869; Conservative
                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                             US-09-993-756A-2
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              GGGCAGGCTCCCGGGCCGTGCCAGGAAGCCGGAAAGCAGCGCCCCCAGTTCCGGAAA
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Sequence 134, Application US/10893315

Sequence 134, Application US/10893315

Sequence 134, Application No. US20050147987A1

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND TITLE OF INVENTION: USES THEREOF

FILE REPREBENCE: LO00786

CURRENT APPLICATION NUMBER: US/10/893,315

CURRENT PILING DATE: 2004-07-19

FRIOR PEPLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 2172

SOFTWARE: FASELSEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13625 TCCAGAATCTGAAGCCCCACTCTGGACCCAGGACATTTGATGAGATCCAAGGAGTTGT 13684
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                                     Gaps
Length 207542;
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                                     Indels
   22;
Score 768.4; DB 22
Pred. No. 1.5e-208;
0; Mismatches 6;
         69.0%;
99.2%;
           Query Match
Best Local Similarity 99.2
Matches 772; Conservative
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Sequence 148, Application US/10893315

Sequence 148, Application WS/10893315

Sequence No. US2005147987A1

PUBLICATION NO. US2005147987A1

APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. CLOOOPS

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

FILE REPRERENCE: CLOOOPS

CURRENT APPLICANTON NUMBER: 60/193, 315

CURRENT APPLICANTON NUMBER: 60/131, 397

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 2172

SOFTWARE FRANCE: PARKSEQ for Windows Version 4.0
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LOCATION: (1)...(207542)
CTHER INFORMATION: n = A,T,C or G
US-10-893-315-148
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ORGANISM: Human
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LENGTH: 207542
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APPLICANT: COUTURIER, Cyril
APPLICANT: UTLANNN, Eugen
TITLE OF INVENTION: Olignoclectides Which inhibit Expression of the OB-RGRP Protein
TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
CURRENT APPLICATION NUMBER: US/10/774,721
CURRENT FILING DATE: 2004-02-09
PRIOR FILING DATE: 2003-04-07
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                              Length 207557;
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                                                                                                                                                                                                                                                                         Score 768.4; DB 22
Pred. No. 1.5e-208;
0; Mismatches 6;
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                                                                                                                                    NAME/KEY: misc_feature

... LOCATION: (1)...(207557)

... OTHER INFORMATION: n = A,T,C

US-10-893-315-134
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.2%;
Matches 772; Conservative
                                                          TYPE: DNA
ORGANISM: Human
FEATURE:
SEQ ID NO 134
LENGTH: 207557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397
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, Sequence 7397, Application US/10956157 , Publication No. US20050118625A1
RESULT 10
US-10-956-157-7397
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Sequence 1, Application US/10774721; Publication No. US20550509042A1; GENERAL INFORMATION: APPLICANT: JOCKERS, Ralf

US-10-774-721-1

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GITCAIGIAGICACGGIGCICTCAGAAAIAIAITAACGCAGICIIGIAGGCAGCIGCCA 240
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                                                                                                                                                                                                 Length 601;
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                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                   Score 599.6; DB 22,
Pred. No. 1.7e-161;
1; Mismatches 0;
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| Publication No. US20040110792A1
| GENERAL INFORMATION:
| TITLE APPLICANT: Ortho-Clinical Diagnostics, Inc.
| TITLE REFERENCE: CDS 293 PCT
| CURRENT APPLICANTION: Methods For Assessing and Tre-
| FILE REFERENCE: CDS 293 PCT
| CURRENT FILING DATE: 2002-10-30
| PRIOR APPLICATION NUMBER: 60/340,938
| PRIOR FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 2172
SEQ TWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 733
LENGTH: 601
                                                                                                                                                                                                   53.8%;
                                                                                                                                                                                                   Query Match 53.8
Best Local Similarity 99.8
Matches 599; Conservative
                                                                                                                      ; TYPE: DNA
; ORGANISM: Human
US-10-893-315-733
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US-10-283-975A-466
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                    APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts,
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEDARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 600
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Sequence 733, Application US/10893315

FROMINICATION No. US20050147987A1

FRUDLICALON No. US20050147987A1

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHIES IN ENOWN GENES ASSOCIATED

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

FILE REPREBENCE: CLO007886

CURRENT APPLICATION NUMBER: US/10/893,315

CURRENT FILING DATE: 2004-07-19
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                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                        53.9%; Score 600; DB 21; L. ilarity 100.0%; Pred. No. 1.3e-161; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                ) ORGANISM: Homo sapiens
US-10-956-157-7397
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 600; Conserv
      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1055
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FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(396)
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LENGTH: 396
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                                                                                                                                                                                                                                                          352 CAAATGGGGAGCCTGCGGCCTTGTGTTGGCAGGCAATGCAGTCATTTTCCTTACAATTCA
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Publication No. US20030040089A1
GENERAL INFORMATION:
APPLICANT: HYBIGENICS
APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
FILE REPERENCE: B4767A
CURRENT APPLICATION NUMBER: US/10/038,010
CURRENT PILING DATE: 2002-07-23
FRIOR APPLICATION NUMBER: US 60/259,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCACTCTGGACCCAGGACA-TTTGATGAGATCC-AANGAGTTGTATGCNCAT
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                                                                                                                                                                                        51.8%; Score 577.4; DB 19; Length 647; 98.6%; Pred. No. 4.4e-155; ive 0; Mismatches 3; Indels 6;
                                                                                              FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(647)
OTHER INFORMATION: N=any base
US-10-283-975A-466
NUMBER OF SEQ ID NOS: 900
SOFTWARE: Patentin version 3.1
SEQ ID NO 466
LENGTH: 647
                                                                                                                                                                                                                          Matches 644; Conservative
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                                                                TYPE: DNA
ORGANISM: HUMAN
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US-10-038-010-23
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GENERAL INFORMATION:

APPLICANT: JOCKERS, Ralf
APPLICANT: COUTURIER, Cyril
APPLICANT: ULHMANN, Eugen
TITLE OF INVENTION: Oliquocoleotides Which inhibit Expression of the OB-RGRP Protein
TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
FILE REFERENCE: FRAVZO03/0005 US NP
CURRENT APPLICATION NUMBER: US/10/774,721
CURRENT FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: 00/461,005
PRIOR APPLICATION NUMBER: 00/461,005
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin version 3.1
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Best Local Similarity 100.0%; Pred. No. 5e-103;
Matches 396; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
LENGTH: 396
TYPE: DNA
ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: gene
LOCATION: (1)..(396)
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Gaps

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240 370

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Sequence 7, Application US/10774721

Sequence 7, Application US/205000942A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JOCKERS, Raif

APPLICANT: COUTURIER, Cyril
APPLICANT: UHLANIN, Eugen
TITLE OF INVENTION: Olignoclectides Which inhibit Expression of the OB-RGRP Frotein
TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
FILE REFERENCE: FRAV2003/0005 US NP
CURRENT FILING DATE: 2004-02-09
FRIOR PAPLICATION NUMBER: 60/461,005
FRIOR PLING DATE: 2003-04-07

PRIOR PLING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 47

SOFTWARE: Patentin version 3.1
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                                             DB 21; Length 396;
5e-103;
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                                               35.5%; Score 396; DB
100.0%; Pred. No. 5e-
ive 0; Mismatches
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NAME/KRY: misc_feature
OTHER INFORMATION: OB RGRP YFP
FEATURE:
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ORGANISM: Artificial Sequence
                                                             Best_Local Similarity 100.
Matches 396; Conservative
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US-10-774-721-7
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Best Local Similarity
       ; OTHER INFORMATION:
US-10-774-721-3
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LOCATION: (1)
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BD125686 Primer fo
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CQ860095 Sequence
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AJ01266 Sequence
BC0696366 Sequence
AJ01268 Mus muscu
AJ720495 Gallus ga
BC010289 Mus muscu
AK67728 Sequence
CR761280 Xenopus I
BC078594 Xenopus I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
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CR385373 Gallus ga
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCGGCAGACATGGCGGCGCTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG
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PB Corporation (NY) (US)
Location/Qualifiers
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CQ16942

    .1114
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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AF139209
CQ696366
AC108402
AC121826
AJ720495
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BC062003
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CR541737
CR541647
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AX677228
CR761280
BC053822
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Matches 1114;
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/db_xref="G1:53790911"
/translation="MAGVXALVALSFSGAIGLTFLMLGCALEDYGVYWPLFVLIFHAI
SPIPHFIAKKVTYNDSACRELAYFFTTGIVVSAFGFPVILARVAVIKWGACGLV
LAGNAVIFLTIQGFFLIFGRGDDFSWEQW"
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compounds for weight gain or loss or diabetes in human or animal
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (17-APR-1997) B.R.P. Bailleul, UPR 0415 CNRS, 22 Rue Mechain, 75014 Paris, FRANCE This is a splice variant from the leptin receptor locus but this variant encodes for a unrelated leptin receptor protein transcribed from one promoter of the leptin receptor locus.
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          PRI 09-SEP-2004
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
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1. ill14
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II14 bp mRNA linear
Homo sapiens mRNA for leptin receptor gene-related
Y12670
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The leptin receptor promoter controls expression
distinct protein
Nucleic Acids Res. 25 (14), 2752-2758 (1997)
97351143
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'gene="OB-RGRP"
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100.0%; Score 1114; DB 9;
Best Local Similarity 100.0%; Pred. No. 2.4e-290;
Matches 1114; Conservative 0; Mismatches 0;
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/number=3

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/gene="OB-RGRP"

/number=4
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Bailleul, B.R.P.
Direct Submission
Submitted (17-APR-1997)
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Homo sapiens
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JP 2002017375-A/3220
22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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ner for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
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1020 TCCTTATCTTTCCAGTGGCTAAACCACTTAACCTCTGGGTGTTACTGCTCGTTGTT
                                TCTCAGC-AATAGACCTGTCAAATTTAGATTATGTTACTCAAATTAAGTTACTCAGC-AATAGA
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                TCTCAGCAAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTATGTTACTTGTTTGG
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                                                                                                  CTGTTCATGTAGTCACGGTGCTCTCAGAAAATATATAACGCAGTCTTGTAGGCAGCTGC
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HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/3220
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASH:
PI SHII,
PI YIRI KAWAI, AI WAKAWATSU, TOMOYASU SUGIYAMA, KEIICHI NACHAMA
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JP 2002017375-A/3220.
Homo sapiens (human)
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SPIEHFIAXXVTXDSAACRELAYFFTTGIVVSAFGFPVILARVAVIKWGACGLV
LAGNAVIFLTIQGFFLIFGRGDDFSWEQW"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                            Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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                                                                                                                                                                              Koga, H.
Primers for synthesizing full length cDNA clones and their use
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                                                                                                                                                                                                            Patent: EP 1396543-A 3842 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
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Sequence 3842 from Patent EP1396543.
CQ783702
CQ783702.1 GI:45503609
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                                                              sapiens (human)
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Matches 1080; Conservative
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I sogai, T. and Otsuki, T.

Direct Submission

I sogai, T. and Otsuki, T.

Direct Submission

I sogai, T. and Otsuki, T.

Direct Submission

Genomics Laboratory; 1532-3 Yana, Kisarzau, Chiba 292-0812, Japan

Genomics Laboratory; 1532-3 Yana, Kisarzau, Chiba 292-0812, Japan

Genomics Laboratory; 1532-3 Yana, Kisarzau, Chiba 292-0812, Japan

Genomics Laboratory; 1532-3 Yana, Sara, Genomics Laboratory of NEDO human cDNA sequencing project supported by Ministry of Seconomy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Institute of Medical Science, University of Tokyo, Laboratory of Sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKO74841 1080 bp mRNA linear PRI 03-SEP-2002 Homo sapiens cDNA FLJ90360 fis, clone NT2RP2003664, highly similar to Homo sapiens mRNA for leptin receptor gene.
                                                                                                                                                                                                                                                                                                                                       Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T., Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y., Ninomiya, K., Nattori, A., Okumura, K., Iwayanagi, T. and Ninomiya, K.
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Catarrhini; Hominidae; Homo.
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/note="cloning vector: pME18SFL3-mRNA from NT2 neuronal
precursor cells after 2-weeks retinoic acid (RA)
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oligo capping; fis (full insert sequence).
Homo sapiens (human)
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/mol_type="mRNA"
/mol_type="mRNA"
/clone="wr2RP2003664"
/cell_line="NT2"
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Mammalia; Eutheria; Primates;
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                                                                                      DB 6; Length 1080;
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Pred. No. 3.6e-278;
0; Mismatches 0;

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    organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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181 TCGTCCTGATTTTCCACGCCATCTCCCCCATCCCCCATTTCATTGCCAAAAGAGTCACCT 241 ATGACTCAGATGCAAACAGTAGTGCCTGTCGGGAACTGGCATATTTCTTCACTGCTGAAA TIGHTHELLINCTGCCTTTGGATTNTCCTGTTATTCTTGCTCGTGTGGCTGTGAAT TITICCTTATATITITGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTTATTC GTCTGGCTTGGGCAGGCTGCCCGGGCCGTGGCAGGAAGCCGGAAGCAGCCGNGCCCCAN GTTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTG GACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGGATTATGGCGTTTACTGGCCCTTAT ATGACTCAGATGCAACCAGTAGTGCCTGTCGGGAACTGGCATATTTCTTCACTACTGGAA TTGTTGTTT-CTGCCTTTGGATT-TCCTGTTATTCTTGCTCGTGTGGCTGTGATC-AAAT GGGGAGCCTGCGGCCTTGTGTTGGCAGGCAATGCAGTCATTTTCCTTACAATTCAAGGGT CATITITACTATGAAATITAATATGCTGGGTTTTTTAATACCTTTATATATCATGTTCACT TTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTATTCTCAGCAAATAGACCTGTCAAAT TTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTATTCTCAGCAAATAGACCTGTCAAT TTAGATTATGTTACTCAAATTATGTTACTTGTTTGGCTGTTCATGTAGTCACGGGGCTCT GGGGAGCCTGCGGCCTTGTGTTGGCAGGCAATGCAGTCATTTTCCTTACAATTCAAGGGT TTTTCCTTATATTTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTTATTC 1 GTCTGGCTTGGGCAGGCTGCCCGGGCCGTGGCAGGAAGCCGGAAGCAGCCGCGCGCCCCCA-Gaps Schnittger, S. Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. Haferlach, T., Schoch, C., Kern, W., Kohlmann, A., Schnittger, Dugas, M., Eils, R., Brors, B. and Mergenthaler, S. Novel genetic markers for leukemias
Novel genetic markers for leukemias
Patent: WO 03039443-A 2116 15-MAY-2003;
Deutsches Krebsforschungszentrum (DE);
Ludwig-Maximilian-Universitaet Muenchen (DE);
Haferlach,
PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (I 4 6; Length 2388 Indels .. .. 95.8%; Score 1067; DB 6; 99.4%; Pred. No. 1.4e-277; attive 0; Mismatches 3; .2388
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 /mol\_type="unassigned DNA"
 /db\_xref="taxon:9606" 657 ò

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Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
CDNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gatthersburg, Maryland;
Sequencing Center (NISC),
Gatthersburg, Maryland;
Web site: http://www.nisc.nih.gov
Contact: nisc_msc@mhgri.nih.gov
Contact: nisc_msc@mhgri.nih.gov
Rkhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Cauan,X., Gupta,J., Haghighi,P.,
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Hansen,N., Ho,S.-L., Masher,M.S., Thomas,P.J., Touchman,J.W.,
McDowell,J., Pearson,R., Stanttripop,S., Thomas,P.J., Touchman,J.W.,
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Young,A., Zhang,L.-H. and Green,E.D.
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Spithfiakkvydbontssackelayffttgivvsafgffyilarvavikwgacgiv
LagnavifliqgfflifgrgddfsweQw"
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94.9%; Score 1057.6; DB 9
Best Local Similarity 99.6%; Pred. No. 4.4e-275;
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                                                                                                                                                                                                                                                                                                                                                                                                 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (11-AUG-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
                                                                                                                                                                                                                                     897 AGACCAAGAGCCTCAACATTTCCTAGGCCTTATTAGAAATGCAGAATCTGAAGCCCCAC 956
                                                                                                                                                                                                                                                                                                                          901 AGACCAAGAGCCTCAACATTTCCTAGAGCCTTATTAGAAATGCAGAATCTGAAGCCCCAC 960
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    (bases 1 to 1092)

                                                                                                                                         TTTTGCTTGGGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCAGGCCTCTCATGACCCA 836
                                                                                                                                                                1017 AGCATCATCATAGAGAAGTAAACATCACCCCAACTTCCTTATCTTTCCAGTGGCTAAAC
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                                  661 TTAGATTATGTTACTCAAATTATGTTACTTGTTTGGCTGTTCATGTAGTCACGGTGCTCT
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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KEYWORDS
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Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramon, R.D., Mullahy, S.J., Bosak, S.A., McBwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Sakalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 19 Row: o Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504978.

Location/Qualifiers
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/db_xref="LocusID:54776IVSAFGFPVILARVAVIKWGACGLVLAGNAVIFLIQGFFLIFGRGDDFSWEQW"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
On Sep 16, 2003 this sequence version replaced gi:15029639.
Contact: mGC help desk
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadanagesystemsbiology.org
contact: amadanagesystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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| Organism="Homo sapiens"
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| db xref="taxon:9606"
| clone="lMAGE:4296363"
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/gene="OBRGRP"
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Strausberg, R.
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1 (Bases 1 to 1056)
2 (Bases 1 to 1056)
3 (Rases 1 to 1056)
3 (Rases 1 to 1056)
3 (Rases 1 to 1056)
4 (Rases 1 to 1056)
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8 (Rase
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Homo sapiens leptin receptor gene-related protein, mRNA (CDNA clone
IMAGE:4296363), partial cds.
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                                                                                                                                                                                 AAGGGTTTTTCCTTATATTTGGAAGAGAGAGATATTTTAGCTGGGAGCAGTGGTAGCACT
                                                                                                                                                                                                                      AAGGGTTTTTCCTTATATTTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCCT
                                                                                                                                                                                                                                                                                                                      TTATTCTGATTACAGTGCATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCAC
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Pred. No. 3.5e-224;
3; Mismatches 2;
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3 1 (bases 1 to 874)
S Akerblom, I.E.
Human leptin receptor-related protein
AL Patent: US 5789138-A 2 04-AUG-1998;
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Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 2 from patent US 5789198.
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Best Local Similarity 99.4%;
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                                                                                         GCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGGACTTTTCTTATGCTGGGATGT
                                                              Gaps
                                              Length 1056;
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               eukaryotic cells"
                                                               Indels
                                               Score 1023.4; DB 9;
Pred. No. 8.1e-266;
0; Mismatches 1;
                  to the vacuole/lysosome of /db_xref="CDD:pfam04133"
                                                 91.9%;
nilarity 99.9%;
Conservative 0
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Best Local Simi
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	454	<800	677	<800	2017	2035
Center: University of Mabilington Center Center Code: UWGC	 	- 008>	3989	3959	1891	1878
		4117	4018	3959	6353	6156
Drafting Center: SC		- 0861	9627	9385	1594	1588
Center project name: chr-1 Center clone name: RP4-630A11 (sc0810)	-	12767	792	800	3180	3218
Sequencing vector: plasmid, 68% of reads		2561	2720	2682	727	<800
Sequencing vector: plasmad; 100/32; 32% of reads Chemistry: Dye-terminator ET; 25% of reads	1353	1330	2477	2477	1891	1878
Chemistry: Dye-terminator big bye; 75% or reads Assembly program: Phrapy version 0.990319		- 008>	2529	2477	6622	6531
Consensus quality: 161032 bases at least Q30 Consensus quality: 161073 bases at least Q30	3743	3611	3828	3959	855	869
Consensus quality: 16110/ DaBes at reast was Insert size: 161112; sum-of-contigs	2498	2561	3173	3194	451	<800
Company of Washington Company of Manager	7241	- 1727	267	<800	5443	5392
Overlapping Sequences: 5: Mapping in progress 5: mai1.430H10 (INWCT.scc702) AC097063, 50135-bp overlap	3987	3930	799	800	10983	10933
	2101	2063	884	899	655	<800
Sequence Quality Assessment: This entry has been annotated with sequence quality	4560	4497	1272	1247	3427	3402
eginmates Computed by the Filtap assembly programmed in manually edited bases have been reduced to quality zero.	1266	1225	4968	4959	430	<800
Quality levels above 40 are expected to make the control of 10,000 by.	3624	3611	1616	1588	1339	1318
Base-by-base quality values are not generally visible as part GenBank flat file format but are available as part	1719	1676	186	<800	3903	3862
of this entry's ASN.1 ille.	225	· 800	9748	9982	1055	1081
This sequence was finished as follows unless otherwise noted:  all regions were either double-stranded or sequenced with an		23955	5416	5448	7669	7660
alternate chemistry or covered by high quality data (1.e., Filed quality >= 30); an attempt was made to resolve all sequencing		9086	5849	5808	7048	7002
problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13	6234	6119	7584	7591	4279	4362
subclone; and the assembly was construct by restriction asser.	094	196	2653	2682	653	<800
Sequence Validation: This sequence has been validated by Multiple Complete Digest	78	<800	1506	1451	2761	2807
<pre>gerprinting. Comparison or the experi yments with sequence-predicted fragme</pre>	5563	5491	6899	6748	7140	7002
The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC.	4515	4497	799	800	95	<800
	3618	3611	10232	9982	15	<800
in the table. There are no significant remaining accompanion between the experimental and predicted values. Uniquely ordered	3628	3611	2996	3022	7722	7660
tragments are separated by dashed lines.  BCORI BglII	4092	4117	3925	3959	6160	6156
SeqDerMap FngrPrnt SeqDerMap FngrPrnt SeqDerMap FngrPrnt	5966	9806	911	899	1068	1081
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106 <800 5998 5808 1247 1212	240	<800	584	<800	3834	3862
3938 3930 5361 5256 4695 4701	4811	4810	2262	2262	1608	1588
4702 4497 9738 9982 3373 3402	3434	3396	234	<800	3928	3862

Oy 997 ATGCACATGAAAGTTTGAGAAGCATCATAGAAAGTAAACATCACACCCAACTTCCT 1056		AUTHORS SUGAROAS. and SUZURIA, X.  TITLE Direct Submission JOURNAL Submission JOURNAL Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, JOURNAL Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, JOURNAL Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratorry of Genome Structure, Human Genome (E-mail:flocknein-dental-46-16)  COMMENT (E-mail:flocknein-dental-46-16) REGOONWY, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Blotechhology (RAB); CDNA library CONSTRUCTION and S'- F-	Scrence, University or Toxyo, Laboratory or Genome Structure, numean Genome Center; 3'-end one pass sequencing; RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.  FEATURES  11614  /organism="Homo sapiens" /mol_type="mRNA" /db_xref="texon:9606" /clone="LNF07412" /clone="LNF07412" /clone="LNF07412" /clone Tibe="thbroblast" /clone Tibe="LNF07412" /clone Tibe="LNF07412" /clone Tibe="LNF07412"	ORIGIN  Query Match
3420 3396 9405 9385 9937 9892 2651 2682 9332 9221 15 6800 685 685 685 68000	ATURES  Location/Qualifiers  source  1161112  Query Match  69.0%; Score 768.4; DB 9; Length 161112;  Best Local Similarity 99.2%; Pred. No. 2.2e-196;  Matches 772; Conservative 0; Mismatches 6; Indels 0; Gaps  33.7 TCGTGTGGCTGTATCAAATGGGGAGCCTGCGGCCTTGTTGGCAGGCA	OY 397 TITCCTTACABLICAGGITTTICCTTAINTITGSAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	Qy         577 CTTTATATATCATCTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTATTCTC 636           Db         30225 CTTTATATATCATGTTCACTTTAAGAAGACTTCATAAGTAGGAGATGAGTTTTATTCTC 30284           Qy         637 AGCAAATAGACTGTCAAATTTAGATTATGTTACTCAAATTATGTTACTTGTTTGGCTGT 696           Db         30285 AGCAAATAGACTGTCAAATTTAGATTATGTTACTCAAATTATGTTACTTGTTTGGCTGT 30344           Qy         697 TCATGTAGTCACGGTGCTCTCAGAAATTAAGTTACTCAAATTATGTTACTTGTTTGGCTGC 756           Db         30345 TCATGTAGTCACGGTGCTCTCAGAAAATTAAACGCAGTCTTGTAGGCAGCTGCCACC 756           Db         30345 TCATGTAGTCACGGTGCTCTCAGAAAATATATAACGCAGCTTGTAGGCCACCC 30404	QY         757         TIATGCAGTGCATCTTTGCTTGGGGATGTTTGGAGAGATAACGCTGA 816           Db         30405         TIATGCAGTGCATCGAAACCTTTTGCTTGGGGATGCTTGGAGAGATAACGCTGA 30464           QY         817         AGCAGGCCTCTCATGACCCAGGAGGCCGGGGTGGATCCCTTTGTGTTGTAGTCCATG         876           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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Patent: WO 2004072293-A 1 26-AUG-2004;

Patent: WO 2004072293-A 1 26-AUG-2004;

Patent: Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)

Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                          CCTGTCAAATTTAGATTATGTTACTCAAATTATGTTACTTGTTTGGCTGTTCATGTAGTC
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Local Similarity 100.0%; Pred. No. 3.4e-164; es 648; Conservative 0; Mismatches 0;
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US-08-691-071-2
Sequence 2, Application US/08691071
SETTLE OF INVENTION: A NOVEL HUMAN LEPTIN TITLE OF INVENTION: RECEPTOR-RELATED PROTEIN TITLE OF INVENTION: RECEPTOR-RELATED PROTEIN CORRESPONDENCES. ADDRESSE: ADDRES
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Pred. No. 4.5e-270;
3; Mismatches 2;
                                             US-09-949-016-11777
US-09-949-016-16295
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COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: SYSTEM: DOS
SOFTWARE: FESTERO, Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,071
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0111 US
TELECOMMUNICATION INFORMATION:
TELEPAN: 415-85-055
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 874 base pairs
TYPE: NUCleic acid
STRANDEDNESS: single
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Matches 869; Conservative
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-839-709-1
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US-09-169-7451-3
US-09-169-74118-3
US-09-1049-7410-3
US-08-137-132-3
US-08-108-1031-3
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US-08-583-153A-3
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US-08-708-562-6
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US-08-708-562-6
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Pred. No. 4.5e-270;
3; Mismatches 2;
                        COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
CORREATING SYFERM: DOS
SOFTWARE: FRASEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/43,370
FILING DATE: Riched Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/691,071
FILING DATE: ANGURE 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REFERENCE/DOCKET NUMBER: PF-0111-1 US
REFERENCE/DOCKET NUMBER: PF-0111-1 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRANCE A15-85-0555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                         78.1%;
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                        LENGTH: 874 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 99.4
Matches 869; Conservative
                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
LIBRARY: HNT2NOT01
CLONE: 492703
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; Sequence 2, Application US/08843370
; Patent No. 2874535
; GENERAL INFORMATION:
    APPLICANT: Akerblom, Ingrid E.
    APPLICANT: Akerblom, Ingrid E.
    TITLE OF INVENTION: GENE-RELATED PROTEIN RECTITLE OF INVENTION: GENE-RELATED PROTEIN NUMBER OF SEQUENCES: 4
    CORRESPONDENCE ADDRESS: ADDRESSE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive STREET: 3174 Porter Drive STATE: CA COUNTRY: U.S.
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Oy 368 GGCCTTGTGTGGCAGGCAATGCAGTCATTTCCTTACAATTCAAGGGTTTTTCCTTATA 427	Partent No. 6607879    Partent No. 6607879   GENERAL INFORMATION:   APPLICANT: Cocks Benjamin G. APPLICANT: Susan G. Stuart   APPLICANT: Susan G. Stuart   TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE   TITLE OF INVENTION: EXPRESSION NUMBER OF SEQUENCES: 1508   CORRESPONDENCE ADDRESS: ADDRESSE: INCYTE PHARMACEUTICALS, INC.	CITY: PALO ALTO CITY: TALO ALTO CITY: TALO ALTO COUNTRY: USA ZIP: 94304 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Loughy disk COMPUTER: MATCH PEFECT 6.1 for Windows/MS-DOS 6.2 CORFWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CORFUTER: WORD PEFECT 6.1 for Windows/MS-DOS 6.2 CORFUTER: WORD DATE: APPLICATION NUMBER: FILING DATE: FILING DATE: CLASSIFICATION: ATTORNEY/AGENT INFORMATION: MAME: ZELLOWHUNDER: FALOOI US TELECOMMUTCATION NUMBER: PA-0001 US TELECOMMUTCATION INFORMATION: TELECOMMUTCATION INFORMATION: TELEFAK: (650) 845-4166	INFORMATION FOR SEC ID NO: 885:   SEQUENCE CHARACTERISTICS:   SEQUENCE CHARACTERISTICS:   ELNGTH: 3800 base pairs   TYPE: nucleic acid   STRANDEDNESS: single   TOPOLOGY: linear   INMEDIATE SOURCE:   LIBRAR: GENBANK   CLONE: g1135594   US-09-023-655-885   Ouery Match
Db   601   TPACTATGAAATTTAATATGCTGGGTTTTTTAATACCTTTATATATA	Db   721   AATATATAACCCAGTCTTGTAGCCACCTCTTAGCAGGCTCTTTT	RESULT 3 US-09-839-709-1 US-09-839-709-1 Sequence 1, Application US/09839709 Patent No. 6517489 Patent No. 6517489 GENERAL INFORMATION: APPLICANT: Miso, Yimin A	Ouery Match

132 ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGGATTATGG 173

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David B.
TITLE OF INVENTION: THE DIAGNOSIS AND METHODS FOR TITLE OF INVENTION: THE DIAGNOSIS AND TERATMENT OF BODY WEIGHT DISORDERS, TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 14.5%; Score 162; DB 3; Length 3871; Best Local Similarity 100.0%; Pred. No. 4.6e-41; Matches 162; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: DIBKACLE
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FeatSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NAME: US/09/069,781B
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/864,564
FILING DATE: 29-ARNIL-1996
APPLICATION NUMBER: US 08/708,123
PILING DATE: 28-MAY-1997
APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/59,485
FILING DATE: 28-APPL-1995
APPLICATION NUMBER: US 08/56,663
APPLICATION NUMBER: US 08/56,663
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: US 08/56,663
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/56,663
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/56,663
FILING DATE: 1-10-C-1995
APPLICATION NUMBER: US 08/56,663
FILING DATE: 1-195
APPLICATION NUMBER: US 08/56,663
FILING DATE: 1-196-1995
APPLICATION NUMBER: US 08/56,663
APPLICATION NUM
                                                          Sequence 3, Application US/09069781B
Patent No. 6287782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coding Sequence 194...3688
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , NAME/KEY:
, LOCATION:
US-09-069-781B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                       US-09-069-781B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ITCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGGCTATTGG 120
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                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tarteglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: Culpepper, Janice A.
APPLICANT: Culpepper, Janice A.
APPLICANT: Culpepper, Janice A.
APPLICANT: Culpepper, MODILATE BODY WEIGHT USING THE OB RECEPTOR UNMBER OF SEQUENCES: 44
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGGATTATGG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: FastSEQ for Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,455B
FILING DATE: 22-JAN-1996
PRIOR APPLICATION NUMBER: 08/591,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
APPLICATION NUMBER: 08/56,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/56,622
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/56,622
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/56,623
APPLICATION NUMBER: 08/56,6363
APPLICATION NUMBER: 08/56,6363
APPLICATION NUMBER: 08/56,6363
APPLICATION NUMBER: 08/56,6363
APPLICATION NUMBER: 08/560,633
APPLICATION NUMBER: 08/560,633
APPLICATION NUMBER: 08/560,633
APPLICATION NUMBER: 08/560,633
APPLICATION NUMBER: 38/5043
REGISTRATION NUMBER: 35,283
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                                               Sequence 3, Application US/08599455B Patent No. 5972621
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-8906
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAWE/KEY: Coding Sequence
; LOCATION: 194...3688
US-08-599-455B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3871 base pairs
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STRANDEDNESS: double
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
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STATE: MA
COUNTRY:
RESULT 5
US-08-599-455B-3
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Gaps

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GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Janice A.
APPLICANT: With a price A.
APPLICANT: WITH A.
APPLICA
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                                                                                                                                                                                                                                                                                                                                     Query Match
14.5%; Score 162; DB 3; Length 3871;
Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGGATTATGG 173
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MEDIUM TYPE: Diskette
COMPUTER IBM Compactible
OPERATING SYSTEM: Windows95
SOFTWARE: TEM COMPACTION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/864,564A
FILING DATE: 28-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/708,123
FILING DATE: 28-MAY-1996
APPLICATION NUMBER: 08/508,524
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/509,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/50,142
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/50,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/56,662
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/56,663
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: MEALELGIOHN, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 3, Application US/08864564A; Patent No. 6395498
                                                                                                                                                                       Coding Sequence 194...3688
                                    TOPOLOGY: unknown
MOLECULE TYPE: CDNA
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 02110-2804
STRANDEDNESS:
                                                                                                                                                              NAME/KEY:
; LOCATION:
US-09-137-132-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-864-564A-3
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Patent No. 6309563
Patent No. 63090563
Patent Information:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS: ADDRESSE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                           61 Trcgggagacarggcgggggrtraaagcrcrcgrggcattarccrrcagrgggggrartgg 120
                                                                                                                                                                                                                                                             72 TTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGGTTATTGG 131
                                    GTCTGGCTTGGGCAGGCTGCCCGGGCCGTGGCAGGAAGCCGGAAGCAGCCGCGCCCCCAG 60
                                                                                 12 GTCTGGCTTGGGCAGCTGCCCGGGCCGTGGCAGGAAGCCGGAAGCCGGAGCGGCGCCCCCAG 71
                                                                                                                                                                                                                                                                                                                                                                                  121 ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGGATTATGG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                        132 ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGGATTATGG 173
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STATE: MA
COUNTY: US
COUNTY: 105
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: Diskette Diskette COMPUTER: Diskette Diskette COMPUTER: Diskette Diskette COMPUTER: Diskette D
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TELECOMMINICATION: INFORMATION:
TELEPHONE: 617-542-5070
TELEFRAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3871 base pairs
TYPE: nuclei
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225 Franklin Street
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194...3688
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                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
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CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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US-08-708-123D-3
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Sequence 3, Application US/09094410

Sequence 3, Application US/09094410

GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tartaglia, Louis A.
APPLICANT: White, David W.
APPLICANT: White, David W.
TITLE OF INVENTION: THE DISCREPTOR AND METHODS FOR
TITLE OF INVENTION: THE DISCREPTOR AND CACHEXIA
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: SO
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TTCGGGAAGACATGGCGGGGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 120
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COMPUTER: TOTALO-2804
COMPUTER: READDABLE FORM:
MEDLIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM COMPUTER: US/09/094,410
APPLICATION NUMBER: US/09/094,410
FILING DATE: 09-JUN-1998
PRIOR APPLICATION NUMBER: 08/708,123
APPLICATION NUMBER: 08/599,455
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/593,153
FILING DATE: 28-DEC-1995
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0;
07334/019002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 Franklin Street
Boston
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-9906
                                                                              TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3871 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                         ; NAME/KEY: Coding Sequence; LOCATION: 194...3688
US-08-864-564A-3
                                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Bost
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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US-09-094-410-3
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Sequence 3, Application US/08708123D

Sequence 3, Application US/08708123D

Sequence 3, Application US/08708123D

GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Tepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson, P.C.
ADDRESSER: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TICGGGAGACAIGGCGGCGIIAAAGCICTCGIGGCAITAICCTICAGIGGGCIAITGG 120
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14.5%; Score 162; DB 3; Length 3871;
Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGGATTATGG 162
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OPERATING SYSTEM: Windows95
SOFTWARE: FastSEM for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/708,123D
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/56,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/56,622
APPLICATION NUMBER: 08/56,623
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/56,63
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,283
ATTORNES/DOCKET NUMBER: 35,283
TELECOMMUNICATION INFORMATION:
TELE
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61 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 120
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   COMPUTER: 1BM COMPUTER:
OPERATING SYSTEM:
SOFTWARE: FastSEQ Version 2.0
SOFTWARE: FastSEQ Version 2.0
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,153A
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/56,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/56,622
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/56,663
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/56,663
FILING DATE: 17-NOV-1995
APPLICATION NUMBER: 08/56,663
FILING DATE: 17-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 37,283
REFERENCE/DOCKET NUMBER: 37,383
REGERVER REGERVER REGER PROCESTION NUMBER: 37,383
REGERVER REGERVER 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 Franklin Street
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 162; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
US-08-583-153A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-570-142D-3
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Sequence 3, Application US/08583153A
Sequence 3, Application US/08583153A
Secont No. 656877
GENERAL INFORMATION:
APPLICANT: Tarper, Robert I.
APPLICANT: Tapper, Robert I.
APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: THE OF EXCEPTOR AND METHODS FOR THE
TITLE OF INVENTION: OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 GTCTGGCTTGGGCAGGCTGCCCGGGCGTGGCAGGAAGCCGGAAGCAGCCGCGGCGCCCCAG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 14.5%; Score 162; DB 4; Best Local Similarity 100.0%; Pred. No. 4.6e-41. Matches 162; Conservative 0; Mismatches 0
            PRILING DATE: 26-APR-1996

APPLICATION NUMBER: 08/599,455

FILING DATE: 22-JAN-1996

APPLICATION NUMBER: 08/599,455

FILING DATE: 22-JAN-1996

APPLICATION NUMBER: 08/570,142

FILING DATE: 1-DEC-1995

APPLICATION NUMBER: 08/569,485

FILING DATE: 08-DEC-1995

APPLICATION NUMBER: 08/56,622

FILING DATE: 04-DEC-1995

APPLICATION NUMBER: 08/56,622

FILING DATE: 04-DEC-1995

APPLICATION NUMBER: 08/56,622

FILING DATE: 27-NOV-1995

APPLICATION NUMBER: 08/56,633

FILING DATE: 27-NOV-1995

APPLICATION NUMBER: 08/56,633

FILING DATE: 27-NOV-1995

ATCRAWGE PROCNET NUMBER: 07334/01901

TELEFRAN: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coding Sequence 194...3688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 3871 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boston
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US-08-708-123D-3
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Sequence 12, Application US/09043816E

Sequence 12, Application US/09043816E

Patent No. 6414128

GENERAL INFORMATION:
APPLICANT: Hilton, Douglas J.
APPLICANT: Hilton, Tracy
APPLICANT: Aicla, Nicola, Timothy
APPLICANT: Alexander, Warren S.
APPLICANT: Alexander, Warren S.
APPLICANT: Alexander, Warren S.
APPLICANT: NG. Abhley
APPLICANT: NG. Ashley
APPLICANTON: A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
TITLE OF INVENTION: BNCODING SAME
FILE REFERENCE: 11268
CURRENT APPLICATION NUMBER: US/09/043,816E

CURRENT FILING DATE: 1998-09-17
NUMBER OF SEQ. ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 Tregggagacareacegegegegerriaangereregegegarranteerregegegegrafieg 120
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Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGGATTATGG 162
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          SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 0734/018001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                CURRENT APPLICATION DUMBER: US/08/638,524B
PILING DATE: 26-APR-1996
PRIOR APPLICATION DATE: 36-APR-1996
PRIOR APPLICATION DATE: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/570,142
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/56,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/56,622
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/56,622
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/56,63
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION: NAME: Medikajohn, Ph.D., Amita L. NAME: M. NAME: MAMITANAME MEDIKAME MEDIKAME MEDIKAME MAMITANAME MEDIKAME MEDIKAME MEDIKAME MAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Coding Sequence LOCATION: 194...3688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3871 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
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US-08-638-524B-3
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Sequence 3, Application US/08638524B

Sequence 3, Application US/08638524B

Barent No. 6548620.

APPLICANT: Tartaglia, Louis A.
APPLICANT: Culpepper, Janice A.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
TITLE OF INVENTION: CACHEXIA

NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
SORRESPONDENCE ADDRESS:
STREET: 225 Franklin Street
CITY: Boston
CITY: Boston
CITY: Boston
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TICGGGAGACAIGGCGGCGTIAAAGCTCTCGIGGCATTATCCTTCAGTGGGGCTATTGG 120
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14.5%; Score 162; DB 4; Length 3871;
Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGGATTATGG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,142D
FILING DATE: 11-DEC-1995
PRIOR APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/56,622
APPLICATION NUMBER: 08/56,622
APPLICATION NUMBER: 08/56,63
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: 08/52,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph. D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 35,283
TELEPHONE: 617-542-5070
TELEPHONE: 617-542-5070
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LOCATION: 194...3688
US-08-570-142D-3
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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US-08-638-524B-3
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9.8%; Score 109.4; DB 3; Length 3909;
Best Local Similarity 91.9%; Pred. No. 4.6e-24;
Matches 113; Conservative 1; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,562
FILING DATE:
CLASSIFICATION A135
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/
FILING DATE: 10/08/97
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M:
REGISTRATION NUMBER: 40,378
REGISTRATION NUMBER: 40,378
REGISTRATION NUMBER: 40,378
TELEPHONE: 415/225-1994
TELEPHONE: 415/225-1994
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Patent No. 6541604
GENERAL INFORMATION:
APPLICANT: Matthews, William
APPLICANT: Bennett, Brian
TITLE OF INVENTION: WSX RECEPTOR
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Prancisco
STRATE: California
COUNTRY: USA
                                                                                                                                      NAME/KEY: unsure
LOCATION: (27)..(68)
OTHER INFORMATION: N is a or g or c or NAME/KEY: unsure
LOCATION: (923)
OTHER INFORMATION: R is g or a
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, OTHER INFORMATION: S is g or c
US-09-043-816E-12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 3909
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ORGANISM: Homo sapiens
PEATURE:
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Search completed: August 18, 2005, 02:55:48
Job time : 236 secs

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Best Local Similarity
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AL709147
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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seq length: 200000000
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Perfect score:
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A1621226 te77a12.x BG170089 602321555 BG564619 602522912 CB990288 AGENCOURT CN480866 UI.H-FT2- CD364970 UI-H-FT2- BE614746 601280203 BI548174 601280203 BI552957 UI-H-FT2- BG166519 UI-H-FT2- BG1652957 UI-H-FT2- BG1652917 UI-H-FT2- BG1652917 UI-H-FT2- BG252917 UI-H-FT2- CA99961 UI-H-FT2- CA99961 UI-H-FT2- CA99961 UI-H-FT2- CA99961 UI-H-FT2- BM549961 UI-H-FT2- BM549961 UI-H-FT2- BM549961 UI-H-FT2- CA99961 UI-H-FT2- BM549961 UI-H-FT2- BM549961 UI-H-FT2- BM549961 UI-H-FT2- BM549961 UI-H-FT2- CA99961 UI-H-FT2- BM549961 UI-H-FT2- BM549961 UI-H-FT2- CA99961 UI-H-FT2- BM549961 UI-H-FT2- CA99961 UI-H-FT2- BM549961 UI-H-FT2-	BX462364 BX362364 BX36264 BX3	.2; DB 5; Length 1040; 7.6e-242;
A1621226 BG170089 CB504619 CB504619 CCD564970 BE51474 CB529627 BG166941 CB529627 BG166941 CB529627 BG166941 CB529627 CB529637 CB529637 CB529637 CB529637 BM549405 BM549405 BM549405 BM549405 BM549405 BM549405 BM549405 BM549405 BM549405 BM549405 BM549405 BM549405 BM549405 BM549405 BM549405 BM549405 BM5590500	BX462364  BX462364  BX462364  BX462364  BX462364  BX462364.2 GI:47065982  BX462364.2 GI:47065982  BX162364.2 GI:4001  DX17 BX162364.2 GI:47065982  BX1623646.2 GI:47065982  BX1623646.2 GI:4706796882  BX1623646.2 GI:47065982  BX1623646.2 GI:47065982  BX1623646.2 GI:4706796882  BX1623646.2 GI:4706796882  BX1623646.2 GI:4706796882  BX1623646.2 GI:4706796882  BX1623646.2 GI:4706796882  BX1623646.2 GI:4706882  BX1623646.2 GI:470682  BX1623666.2 GI	Score 917.2, Pred. No. 7
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0 00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1  BX462364  LOCUS  DEFINITION  ACCESSION  VERYWORDS  SOURCE  AUTHORS  TITLE  JOURNALL  COMMENT  FEATURES  SOURCE  SOURCE  ONLIGIN	Query Match Best Local

AL550884 AL650884 I050 bp mRNA linear EST 25-MAR-2004 DEFINITION AL550884 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0D1065YP15 5-PRIME, mRNA sequence. AL550884.3 GI:45751247 AL550884.3 GI:45751247 KEYWORDS EST. Homo sapiens (human) NGANISM HOMO sapiens	SS	ORIGIN  Query Match  B1.1%; Score 903.4; DB 1; Length 1050;  Best Local Similarity 95.8%; Pred. No. 58-238;  Matches 963; Conservative 6; Mismatches 32; Indels 4; Gaps 4;  CGGGGCCCAGTTCGGGAGACATCGCGGGCGTTAAAGCTCTCGTGCATTATCCTTCAGT 109  CGCGCCCCAGTTCGGGAGACATCGCGGGCGTTAAAGCTCTTGTGGCATTATCCTTCAGT 60  Db 1 CGCGCCCCAGCTCGGGAGACATCGCGGGCGTTAAAGCTCTTGTGGCATTATCCTTCAGT 60  Oy 110 GGGGCTATTGGACTGACTTTTTTTATGCTGGGATTATGCGCATTATCCTTCAGT 120  CO 110 GGGGCTTATTGACTGCTGGCGGGCGTTAAGAGGATTATGGCGTTTAC 169  Oy 170 TGGCCCTTATTGACTGCTGCATTTTCTTATGCTGCCAAA 180  Db 121 TGGCCCTTATTCGTCCTAATTTCCAGCCCATTCCCCCATTCATT	
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/mol_type="mRNA"

/db xref="texon:9606"
/clone="CSODIO72YL004"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
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sites of the pCMVSPORT 6 vector. Library was normalized."
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Z rue Gaston Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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AL552981.3 GI:45857751
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1. (bases 1 to 1026)
1. (Jases 1 to 1026)
1. (Jases 1 to 1026)
1. (Pall-length Chubr, C., Jessee, J. and Polayes, D.
Full-length CDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31274795.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITATICTGATTACAGTGCATTGAATTTCTTAGAACTCATACTATCTGTATACAGGCA
                                                                                        GTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTTATTCTCAGCAAATAGACCT
                                                                                                                                                                                                 GTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTATTCTCAGCAAATAGACCT
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957

LOCUS DEFINITION

RESULT 3 ALS52981

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

899

950

190 AAGAGTCACCTATGACTCAGATGCAACCAGTAGTGCCTGTCGGGAACTGGCATATTTCTT 249 289 CACTACTGGAATTGTTTCTGCCTTTGGATTTCCTGTTATTCTTGCTGTGTGGTGT 348 250 CACTACTGGAATTGTTTTTTGTGTTTTCTGGATTTCTTGCTTTTTTTT	409 TCAAGGGTTTTTCCTTATTTGGAAGAGATGATTTTAGCTGGGAGCAGTGGTAGCA 468 370 TCAAGGGTTTTTCCTTATTTGGAAGAGAGATGATTTTTAGCTGGGAGCAGTGGTAGCA 429 469 CTTTATTCTGATTACAGTGCATTGAATTTCTTAGAACTCATACTTGTGTATACAGTGTGGTAGA 430 CTTTATTCTGATTACAGTGCATTGAATTTCTTAGAACTCATACTGTATACAGTGTGG 528 430 CTTTATTCTGATTACAGTGCATTGAATTTATAATACTCATACTGTATACTGTGGC 489 529 ACATGCGGCATTTTACTATGAAATTTAATAATGCTGGGTTTTTTAATAATACTGTATAACAGTGGGAATAAATA	709 670 769 729 889 8848 848	B-FRIME, mRNA sequence.  ESTON BX417586.2 GI:46927707 BX417586.2 GI:46927707 BX417586.2 GI:46927707 BX417586.2 GI:46927707 BX417586.2 GI:46927707 BX417586.2 GI:46927707 BXA17586.2 GI:46927707 BXA17586.2 GI:46927707 BYONED BYON
8888	8 8 8 8 8 8 8 8	QY Db OY OY OY OY OY Db OY Db CY	ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT
850 TGTGGCCCACAGAACAAGAGCCTCCACATTTCCTAGAGSCTTATTWGAAATGCAKGATCT 909 947 GAAGCCCCACTCTGGACCTCAGGACATTTTGATGAGATCCAAAGGACTTGTATGCACATGA 1006	RESULT 4  BX417049  LOCUS  BX417049  BX417049	Contact: Generators  Contact: Generators  Contact: Generators  2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  Email: seqrefeGenoscope.cns.fr, Web : www.genescope.cns.fr  Email: seqrefeGenoscope.cns.fr, Web : www.genescope.cns.fr  Int the the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  was not normalized. Library was constructed by Life Technologies, a  division of Invitrogen.  This sequence belongs to sequence cluster; see  http://www.genoscope.cns.fr/cdna?s=CSODE003CE12QP1&c=384.f.  FEATURES  Location/Qualifiers  Location/Qualifiers    Organism="Homo sapiens"     Ab xref="texton:8606"     Cilone   Tib="texton:8606"     Cilone   Tib="texton:PCMVRTA"     Cilone   Tib="texton:8606"     Cilone   Tib="texton:PCMVRTA"     Cilone   Tib="texton:8606"     Cilone   Tib="texton:8606"     Cilone   Tib="texton:PCMVRTA"     Cilone   Tib="texton:PCMVRT	

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 786)

2. Li, W.B., Guber, C., Jessee, J. and Polayes, D.

1. Full-length cDNA libraries and normalization

2. In Thoublished (2001)

3. On Feb 16, 2001 this sequence version replaced gi:31292526.

3. The Gaston Cremicux, CP 5706 - 91057 ENRY cedex - FRANCE

Email: seqref@genoscope.cna.fr. Web: www.genoscope.cna.fr.

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and Econ V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                          EST 05-APR-2004
                                        o mRNA linear EST 05-APR-2004
COT 25-NORMALIZED Homo Bapiens cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                   TTGTAGTCCATGCTATTAAAAGTGTGGCCCACAGAGCCAAGAGCCTCAACATTTCCTAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CSODIO27AF09QP1&c=384.f.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.4%; Score 784.4; DB 1;
99.9%; Pred. No. 3.5e-205;
tive 0; Mismatches 1;
                                                                                                                                                                                                                        AL571122 Homo sapiens PLACENTA COT 25-NORW
AL571122 Homo sapiens PLACENTA COT 25-NORW
Clone CSODI027KK17 5-PRIME, mRNA sequence.
AL571122
                                                                                           CCTTATTAGAAATGCAGAATCTGAAGCCCCACT 957
                                                                                                                            -criariadaargcadarcrdaagcccacrcr 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI027YK17"
                                                                                                                                                                                                                                                                                              AL571122.3 GI:46237227
EST.
                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                     RESULT 6
AL571122
LOCUS
DEFINITION
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AUTHORS
TITLE
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COMMENT
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KEYWORDS
SOURCE
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                                                                                                         /mol_type="mRNA"
//mol_type="mRNA"
//mol_type="texon:9606"
/clone="CSODE010YLO3"
//tissue_type="PLACENTA"
//tissue_type="PLACENTA"
//tissue_type="PLACENTA"
//tissue_type="PLACENTA"
//note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, with a NotI-oligo(dT) primer. Five prime end enriched, the Not I and ECORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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This sequence belongs to sequence cluster 384.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODE010CF02QP1&c=384.f.
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                                                                                                                                                                                                                                                                                                                                     Length 1004;
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71.0%; Score 790.6; DB 5;
al Similarity 97.1%; Pred. No. 7.1e-207;
848; Conservative 0; Mismatches 19;
                                                                                           organism="Homo sapiens"
                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches 84
                                                      PEATURES
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BOKFZD686B1965_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZD686B1965_5', mRNA sequence.
AL709947.1 GI:19693302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No sl sequence
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 805)
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                                                                                                                                                                                                                                                                                                            CCTTATGCAGGGATCGAAACCTTTTGCTTGGGGATGTGCTTGGAGAGGCAGATAACGCT
                                                                                   CTGTATACATGTGCACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTTAAT
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Contact: MIPS
MIPS
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Site_1: SfiIA; Site_2: SfiIB;
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                                                                                                                                                                      Indels
                                                                                                                                          Score 776.8; DB 1;
Pred. No. 4.4e-203;
0; Mismatches 2;
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|dow_stage="adult"
|lab_host="DH108"
|clone_lib="686 (synonym: hl
/note="Vector: priplEx2; si
cbNA-collection"
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BUNDENISS 11-AUG-2002 AGENCOURT 10029380 NIH_MGC_40 Homo sapiens CDNA clone IMAGE:6482247 S', mRNA sequence.
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/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 40"
/note="Organ: prostate; Vector: pOTB7; Site_1: Xho1;
Site_2: EcoR1; DONA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis Xit (Stratagene) and Superscript II RT (Life Technologies).
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S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2664 row: o column: 16
High quality sequence stop: 591.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                       435 CCTTATATTTGGAAGAAGAGAGATGATTTTTAGCTGGGGAGCAGTGGTAGCACTTTATTCTGAT
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                           CCTTATATTTTGGAAGAGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTTATTCTGAT
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6482247"
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                           EST 23-APR-2004
                         o mRNA linear EST 23-APR-2004
COT 25-NORMALIZED Homo sapiens cDNA
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                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 811)
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/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                                                                                                                                 Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length CDNA libraries and normalization Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30439226.
Contact: Genoscope
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                      BX378815 . BX378815 Homo Bapiens PLACENTA COT 25-NORMZ CIONE CS0D1026YOLS 5-PRIME, MRNA BEQUENCE.
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Pred. No. 1.4e-202;
1; Mismatches 6;
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/ organism="Homo sapiens"
/mol_type="mkNa"
/db_xref="taxon:9606"
/clone="ImAdSs:6188548"
/tissue_type="melanotic melanoma"
/lab_host="bH10B (phage-resistant)"
/clone=lib="NHH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: Not1;
/note="Organ: skin; Vector: pCMV-spoRT6; Site 1: Not1;
/wherage insert size 2 kb. Library constructed by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ACTGGGGCTATTGGACTGTTTTCTTATGCTGGGATGTGCCTTAGAGGATTATGGCGTT 120
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                                                  E 1 (bases 1 to 914)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDN Library Preparation: Life Technologies, Inc.

CDN Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LibM13512 row: d column: 21

High quality sequence stop: 678.
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TACTGGCCCTTATTCGTCCTGATTTTCCACGCCATCTCCCCCATCCCCCATTTCATTGC
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                                                                                    Indels
 is a NIH MGC Library."
                                                69.3%; Score 771.6; DB 5;
larity 98.4%; Pred. No. 1.3e-201;
Conservative 0; Mismatches 9;
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CF594097 835 bp mRNA linear EST 26-SEP-2003
AGENCOURT 15624279 NIH MGC_147 Homo sapiens CDNA clone
IMAGE:30528070 5', mRNA sequence.
GCCTTAGAGGATTATGGCGTTTACTGGCCCTTATTCGTCCTGATTTTCCACGCCATCTCC 130
                                                                                                                                                                                                                                                                                 311 AATGCAGTCATTTTCCTTACAATTCAAGGGTTTTTCCTTATATTTGGAAGAGGAGATGAT 370
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (base) 1 to 835)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Onpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda. MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
                                 251 GTTATTCTTGCTCGTGTGGGTGTGTGTATCAAATGGGGAGCCTGCGGGCCTTGTGTTTGGCAGGC
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NH1 MGC 72"
/note="Togan: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
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I (bases 1 to 899)
NH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                     CCTGTCAAATTTAGATTATGTTACTCAAATTATGTTACTTGTTTGCCTGTTCATGTGAGTC
                                                                                                                                           ACGGTGCTCTCAGAAAATATATTAACGCAGTCTTGTAGGCAGCTGCCACCTTATGCAGTG
                                                                                                                                                                                                                                   CATCGAAACTTTGGCCTTGGGGATGTGCTTTGGAGAGGCAGATAACGCTGAAGCANGCCT
                    CATGLICACTITAAGAAAGACTICATAAGTAGGAGATGAGGTTTTATTCICAGCAAATAGA
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13505 row. b column: 20
High quality sequence stop: 638.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6158131"
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/organism="Homo sapiens"
/mol type="mRNA"
/dol type="mRNA"
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/tissue_type="Human Placenta"
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/lone lib="NIH MGC_147"
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/rTTTTTTTTTTTTTTTTTTTTVTV-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci,
preparation). Library constructed by M. Brownstein
(NIMM/NHGRI, Netional Institutes of Health). Note: This is
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  Brownstein (NHGRI) with help
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cDNA Library Preparation: Michael J. Brownstein (NHGRI) wit:
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.AG.B. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
plate: NDAMG13 row: g column: 23
High quality sequence stop: 589.
High quality sequence stop: 589.
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llarity 98.9%; Pred. No. 2.2e-199;
Conservative 0; Mismatches 6;
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St Mil-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Ontact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: NDCM154 row: o column: 14

High quality sequence stop: 577.

High quality sequence stop: 577.
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AGENCOURT_13666636 NIH_MGC_184 Homo sapiens CDNA clone
IMAGE:30353725 5', mRNA sequence.
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98.7%; Pred. No. 6.6e-195;
iive 0; Mismatches 8;
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Search completed: August 18, 2005, 02:51:55 Job time : 4261 secs
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DKFZp686G13116 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp68GG13116 5', mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 739)
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
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No s1 sequence available.

No s1 sequence available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin. Charlottenburg, GERMANY; Email: clone@rzpd.de.
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Site_1: SfiIA; Site_2: SfiIB;
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/note="Vector: pTriplEx2;
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/organism="Homo sapiens"
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/dev stage="adult"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Unpublished (1999)
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Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2005
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- nucleic search, using sw model OM nucleic

August 17, 2005, 15:40:42; Search time 700 Seconds (without alignments) 9420.845 Million cell updates/sec Run on:

US-10-774-721-21 Title: Perfect score: Sequence:

1 gtctggcttgggcaggctgc......gttacctgctcatttgttta 1114

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

Total number of hits satisfying chosen parameters:

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length: 0 length: 2000000000 seg seg 80 080 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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## SUMMARIES

D Description	ADR27672 Adr27672 Leptin re	ADT71341 Human OB-		AK94760 Auman ful	ADL31809 Full len	ADF81560 Leukaemia	AS81135 AAS81135 DNA encod	AAV17683 CDNA enco	ADR27652 Leptin re			ADL29733 5' end of	ADL28325 5'	ADE85249 Ade85249 Farnesyl	4	ADL29084 3' end of	ABS51017 Abs51017 Human cDN	ADR27654 Human lep	ADR27658 OB-RGRP	י ממנת מני למלבניבלא
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& Query Match	100.0	100.0	8.66	96.0	96.0	95.8	81.6	78.1	58.2	52.8	52.8	52.8	52.8	51.8	44.7	44.7	35.5	35.5	35.3	200
Score	1114	1114	1111.6	1069	1069	1067	909.2	869.6	648	588.4	588.4	588.4	588.4	577.4	498.4	498.4	396	396	393	000
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## ALIGNMENTS

Leptin receptor related protein, OB-RGRP, nucleotide sequence, SEQ ID 21. Osteopathic, Anorectic, Antidiabetic, Cytostatic, Antiinflammatory; BP. ADR27672 standard; DNA; 1114 (first entry) 04-NOV-2004 human; ds. ADR27672; RESULT 1 ADR2767 

Immunomodulatory; Anabolic; Endocrine; Antianemic; Antianglogenic; Imptin receptor related protein; OB-RGRP; leptin receptor; leptin related disorders; steoporosis; calcification; obesity; diabetes; anorexia; sexual maturity disorder; haematopolesis; anglogenesis; thrombus formation; immunity; inflammation; fetal development; cancer;

Homo sapiens

FR2850971-A1.

13-AUG-2004.

10-FEB-2003; 2003FR-00001543.

10-FEB-2003; 2003FR-00001543

(AVET ) AVENTIS PHARMA SA. (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

Uhlmann E; Couturier C, Jockers R,

WPI; 2004-595751/58.

New oligonucleotides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and angiogenesis

Claim 12; SEQ ID NO 21; 104pp; French.

The present invention relates to a leptin receptor related protein (OB-

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CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises specifically with and inhibits the expression of ADR27652. The ON promotes expression of leptin receptors on the cell surface and may contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a criethyleneglycol residue at the 3'-end. Also claimed are interfering RNA triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA (iRNA) of 15-2s nt that hybridize specifically with ABR27672, and inhibit cc expression of OB-RGRP. Also claimed are fusion proteins (FPS) and their coding sequences comprising OB-RGRP or MY047 (thought to be a member of coding sequences comprising OB-RGRP or MY047 (thought to be a member of the OB-RGRP family, shares 68* homology with OB-RGRP), and a protein that cod a detecting compounds that modify the interaction between correct leptin receptor and OB-RGRP proteins, which can be used to prevent or treat leptin-related disorders. On also related interfering RNA, are used for prevention and/or treatment of leptin-related disorders, e.g. osteoporosis (or other conditions involving reduced bone density, and calcification; obesity; diabetes; anorexia; disorders of sexual maturity, and inflammation, fetal development and cancer.
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1020 1080 1080 are 960 840 840 900 900 960 Antidiabetic; anorectic; weight loss; weight gain; diabetes; LEPROTL1; leptin receptor overlapping transcript-like 1; OB-RGRP; leptin receptor gene related protein; intracellular transport; obesity; human; gene; ds. The invention relates to a method for identifying compounds (I) that TCAICATAGAGAAGTAAACATCACACCCAACTTCCTTTCCAGTGGCTAAACCACT CAAGAGCCTCAACATTTCCTAGAGCCTTATTAGAAATGCAGAATCTGAAGCCCCACTCTG GGCCGGGGTGGATCCCTTTGTGTTGTAGTCCATGCTATTAAAAGTGTGGCCCACAGAC GACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGAAAGTTTTGAGAAGCA GCTTGGGGATGTGCTTGGAGGCAGATAACGCTGAAGCAGGCCTCTCATGACCCAGGAA GGCCGGGGTGGATCCCTCTTTGTGTTGTAGTCCATGCTATTAAAAGTGTGGCCCACAGAC AAAIAIIAITAACGCAGTCTTGTAGGCAGCTGCCACCTTATGCAGTGCATCGAAACCTTTT of of Identifying compounds useful for treating loss or gain of weight diabetes, from their ability to modulate expression or transport proteins related to the leptin receptor. TAACCTCTCTGGGTGTTACCTGCTCAITTGTTTA 1114 ŝ Belouzard Disclosure; SEQ ID NO 4; 38pp; French. seg id 4. Location/Qualifiers 71. .466 /\*tag= a /product= "OB-RGRP" Seron K, BP. (CNRS ) CNRS CENT NAT RECH SCI 10-MAR-2003; 2003FR-00002931. 10-MAR-2003; 2003FR-00002931. Human OB-RGRP gene sequence, ADT71341 standard; DNA; 1114 (first entry) Υ, Rouille WPI; 2004-671009/66. P-PSDB; ADT71342. FR2852397-A1 Bailleul B, sapiens 17-SEP-2004. 16-DEC-2004 ADT71341; 1081 841 ( 841 961 961 1021 901 721 781 Ношо RESULT 2 ADT71341

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active against loss or gain of weight or diabetes in humans or animals. The method comprises measuring the effect of a test compound on the expression of at least one of the genes LEPROTIA (leptin receptor overlapping transcript-like 1) or OB-RGRP (leptin receptor gene related protein). Alternatively the method comprises measuring the effect of the compound on intracellular transport as far as the cell membrane (CM), the presence at CM, and internalisation from the membrane of proteins (X) encoded by the specified genes, or parts of them. Compounds of the invention are used to treat or prevent obesity, weight loss and diabetes. The current sequence represents the human OB-RGRP gene sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardioactive; immunomodulatory; muscular active; vulnerary; agastrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer.
                                                                                                     CAAGAGCCTCAACATTTCCTAGAGCCTTATTAGAAATGCAGAATCTGAAGCCCCACTCTG
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cardiovascular, renal, and proliferative disorders. The proteins m be used in the treatment of wounds and infections diseases. Solymucleotide sequences AAF18425 - AAF18433 and peptide AAB585499 used in the course of the invention for the identification and characterisation of the polymucleotide and protein sequences
                                                         Length 2732;
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                                           Sequence 2732 BP; 777 A; 516 C; 546 G; 887 T; 0 U; 6 Other;
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful length clones were obtained by construction of full length enriched cDNA length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers inhabet the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
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K, Kojima S, Otsuki T, Koga
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02-MAY-2000; 2000JP-00183765.
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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
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T, Koga
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0; Mismatches 0; Indels 1;
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S, Otsuki
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a T, Nagai K, Kojima
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Wakamatsu A, Sugiyama T,
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Cytostatic; Gene therapy; leukaemia; ss. Leukaemia-related DNA sequence #2116.

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ADF81560 standard; DNA; 2388

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method (MI) for determining the subtype of leukaemia cells and whether a patient sample contains leukaemia cells. The method comprises determining the expression profile of a group of markers in a patient sample. The method is useful for determining the presence of leukaemia cells, its types or subtypes, and for the preparation of a medicament for treating leukaemia.
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Pred. No. 4.4e-311;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Kohlmann A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, SEQ ID NO 2116; 2938pp; English.
                                                                                                                                                                                                                                                       DEUT KREBSFORSCHUNGSZENTRUM.
UNIV LUDWIG MAXIMILIANS.
HAFERLACH T.
SCHOCH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brors B, Mergenthaler S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kern W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.8%;
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Best Local Similarity 99.4%;
Matches 1111; Conservative
                                                                                                                                                                    05-NOV-2001; 2001EP-00126244.
30-APR-2002; 2002EP-00009758.
                                                                                                          04-NOV-2002; 2002WO-EP012303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schoch C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-505037/47.
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WO2003039443-A2
                                                                                                                                                                                                                                                                                                                                                                                              KERN W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357
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                                                                                                                                                                                                                                                                                                 (UYLU-)
(HAFE/)
(SCHO/)
                                                                                                                                                                                                                                                                       (DEKR-)
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                                                                                                                                                                                                                                                                                                                                                                                              KERN/)
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reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (11). The polymotecrides are also used and in recombinant production of (11). The polymotecrides are also used in diagnostics as expressed sequence tags for identifying expressed sequence involving (II). It is useful in gene therapy techniques to restore normal cusful for to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in facilitations of mutentions responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AA&64197-AA$94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in the contract of the invention of the contract of the invention of the contract of the contract
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                                                                                                 wew includes polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 909.2; DB 5;
Pred. No. 1.4e-263;
0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 16939; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
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  Tang YT
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95.8%;
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Matches 1086; Conservative
  RT, Liu C,
                                               WPI; 2001-639362/73
                                                                         P-PSDB; ABG16948
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGAAAATATTAACGCAGTCTTGTAGGCAGCTGCCACCTTATGCAGTGCATCGAAACC 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITICCTTATATITIGGAAGAGAGATGATITITAGCIGGGAGCAGIGGIAGCACTITATIC 480
                                                                                                                                                                                                                                                                                                                                                                    TTAGATTATGTTACTCAAATTATGTTACTTGTTTGGCTGTTCATGTAGTCACGGTGCTCT 720
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                                                                         TGATTACAGTGCATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGG
                                                                                                                                       CATITIACIATGAAATITAATATGCTGGGTTTTTTAATACCTTTATATATATGTTCACT
                                                                                                                                                               CATTITACTATGAAAITTAATATGCTGGGTTTTTTAATACCTTTATATATATCATGTTCACT
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2000US-00649167,
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23-AUG-2000;
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237 240 296 300 352 360 420

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The present sequence encodes a human leptin receptor gene-related protein (LRGRP). The cDNA sequence was first isolated in Incyte clone 492703 from (LRGRP) that cDNA library through a computer generated search for the hNT2 cell line cDNA library through a computer generated search for amino acid sequence alignments. The LRGRP protein has some homology to Saccharomyces cerevised proteins of Caenorhabditis elegans ORF C30B.2 and treat metabolic, reproductive and developmental disorders, whilst treat metabolic, reproductive and developmental disorders, whilst antagonists of LRGRP can be used to treatment of cancer or connective tissue disorders e.g. rheumatoid arthritis and Sjogren's syndrome. Polynucleotides which hybridise to the LRGRP nucleotide sequence can be used for detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTGACTITICITATGCTGGGATGTGCCTTAGAGGATTATGGCGTTTACTGGCCCTTATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTTATATTTTCGAAGAGGAGGATGATTTTAGCTCGGAGCAGTGGTAGCACTTTATTCTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCGGGAGACATGGCCGCGTTAAAGCTCTCGTCGCATTATCCTTCAGTCGGCCTATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGTCCTGATTTTCCACGCCATCTCCCCCATTCCATTGCCAAAAGAGTCACTA
                                                                                                                                                                                 DNA encoding human leptin receptor gene-related protein - useful for, e.g. screening for drugs used in treatment of metabolic, reproductive, developmental and connective tissue disorders or cancer.
                                                                                                                                                                                                                                                                                                                                                                                               Length 874;
                                                                                                                                                                                                                                                                                                                                                                          Seguence 874 BP; 192 A; 182 C; 214 G; 283 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                               Score 869.6; DB 2;
Pred. No. 1.1e-251;
3; Mismatches 2;
                                                                                                                                                                                                                               Claim 5; Fig 1A-C; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 78.1%;
Best Local Similarity 99.4%;
Matches 869; Conservative 3
                                                                                 96US-00691071.
97US-00843370.
                                                              97WO-US014191
these bases"
                                                                                                                  PHARM INC.
                                                                                                                                                           WPI; 1998-145624/13.
                                                                                                                                                                      P-PSDB; AAW48322
                                                                                                                   (INCY-) INCYTE
                                                                                   01-AUG-1996;
15-APR-1997;
                      WO9805792-A2
                                                               25-JUL-1997;
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these bases"
349. 350
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/note= "intron contained in genomic sequence
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                                                                                                                                                                                                                   GGCCTCTCATGACCCCAGGAAGGCCGGGGTGGATCCCTCTTTGTGTTGTAGTCCATGCTAT
                                                                                                                                                                                                                                                              TAAAAGTGTGGCCCACAGACCAAGAGCCTCAACATTTCCTAGAGCCTTATTAGAAATGCA
                                                                                                                                                                                                                                                                                                        sequence between
                                                                                                                                                                                 TGCACATGC-GGCATTTTACTATGAAATTTAATATGC---TGGGTTTTTTAATACCTTTA
                                                   TATATCATGTTCACTTTAAG-AAAGACTTCATAAGTAGGAGATGAGTTTTATTCTCAGGA
                                                                                            AATAGACCTGTCAAATTTAGATTATGTTACTCAAATTATGTTACTTGTTTGGCTGTTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encodiong a novel human leptin receptor gene-related protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
Leptin receptor related protein; OB-RGRP; leptin receptor;
leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
                                                                                                                                                                                                                                                     ATTATGTTACTCAAATTATGTTACTTGTTTGGCTGTTCATGTAGTCACGGTGCTCTCAGA 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTTGGGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCAGGCCTCTCATGACCCAGGAA 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leptin receptor related protein, OB-RGRP, nucleotide sequence, SEQ ID 1.
                                      TACAGTGCATTGAATTTCTTAGAACTCATACTGTATACATGTGCACATGCGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anorexia; Bexual maturity disorder; haematopoiesis; angiogenesis; thrombus formation; immunity; inflammation; fetal development; cancer;
                                                                                             TTACTATGAAATTTAATATGCTGGGTTTTTTAATACCTTTATATATCATGTTCACTTTAA
                                                                                                                   GAAAGACTTCATAAGTAGGAGATGAGTTTTTATTCTCAGCAAATAGACCTGTCAAATTTAG
                                                                                                                                                                                              GAAAGACTTCATAAGTAGGAGATGAGTTTTATTCTCAGCAAATAGACCTGTCAAATTTAG
                                                                                                                                                                                                                                                                           ATTATGTTACTCAAATTATGTTACTTGTTTGGCTGTTCATGTAGTCACGGTGCTCTCAGA
                                                                                                                                                                                                                                                                                                                                                                     AAATATTAACGCAGTCTTGTAGGCAGCTGCCACCTTATGCAGTGCATCGAAACCTTTT
                                                                                                                                                                                                                                                                                                                                AAATATATAACGCAGTCTTGTAGGCAGCTGCCACCTTATGCAGTGCATCGAAACCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New oligonucleotides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        874
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(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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Specifically with and inhibite the expression of ADR27652. The ON promotees expression of ADR27652. The ON promotees expression of leptin receptors on the cell surface and may contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA (TRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their coding sequences comprising OB-RGRP or MY047 (thought to be a member of the OB-RGRP family, shares 68# homology with OB-RGRP), and a protein that is a donor or acceptor of energy e.g. luciferase or yellow fluorescent protein (YFP) for detecting compounds that modify the interaction between the leptin receptor and OB-RGRP proteins, which can be used to prevent or treat leptin-related disorders. ON, also related interfering RNA, are used for prevention and/or treatment of leptin-related disorders, e.g. cateoporosis (or other conditions involving reduced bone density); calcitication; obesity; diabetes; anorexia; disorders of sexual maturity, hemmatopolesis, anglogenesis, thrombus formation, regulation of immunity and inflammation, fetal development and cancer.
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Pred. No. 8.8e-185;
0; Mismatches 0;
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AAK93306 standard; cDNA; 629

The present invention relates to a leptin receptor related protein (OB-

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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence encoded by the clone. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
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                                                                                                                                                                                                                                                                                                                                                                                      Primers useful for synthesizing full length cDNA clones and their use
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                                                                                                                                                                                                                                                                                                                                Koga
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                                                                                                                                                                                                                                                                                                                    Ishii S, Kawai Y;
3, Otsuki T, Koga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 629 BP; 144 A; 129 C; 140 G; 211 T; 0 U; 5 Other;
                                                                                          Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
                                                              Human cDNA clone representative sequence, SEQ ID NO: 1766.
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Pred. No. 8.8e-167;
0; Mismatches 6;
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Wakamatsu A, Sugiyama T, Nagai K, Kojima S,
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98.6%;
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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The invention relates to primers for synthesising full length CDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful length clones were butained by construction of full length encoded by the CDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO Primers useful for synthesizing full length cDNA clones and their use 540 631 420 511 480 571 391 360 451 TATCTGTATACATGTGCACATGTGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTT **AATACCTTTATATATCATGTTCACTTTAAGAAGACTTCATAAGTAGGAGATGAGTTTTA** TGGGAGCAGTGGTAGCACTTTATTCTGATTACAGTGCATTGAATTTCTTAGAACTCATAC rarcretaracarerecacarecescarrrracrareaaarrraararecreeerrrr GTCATTTTCCTTACAATTCAAGGGTTTTTCCTTATATTTGGAAGAGGAGATGATTTTAGG Ĥ Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y; Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga Claim 2; SEQ ID NO 358; 1380pp + Sequence Listing; English. Human; full length cDNA; cDNA synthesis; oligo-capping; ss. 662 Human cDNA 5'-end sequence, SEQ ID NO: 358. TTCTCAGCAAATAGACCTGTCAAATTTAGAT 600 TTCTCANC-AATAGACCTGTCAAATTTAGAT BP. 08-JUL-1999; 99JP-00194486. 11-JAN-2000; 2000JP-00118774. 02-MAY-2000; 2000JP-00183765. 07-JUL-2000; 2000EP-00114089 AAK91898 standard; cDNA; 629 06-NOV-2001 (first entry) genetic manipulation. (HELI-) HELIX RES INST WPI; 2001-524255/58 Homo sapiens EP1130094-A2 05-SEP-2001. AAK91898; 301 392 452 421 512 481 572 632 332 830 RESULT 11 2 AAK91898 g g à ò ద 8 셤 셤 õ g ò

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       T; 0 U;
                      Score 588.4; DB 4;
Pred. No. 8.8e-167;
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This invention relates to a novel primers useful for synthesising full length CDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is the 5' end of a representative human DNA cluster of the invention.
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S, Otsuki T, Koga
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                                                                                                                                                                                                               Ota T, Nishikawa T, Isogai T, Hayashi K,
Wakamatsu A, Sugiyama T, Nagai K, Kojima
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08-JUL-1999; 99JP-00194486.
11-JAN-2000; 2000JP-00118774.
02-MNY-2000; 2000JP-00183865.
07-JUL-2000; 2000EP-00114089.
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Best Local Similarity 98.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATACCTTTATATATATCATCTTCACTTTAAGAAAGAC-TCATAAGTNGGANATGAGTTTTA
CCCCATTTCATTGCCAAAAGAGTCACCTATGACTCAGATGCAACCAGTAGTGCCTGTCGG
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                                                                     GAACTGGCATATTTCTTCACTACTGGAATTGTTGTTTCTTGCCTTTGGATTTCCTGTTATT
                                                                                                                                           TATCTGTATACATGCGCACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTT
                                               GAACTGGCATATTTCTTCACTACTGGAATTGTTGTTTCTGCCTTTGGATTTCCTGTTATT
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transferase inhibitor, by analyzing the expression of gene that
differentially modulated in the presence of the inhibitor.
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quinolinone; leukemia; cancer.
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30-OCT-2001; 2001US-0340081P.
30-OCT-2001; 2001US-0340938P.
30-OCT-2001; 2001US-0341012P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polymucleotide sequence is the 5' end of a full length human cDNA sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                           numan; medicine; signal transduction; glycoprotein; transcription; oligo-capping method; ss.
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T, Koga
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S, Otsuki
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Best Local Similarity 98.6%; Pred. No. 8.8e-167;
Matches 622; Conservative 0; Mismatches 6;
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K, Kojima
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                                     cawa T, Isogai T,
Sugiyama T, Nagai
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2000EP-00114089.
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11-JAN-2000; 2
02-MAY-2000; 2
07-JUL-2000; 2
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                                                                                                                                                                                                                                                                           20-MAY-2004
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patient will respond to treatment with a FTI such as (B) -6-[amino(4-chlorophenyl) (1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a patient with leukemia with FTI if the analysis indicates that the patient will respond. This sequence corresponds to a mone whose remaining the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                479
                                                                             will respond. This sequence corresponds to a gene whose expression may be modulated in the presence of FTI.
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                                                                                                                                                                                                                             CAAATGGGGAGCCTGCGGCCTTGTGTTGGCAGGCAATGCAGTCATTTTCCTTACAATTCA
                                                                                                                                                                                                                                                  AGGGTTTTTTCCTTATATTTGGAAGAGGAGATGATTTTTAGCTGGAGCAGTGGTAGCACTT
                                                                                                                                                                                                                                                                                                                AGGGTTTTTCCTTATATTTGGAAGAGGAGATTTTTAGCTGGGAGCAGTGGTAGCTT
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                                                                                                                                                              DB 10; Length 647;
                                                                                                                             Sequence 647 BP; 174 A; 122 C; 144 G; 205 T; 0 U; 2 Other;
                                                                                                                                                                                              3; Indels
                                                                                                                                                          51.8%; Score 577.4; DB 10; 98.6%; Pred. No. 1.9e-163; ive 0; Mismatches 3;
                                                                                                                                                                                              644; Conservative
                                                                                                                                                                             Similarity
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full length cDNA; cDNA synthesis; oligo-capping;
                                                                                                           ID NO: 1117
                                                                                                           SEO
                                                    BP.
                                            657/c
AAK92657 standard; cDNA; 546
                                                                                                           sequence,
                                                                                          entry)
                                                                                        (first
                                                                                                           cDNA 3'-end
                                                                                                                                                 Homo sapiens
                                                                                                                                                                    EP1130094-A2
                                                                                         06-NOV-2001
                                                                     AAK92657
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CAAAGGAGTTGTATGCACATGAAAGTTTGAGAAGCATCATCATAGAGAAGTAAACATCAC

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CAAAGGAGTTGTATGCACATGAAAGTTTGAGAAGCATCATCATAGAGAAGTAAACATCAC

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1045 ACCCAACTTCCTTATCTTTCCAGTGGCTAAACCACTTAACCTCTCTGGGTGTTACCTGCT 1104

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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 3'-end of a CDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
                                                                                                                                                                                                                                                                          their use
                                                                                                                                                                                                     Ξ
                                                                                                                                                                                     Ishii S, Kawai Y;
S, Otsuki T, Koga
                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                            Primers useful for synthesizing full length cDNA clones
                                                                                                                                                                                                                                                                                                                            + Sequence Listing; English
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                                                                                                                                                                                     Hayashi K,
K, Kojima
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a T, Nagai
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                                                                                99JP-00194486.
2000JP-00118774.
2000JP-00183765.
                                                07-JUL-2000; 2000EP-00114089
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Wakamatsu A, Sugiyama T,
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Search completed: August 18, 2005, 00:13:52 Job time : 709 secs

## SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 70%

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.



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25 1 US-10-809-189-125800 Sequence 25 1 US-10-956-157-314866 Sequence 25 1 US-10-956-157-31486 Sequence 25 1 US-10-719-956-15848 Sequence 25 1 US-10-719-956-13388 Sequence	3.6 1.7 25 1 US-10-719-956-251988 Sequence 3.6 1.7 25 1 US-10-719-956-255221 Sequence 8.6 1.7 25 1 US-10-719-956-365165 Sequence 8.6 1.7 25 1 US-10-719-956-365165 Sequence	8.2 1.6 25 1 US-10-050-2501-05072 8.2 1.6 25 1 US-10-179-900-707 Sequence 8.3 1.6 25 1 US-10-719-900-18782 Sequence	8.2 1.6 25 1 US-10-956-157-250112 Sequence 8.2 1.6 25 1 US-10-843-527-4769 Sequence	8.2 1.6 25 1 US-10-843-527-233408 Sequence	18 1.6 18 1 US-08-779-457-30 Sequence	8 1.6 18 1 US-08-779-457-31 Sequence 8 1.6 18 1 US-10-214-802-30 Sequence	1.6 18 1 US-10-214-802-31 Sequence	1.6 18 1 US-10-921-710-31 Seguence	1.6 25 1 US-10-/19-900-300039 Coguence 1.6 25 1 US-10-719-900-708562 Sequence	1.6 25 1 US-10-719-900-793561 Sequence	1.6 25 1 US-10-719-956-152720 Sequence	1.6 25 1 US-10-719-956-356718 Sequence	1.6 25 1 US-10-719-956-571667 Sequence	1.6 24 1 US-09-841-366A-60 Sequence	1,6 24 1 US-1942-863-263 Coguence 1,6 24 1 US-10-314-810-60 Sequence	1.6 25 1 US-10-098-263B-87092 Sequence	1.6 25 1 US-10-/19-900-143150 50416000 1.6 25 1 US-10-719-900-217495 Sequence	1.6 25 1 US-10-719-900-266991 Sequence	1.6 25 1 US-10-719-900-685910 Sequence 1.6 25 1 US-10-719-900-685910	1.6 25 1 US-10-719-900-718042 Sequenc	1.6 25 1 US-10-719-900-767443 Sequenc	1,6 25 1 US-10-719-900-878894 Sequence	1.6 25 1 US-10-719-900-899808 Sequenc	1.6 25 1 US-IU-809-189-20048 3-4-255	1.6 25 1 US-10-956-157-97218 Sequence	1.6 25 1 US-10-956-157-155162 Sequenc	1,6 25 1 US-10-843-527-8674 Sequence	1.6 25 1 US-10-843-527-105776 Sequence	1.6 25 1 US-10-843-52/-152401 Codemon	1.6 25 1 US-10-681-773-16943 Sequence	1.6 25 1 US-10-681-7/3-103264 Sequence	1.6 25 1 US-10-719-956-48483 Sequence	1.6 25 1 US-10-719-956-357405 Sequence	1.6 25 1 US-10-719-956-649616 Sequence	1.6 25 1 US-10-719-956-685651 Sequence 005051, 1.5 21 1 US-10-231-778-208 Sequence 208, App	1.5 24 1 US-09-911-088-1 Sequence 1, Appli	1.5 24 1 US-10-913-085-1 Sequence 1, 4	1.5 21 1 US-10-751-736-44458 Sequence 444	1.5 23 1 US-09-990-940-23 Sequence 23,	1.5 23 1 US-10-913-280-633 Sequence 633	1.5 23 1 US-11-038-360-23 Sequence 23,	1.4 16 1 US-10-7/4-721-43 Coquence 47,	1.4 20 1 US-10-159-339-21 Sequence 21,

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Sequence 18965, A Sequence 18966, A Sequence 18966, A Sequence 18969, A Sequence 18969, A Sequence 18969, A Sequence 2564, Ap Sequence 2564, Ap Sequence 2564, Ap Sequence 211, App Sequence 181, App Sequence 186, App Sequence 186, App Sequence 187, App Sequence 217, App Sequence 2564, Ap Sequence 217, App Sequence 599, App Sequence 599, App	Sequence 89, Appl Sequence 222, Appl Sequence 222, Appl Sequence 124, Appl Sequence 124, Appl Sequence 24, Appl Sequence 24, Appl Sequence 1179, Appl Sequence 1179, Appl Sequence 2567, Appl Sequence 6281, Appl Sequence 6281, Appl Sequence 6281, Appl Sequence 619, Appl Sequence 619, Appl Sequence 619, Appl Sequence 619, Appl Sequence 1483, Appl Sequence 4245, Appl Sequence 4443, Appl Sequence 9117, Appl Sequence 91117, Appl Sequence 9117, Appl Sequence 91117, Appl Sequence 91117, Ap
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Publication No. US20050118625A1
GENERAL INFORMATION:
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Matches 25; Conservative
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Matches 25, Conservative
                                 LENGTH: 25
TYPE: DNA
ORGANISM: Probe Sequence
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US-10-956-157-58126
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SEQ ID NO 58124
LENGTH: 25
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                                                    Sequence 58122, Application US/10956157

| Sequence 58122, Application US/10956157
| Publication No. US20050118625A1
| GENERAL INFORMATION:
| APPLICANT: Wyeth
| APPLICANT: Wounts, William
| TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
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| TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
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| TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
| TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
| TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
| TITLE OF INVENTION: HUMAN PROTEASES
| TITLE OF INVENTION: HUMAN PROTEASES AND HUMAN PROTEASES
| TITLE OF INVENTION: HUMAN PROTEASES PROTEATION ASSOCIATED H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wounts, William
TITLE OF INVERTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN GSTECDARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (Am 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 58123
LENGTH: 25
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GENERAL INFORMATION:

APPLICANT: Wyeth

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION UMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805
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23;
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llarity 100.0%; Pred. No. 23.
Conservative 0; Mismatches
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Sequence 58123, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
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US-10-956-157-58122
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; ORGANISM: Probe Sequence
US-10-956-157-58123
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Best Local Similarity
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Sequence 58125, Application US/10956157
Publication No. US20050118625A1
Publication No. US20050118625A1
APPLICANT: Wounts William
APPLICANT: Mounts William
APPLICANT: Mounts William
TITLE OF INVENTION: UNDER: US/10/956,157
CURRENT PLING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 25
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APPLICANT: Wyeth
APPLICANT: Wouth, William
APPLICANT: Mounts, William
APPLICANT: Mounts, William
APPLICANT: Wouth,
TITLE OF INVENTION: NUCLEIC ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 58126
LENGTH: 25
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100.0%; Pred. No. 23;
tive 0; Mismatches (
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Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches
2.2%; Score 25; DB 1;
100.0%; Pred. No. 23;
tive 0; Mismatches
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GENERAL INCOME.

GENERAL INCOME.

APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: MOUNTS, William
APPLICANT: MOUNTS, WILLIAM
APPLICANTON: HUMAN OSTBOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043600 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 88130
LENGTH: 25
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITTIES OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NUMBER: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFFWARE: PATCHIL VETSION 3.2
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                                                                                   2.2%; Score 25; DB 1; Length 25; 100.0%; Pred. No. 23; tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches
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US-10-956-157-58131
Sequence 58131, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
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ORGANISM: Probe Sequence
US-10-956-157-58131
                                                                                                     Query Match 2.2
Best Local Similarity 100.
Matches 25; Conservative
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US-10-956-157-58130
TYPE: DNA
ORGANISM: Probe Sequence
US-10-956-157-58129
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Best Local Similarity
Matches 25; Conserv
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US-10-956-157-58130
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LENGTH: 25
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APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTBOARTHRIIIS AND HUMAN PROTEASES
FILE REFERENCE: 0319865-043000 (Am 101081)
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFFWARE: PALCHLIN VERSION 3.2
SEQ ID NO 58129
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APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NUMBER: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 58128
LENGTH: 25
                     ESULY, Application US/10956157
Sequence 58127, Application US/10956157
Sequence 58127, Application US/10956157
Sequence 58127, Application US/10956157
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounte, William
APPLICANT: WOUNTEN USCEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REPERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOCTOARE: Patentin version 3.2
SEQ ID NO 58127
LENGTH: 25
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2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels
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US-10-956-157-58128
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Gaps

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Publication No. US20050118625A1

Publication No. US20050118625A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: HUMAN OSTEOARTHAITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,1157
CURRENT FILLING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 58135
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CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PATENTIN VERSION 3.2
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Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches
                                                                                           Query Match 2.2%; Score 25; DB Best Local Similarity 100.0%; Pred. No. 23; Matches 25; Conservative 0; Mismatches
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Best Local Similarity 100.8
Matches 25; Conservative
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58134
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ORGANISM: Probe Sequence
US-10-956-157-58135
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ORGANISM: Probe Sequence
US-10-956-157-58136
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US-10-956-157-58135
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US-10-956-157-58137
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LENGTH: 25
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Sequence 58133, Application US/10956157

Fublication No. US20050118625A1

Sequence 58133, Application US/10956157

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounts, William

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION WMBER: US/10/956,157

CURRENT PILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SEQ ID NOS: 319805

SEQ ID NO 58133

LENGTH: 25
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US-10-956-157-58134

US-10-956-157-58134

US-10-956-157-58134

Sequence $8134 Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Weeth

APPLICANT: Wounts, William

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

FILE REPERENCE: 01996-043000 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT PILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: PATENTIN version 3.2

SEQ ID NO $8134
                 Sequence 58132, Application US/10956157

Bublication No. US20050118625A1

GENERAL INFORMATION:
APPLICANT: Worth
APPLICANT: Wounts, William
TITLE OF INVENTION: HUMAN OSTEDARTHRITS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTEDARTHRITS AND HUMAN PROTEASES

TITLE REPERENCE: 031896-043000 (AM 101081)
CURRENT PILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE PatentIn version 3.2

SEQ ID NO 58132

LENGTH: 25
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; ORGANISM: Probe Sequence
US-10-956-157-58132
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ORGANISM: Probe Sequence
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Best Local Similarity
US-10-956-157-58132
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RESULT 21
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APPLICANT: Wyeth
APPLICANT: Worth
APPLICANT: Wounts, William
APPLICANT: Wounts, WILLIAM
APPLICANT: Wounts, WICLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION VUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 58140
LENGTH: 25
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Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches (
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                                                                          2.2%; Score 25; DB 1; ilarity 100.0%; Pred. No. 23; Conservative 0; Mismatches
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US-10-956-157-58142
; Sequence 58142, Application US/10956157
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US-10-956-157-58140
i. Sequence 58140, Application US/10956157
j. Publication No. US20050118625A1
j. GENERAL INFORMATION:
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Best Local Similarity 100.0
Marches 25; Conservative
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ORGANISM: Probe Sequence
US-10-956-157-58141
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, ORGANISM: Probe Sequence
US-10-956-157-58139
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Best Local Similarity
Matches 25; Conserv
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US-10-956-197-58139
US-10-956-197-58139
US-10-956-197-58139
Sequence 58139, Application US/10956157
Sequence 58139, Application US/20050118625A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: WOUNTION: UNCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: UNMERR: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 58139
LENGTH: 25
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Publication No. US20050118625A1
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Weeth
APPLICANT: Weeth
TITLE OF INVENTION: HUMAN OSTEOARTHEITS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEOARTHEITS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEOARTHEITS AND HUMAN PROTEASES
TITLE OF INVENTION: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PATENTIN Version 3.2
SEQ ID NO 58138
LENGTH: 25
                                                                                                                                APPLICANT: Mounts, William APPLICANT: Mounts, William APPLICANT: Mounts, William APPLICANT: Mounts): NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES FILE REFERENCE: 031896-043000 (AM 101081) CURRENT APPLICATION NUMBER: US.10/956,157 CURRENT FILING DATE: 2004-10-04 NUMBER OF SEQ ID NOS: 319805 SOFTWARE: Patentin version 3.2 SSEQ ID NO $8137 LENGTH: 25
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                           Sequence 58137, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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ORGANISM: Probe Sequence
US-10-956-157-58138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
) ORGANISM: Probe Sequence
US-10-956-157-58137
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Sequence 126134. Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

TITLE OF INVENTION: HUMAN OSTEOARTHATIS AND HUMAN PROTEASES

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: Patentin version 3.2

SEQ ID NO 126134
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REDICATION NO. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

TIPLE OF INVENTION: WIlliam

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

FILE REPERBERCE: 031896-043000 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT PILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805
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Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches
                                                  2.2%; Score 25; DB
100.0%; Pred. No. 23;
ative 0; Mismatches
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SEQ ID NO 133680
LENGTH: 25
                                                     Query Match
Best Local Similarity 100.
Matches 25; Conservative
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US-10-956-157-126134
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US-10-956-157-126134
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APPLICANT: Wounts, william
APPLICANT: Wounts, william
APPLICANT: Wounts, william
TITLE OF INVERTION: UCLERC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN GSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 58143
LENGTH: 25
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: WILLIAM
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REPERENCE: 031896-043000 (Am 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTMARE: Patentin version 3.2
SOFTMARE: Patentin version 3.2
LENGTH: 25
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APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
TITLE OF INVENTION: WOCHEC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NOS: 312805
SOFTWARE: Patentin version 3.2
SEQ ID NO 58144
LENGTH: 25
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23;
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23;
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100.0%; Pred. No. 23;
ive 0; Mismatches
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Best Local Similarity 100.
Matches 25; Conservative
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US-10-956-157-58143
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ORGANISM: Probe Sequence
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US-10-956-157-58143
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Best Local
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Sequence 158422. Application US/10956157

Sequence 158422. Application World US/20050118625A1

Publication No. US20050118625A1

GENERAL INFORMATION:
APPLICANT: Wouth
APPLICANT: Wouth
APPLICANT: Wouth
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WILL
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WILL
TITLE OF INVENTION: UNCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WILL
TITLE OF INVENTION: UNCLEIC ACID AND 10081)
CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: Patentin version 3.2

SEQ ID NO 158472
                                                                                                                                                                                                                           RESULT 30

US-10-956-157-146569

US-10-956-157-146569

Sequence 146569, Application US/10956157

Sequence 146569, Application Wo. US20050118625A1

Sequence 146569, Application No. US20050118625A1

APPLICANT: Wyeth MUMAN OSTEDARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTEDARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTEDARTHRITIS AND HUMAN PROTEASES

CURRENT FILING DATE: 2004-110-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE Patentin version 3.2

SEQ ID NO 146569

LENGTH: 25
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DB 1; Length 25; 23;
                                                0; Indels
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100.0%; Pred. No. 23;
tive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches
                                                     0; Mismatches
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US-10-956-157-168122
US-10-956-157-168122, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
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       2.2%; Score 25;
100.0%; Pred. No.
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                                                                                                   897 AGACCAAGAGCCTCAACATTTCCTA 921
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Matches 25; Conservative
               Query Match
Best Local Similarity 100.
Matches 25; Conservative
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ORGANISM: Probe Sequence
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US-10-956-157-146569
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US-10-956-157-158472
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US-10-956-157-140715
US-10-956-157-140715
Sequence 140715, Application US/10956157
Sequence 140715, Application US/10956157
Sequence 140715, Application No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Worth
CTTLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFREENCE: 031996-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956.157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SEQ ID NO 140715
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mounts, William ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH TITLE OF INVENTION: HUMAN OSTEOARFRITIS AND HUMAN PROTEASES FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US.10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 140388
LENGTH: 25
                                   APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Mounts, William
APPLICANT: Mounts, William
APPLICANT: Mounts ADD ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031895-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 25
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23;
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00.0%; Pred. No.
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Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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Best Local Similarity 100.
Matches 25; Conservative
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; ORGANISM: Probe Sequence
US-10-956-157-140715
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ORGANISM: Probe Sequence
                                                                                                                                                                                                                                                                                                                             ORGANISM: Probe Sequence US-10-956-157-137776
               GENERAL INFORMATION:
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US-10-956-157-140388
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Sequence 198863, Application US/10956157
Publication No. US20050118625A1
Publication No. US20050118625A1
Publication No. US20050118625A1
APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Wounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: UNMERR: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Pacentin version 3.2
SEQ ID NO 198863
LENGTH: 25
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TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 199300
LENGTH: 25
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     2.2%; Score 25; DB 1;
100.0%; Pred. No. 23;
tive 0; Mismatches (
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23;
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Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches
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                                                                                                               823 CCTCTCATGACCCAGGAAGGCCGGG 847
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Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William
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; Sequence 204733, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INPORMATION:
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                                                           Conservative
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US-10-956-157-198863
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Best Local Similarity
Matches 25; Conserv
        Query Match
Best Local Similarity
Matches 25; Conserv
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US-10-956-157-199300
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US-10-956-157-198286

US-10-956-157-198286

US-10-956-157-198286

Sequence 198286, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Mounts, William
TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805

SOOFWARE: PatentIn version 3.2

SEQ ID NO 198286

LENGTH: 25
APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: 20/4-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SOCTUBENCE: 25
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Sequence 182572, Application US/10956157

Sequence 182572, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:
APPLICANT: Wyeth

APPLICANT: Wounts, William

APPLICANT: Wounts, WILLIAM

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

TITLE OF INVENTION: HUMAN GSTEOARTHRITES AND HUMAN PROTEASES

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT PILLING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: PATENTIN version 3.2
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Best Local Similarity 100.0%; P
Matches 25; Conservative 0;
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; ORGANISM: Probe Sequence
US-10-956-157-168122
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) ORGANISM: Probe Sequence
US-10-956-157-182572
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LENGTH: 25
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US-10-956-157-216427

US-10-956-157-216427

Sequence 216427, Application US/10956157

Sequence 216427, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

TITLE OF INVENTION: HUMAN OSTEOMETHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SEQ ID NO 216427

LENGTH: 25

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APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts,
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION WUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 215150
LENGTH: 25
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100.0%; Pred. No. 23;
:ive 0; Mismatches
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1 Similarity 100.0%; Pred. No. 23; 25; Conservative 0; Mismatches
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US-10-956-157-225248
US-10-956-157-225248
Sequence 225248, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
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                                                                                                      761 GCAGTGCATCGAAACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25; Conservative
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US-10-956-157-216427
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ORGANISM: Probe Sequence
US-10-956-157-215150
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Best Local Similarity
             Best Local Similarity
                                                                                                                                                                                                                                                                    RESULT 40
US-10-956-157-215150
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                                                    Matches
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Sequence 214737, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wyeth

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: Patentin version 3.2

SEQ ID NO 214337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 38
US-10-956-157-209653
US-10-956-157-209653
Sequence 209553, Application US/10956157
Sequence 209553, Application US/20050118625A1
Sequence 209553, Application No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: HUMAN GSTEOARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN GSTEOARTHRITIS AND HUMAN PROTEASES
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILLING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319905
NUMBER OF SEQ ID NOS: 319905
SOFTWARE: PATCHLIN Version 3.2
         APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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CRGANISM: Probe Sequence
US-10-956-157-214737
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Query Match
Best Local Similarity 100.
Matches 25; Conservative
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US-10-956-157-209653
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ORGANISM: Probe Sequence
US-10-956-157-204733
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LENGTH: 25
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Query Match

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TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REPERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 225248
LENGTH: 25
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TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTRRITIS AND HUMAN PROFEASES
FILE REPREBNICE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SEQ ID NO 211080
LENGTH: 25
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CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin Version 3.2
SOFTWARE: Patentin Version 3.2
LENGTH: 25
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Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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Matches 25; Conservative
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; ORGANISM: Probe Sequence
US-10-956-157-225248
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ORGANISM: Probe Sequence
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ORGANISM: Probe Sequence
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Matches 25; Conserv
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US-10-956-157-231080
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US-10-956-157-225301
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APPLICANT: Wyeth
APPLICANT: Woth
MOULE, William
APPLICANT: MOULE, ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
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Sequence 239416, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:
APPLICANT: Wounts, William
APPLICANT: Wounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 239416
LENGTH: 25
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APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
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.00.0%; Pred. No.
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                                          904 GAGCCTCAACATTTCCTAGAGCCTT 928
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Best Local Similarity 100.1
Matches 25; Conservative
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Best Local Similarity 100.
Conservative
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ORGANISM: Probe Sequence
US-10-956-157-239117
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US-10-956-157-239416
25;
Matches
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Sequence 250507, Application US/10956157

Sequence 250507, Application US/10956157

Sequence 250507, Application No. US20050118625A1

Sequence 250507, Application No. US20050118625A1

SEQUENCE OF TOTAL OF THE PROPERTY OF TITLE OF INVENTION: HUMAN OSTECAFFRITIS AND HUMAN PROTEASES

TITLE OF INVENTION HUMAN OSTECAFFRITIS AND HUMAN PROTEASES

TITLE OF INVENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mounts, william
APPLICANT: Mounts, william
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WILL
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT PAPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 254092
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APPLICANT: Mounte, William
IITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WI'I
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
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Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches
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; Publication No. US20050118625A1
; GENERAL INFORMATION:
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                701 GTAGTCACGGTGCTCTCAGAAATA 725
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US-10-956-157-254092
Sequence 254092, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
                                                         1 GTAGTCACGGTGCTCTCAGAAATA
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Best Local Similarity 100.0
Matches 25; Conservative
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US-10-956-157-250507
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US-10-956-157-261903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MOUNTS, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REPERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION VUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PATENTIN VERSION 3.2
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TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
SEQ ID NO 244137
LENGTH: 25
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100.0%; Pred. No. 23;
iive 0; Mismatches 0; Indels
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00.0%; Pred. No.
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Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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Query Match
Best Local Similarity 100.
Matches 25; Conservative
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Best Local Similarity 100.0
Matches 25; Conservative
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ORGANISM: Probe Sequence
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CORGANISM: Probe Sequence
US-10-956-157-244137
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US-10-956-157-247073
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LENGTH: 25
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Sequence 26926, Application US/10956157
Publication No. US20050118625A1
GEBREAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: HUMAN OSTEOARTHAITIS AND HUMAN PROTEASES
FILE REPERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 269226
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Publication No. US/2056118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wyeth

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

TITLE OF INVENTION: NUMBER: US/10/956,157

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: PATENTIN VERSION 3.2
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Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William
TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES
FILE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES
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Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches
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         618 GGAGATGAGTTTTATTCTCAGCAAA 642
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; ORGANISM: Probe Sequence
US-10-956-157-292875
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US-10-956-157-267654
Sequence 267654, Application US/10956157
Sequence 267654, Application US/10956157
Sequence 267654, Application No. US20050118625A1
GENERAL INFORMATION:
MEDIICATION:
MOUNTE, William
TITLE OF INVENTION: WILLE OF SECONTRALTIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEOARTHATIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEOARTHATIS AND HUMAN PROTEASES
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
LENGTH: 25
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Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Worth
APPLICANT: Wor
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23;
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100.0%; Pred. No. 20,
0; Mismatches
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FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT PEPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
SEQ ID NO 251903
LENGTH: 25
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Best Local Similarity 100.04
Matches 25; Conservative
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-261903
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CRGANISM: Probe Sequence
US-10-956-157-265849
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ORGANISM: Probe Sequence
US-10-956-157-267654
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US-10-956-157-265849
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Sequence 309122. Application US/10956157
Sequence 309122. Application US/10956157
Sequence 309122. Application No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Weeth
APPLICANT: Weeth
APPLICANT: Went
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WIT TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WIT TITLE OF INVENTION: NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 309122
LEMETH - 1. SEQ ID NO 309122
                                                                                                                                                                                               Sequence 308375. Application US/10956157
Sequence 308375. Application US/20950118625A1
Sequence 308375. Application No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Weath
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, APPLICANTON: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: UNABER: US/10/956,157
CURRENT PLICE DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
SEQ ID NO 308375
TEMPORAL SECOND NOS SEQ ID N
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US-10-956-157-316779, Application US/10956157
Sequence 316779, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Myear
APPLICANT: Mounts, William
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REPRENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.2%; Score 25; DB 1; Length 25; 100.0%; Pred. No. 23; tive 0; Mismatches 0; Indels
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Pred. No. 23;
Mismatches 0
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Pred. No.
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ch 2.2%; SC4
1 Similarity 100.0%; P1
25; Conservative 0;
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ORGANISM: Probe Sequence
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Best Local Similarity
Matches 25; Conserv
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US-10-956-157-309122
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US-10-956-157-304297
Sequence 304297, Application US/10956157
Sequence 304297, Application US/10956157
Sequence 304297, Application US/10956157
Sequence 304297, Application US/10956157
GENERAL INFORMATION: Worths, William
APPLICANT: Wounts, William
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US-10-956-157-301719
Sequence 301719-Application US/10956157
Sequence 301719-Application US/10956157
Sequence 301719-Application No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Weeth
APPLICANT: Weeth
APPLICANT: Weeth
TITLE OF INVENTION: HUPAN OSTGOARTHEITIS AND HUPAN PROTEASES
TITLE OF INVENTION: HUPAN OSTGOARTHEITIS AND HUPAN PROTEASES
TITLE OF INVENTION: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SEQ ID NO 301719
LENTH: 25
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100.0%; Pred. No. 23;
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23;
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                                           CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
SEQ ID NO 298706
LENGTH: 25
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Matches 25; Conservative
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CORGANISM: Probe Sequence
US-10-956-157-304297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Probe Sequence US-10-956-157-301719
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Best Local Similarity
Matches 25; Conserva
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Sequence 32, Application US/10774721
Publication No. US20050009042A1
GENERAL INFORMATION:
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                                                         US-10-719-956-674672

Sequence 674672, Application US/10719956

Publication No. US2040146910A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVERNION: Methods of Genetic Analysis of Rat

FILE REFERENCE: 3527.

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT APPLICATION NUMBER: 60427,836

PRIOR FILING DATE: 2002-11.20

PRIOR FILING DATE: 2002-11.20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 674672

LENGTH: 25
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Bublication No. US20040146910A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT FILING DATE: 2003-11-20;
FRIOR PAPLICATION NUMBER: US/10/719,956;
CURRENT FILING DATE: 2003-11-20;
FRIOR FILING DATE: 2003-11-20;
NUMBER OF SEQ ID NOS: 699466;
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 345761
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0; Mismatches
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95.8%; Pred. No. 48
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1 GGAACTGGCATATTTCTTCACCACT 25
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Best Local Similarity 96.0%;
Matches 24; Conservative
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US-10-719-956-345761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Rattus norvegicus
US-10-719-956-674672
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Best Local Similarity
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US-10-774-721-32/c
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Publication No. US20050118625A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Worth
APPLICANT: Worth
APPLICANT: Worth
APPLICANT: When NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
ITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
ITLE OF INVENTION: USCHAOO (AM 101081)
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE PRILES PATENTION: VERSION 3.2
LENGTH: 25
LENGTH: 25
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; Fublication No. US20040146910A1
; GRNERAL INFORMATION:
APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REPERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR PAPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 417007
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                                                                                                                                                                                                                                                                                    Score 25; DB 1; Length 25; Pred. No. 23;
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                       NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 316779
LENGTH: 25
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; ORGANISM: Rattus norvegicus
US-10-719-956-417007
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Matches 24; Conservative
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Matches 25; Conservative
                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-316779
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; ORGANISM: Probe Sequence
US-10-956-157-317103
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US-10-719-956-417007
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Length 25;

DB 1;

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ORGANISM: Rattus norvegicus US-10-719-956-674671
2.0%;
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Query Match
Best Local Similarity 92.0%
Matches 23; Conservative
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US-10-719-900
US-10-719
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   CURRENT APPLICATION NUMBER: US/10/774,721
CURRENT FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: 60/461,005
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: 0301543
PRIOR PILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin version 3.1
SEQ ID NO 32
LENGTH: 22
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US-10-719-900-377733
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US-10-774-721-32
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US-10-956-417006

y Sequence 417006, Application US/10719956

publication No. US20040146910A1

publication No. US20040146910A1

TURE OF INVENTION: Wethods of Genetic Analysis of Rat

TITLE OF INVENTION: Wethods of Genetic Analysis of Rat

FILE REPRENCE: 3527.1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT PILING DATE: 2002 11.20

PRIOR FILING DATE: 2002 11.20

PRIOR FILING DATE: 2002 11.20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGHH: 25

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"LENGHH: 25
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2.0%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 56;
Matches 23; Conservative 0; Mismatches 2; Indels
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                           2; Indels
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Best Local Similarity 92.0%; Pred. No. 56;
Matches 23; Conservative 0; Mismatches
Score 21.8; DB; pred. No. 56; 0; Mismatches
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Publication No. US20040146910A1
GENERAL INFORMATION:
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US-10-719-956-445812
Sequence 445812, Application US/10719956
; Publication No. US20440146910A1
; GRNERAL INFORMATION:
    APPLICANT: Xue Mei Zhou
; TITLE OF INVERNION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT PILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002 11 20
; RNDMERE OF SEQ. ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 445812
; LENGTH: 25

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Pred. No. 74;
0; Mismatches 2; Indels
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 35.71
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR PILING DATE: 2002 11 20
PRIOR PILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 345760
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TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REPERENCE: 35.71
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR PILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE NCOATRAY Probe Sequence Listing Generator V 1.1
SEQ ID NO 446463
LENGTH: 25
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Best Local Similarity 91.7%; Pred. No. 74;
Matches 22; Conservative 0; Mismatches
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; Sequence 456463, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 GAGGATTATGGCGTTTACTGGCCC 175
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Best Local Similarity 91.7%;
Matches 22; Conservative (
                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-345760
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CRGANISM: Rattus norvegicus
US-10-719-956-445812
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; ORGANISM: Rattus norvegicus
US-10-719-956-456463
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Sequence 377731, Application US/10719900

Publication No. US20050026164A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

ITLE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 35281

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR PILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 377731

LENGTH: 25
                                                                                                                                                                                                                        Sequence 110791. Application US/10098263B
; Sequence 110791. Application US/10098263B
; Publication No. US2003104410A1
; GENERAL INFORMATION:
; AFPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT APPLICATION NUMBER: US/10/098,263B
; RIOR APPLICATION NUMBER: 0203-01-08
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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  DB 1; Length 25;
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Pred. No. 87;
0; Mismatches
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1.8%; Score 20.2; E
Best Local Similarity 88.0%; Pred. No. 87;
Matches 22; Conservative 0; Mismatches
1.9%; Score 20.8; I
llarity 91.7%; Pred. No. 74;
Conservative 0; Mismatches
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; Sequence 92897, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
                                                                                                                             1 GGGCGTTAAAGCTCTTGTGGCACT 24
                                                                                      76 GGCGTTAAAGCTCTCGTGGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%;
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Best Local Similarity 88.0°
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Xue Mei Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapien
US-10-098-263B-110791
                      Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                        JS-10-098-263B-110791
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US-10-719-900-377731
  Query Match
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us-10-774-721-22/c

sequence 22, Application US/10774721

sequence 22, Application Wo. US2005009042A1

sublication No. US2005009042A1

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density of US2005009042A1

subministry of US2005009042A1

subministry of US2005009042A1

subministry of US2005009042A1

subministry of UNCANTION: Olignoclectides Which inhibit Expression of the OB-RGRP Protein TITLE OF INVENTION: Bugen Proteins Of the OB-RGRP Family And The Leptin Receptor TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor TITLE OF INVENTION NUMBER: US/10/774,721

current Filing DATE: 2003-04-07

subministry APPLICATION NUMBER: 00/461,005

subministry APPLICATION
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Sequence 23, Application US/10774721

Publication No. US20050009042A1

GENERAL INFORMATION:

APPLICANT: COCTURERS, Ralf

APPLICANT: COTTURERS, Cyril

APPLICANT: COTTURERS, Cyril

APPLICANT: UHLANN, Eugen

TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction

TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor

TITLE REFREENCE: FRAY2003/0005 US NP

FILE REFREENCE: FRAY2003/0005 US NP

CURRENT FILING DATE: 2004-02-09

PRIOR APPLICATION NUMBER: 60/461,005

PRIOR FILING DATE: 2003-04-07

PRIOR APPLICATION NUMBER: 0301543
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1.8%; Score 20; DB 1;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches
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COTHER INFORMATION: antisens AS14
US-10-774-721-2
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                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
FEATURE:
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US-10-774-721-23/c
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Sequence 2, Application WS/10774721
Sequence 2, Application No. US2005009042A1
Publication No. US2005009042A1
Septication No. US2005009042A1
GENERAL INFORMATION:
APPLICANT: OUCKERS, Ralf
APPLICANT: COUTURIER, Cyril
APPLICANT: COUTURIER, Cyril
APPLICANT: UNIMARN, Eugen
TITLE OF INVENTION: Olignocleotides Which inhibit Expression of the OB-RGRP Protein
TITLE OF INVENTION: Between Protecting Compounds Which Modify The Interaction
TITLE OF INVENTION: Between Protecting Compounds Which Modify The Interaction
TITLE OF INVENTION: Between Protecting Compounds Which Modify The Interaction
TITLE OF INVENTION NUMBER: US/10/774,721
CURRENT APPLICATION NUMBER: 00/401,005
PRIOR APPLICATION NUMBER: 0301543
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
SOFTWARE: PatentIn version 3.1
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; Sequence 133897, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
    APPLICANT: YUE Mei Zhou
    TITLE OF INVENTION: Methods of Genetic Analysis of Rat
    TITLE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
    PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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TITLE OF INVENTION: Methods of Genetic Analysis of Rat FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILLING DATE: 2003-11-20
PRIOR PILLING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 92897
LENGTH: 25
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Pred. No. 87;
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Best Local Similarity 88.0%;
Matches 22; Conservative (
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CRGANISM: Rattus norvegicus
US-10-719-956-133887
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-92897
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US-10-719-956-133887
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Sequence 26, Application US/1074721
; Sequence 26, Application US/10774721
; Sequence 26, Application NO. US2050009042A1
; Publication NO. US2050009042A1
; GENERAL INFORMATION:
    APPLICANT: JOCKERS, Ralf
; APPLICANT: JOCKERS, Cyril
; APPLICANT: UHLWANN, Eugen
; TITLE OF INVENTION: Olignoclectides Which inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRAV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT PILING DATE: 2003-04-07
; PRIOR FILING DATE: 2003-04-07
; PRIOR FILING DATE: 2003-04-10
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO SE
    LENGTH: 20
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Sequence 27, Application US/1074721
Publication No. US20050009042A1
GENERAL INFORMATION:
APPLICANT: JOCKERS, Raif
APPLICANT: COUTURIER, Cyril
APPLICANT: UNIMANN, Bugen
TITLE OF INVENTION: Olignocleotides Which inhibit Expression of the OB-RGRP Protein
TITLE OF INVENTION: Olignocleotide Ombounds Which Modify The Interaction
TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
TITLE OF INVENTION: UNIMERE: US/10/774,721
CURRENT APPLICATION NUMBER: US/10/774,721
CURRENT FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: 60/461,005
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100.0%; Pred. No. 58;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
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.00.0%; Pred. No. 58;
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Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches,
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      PRIOR APPLICATION NUMBER: 0301543
PRIOR FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 20
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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Matches 20; Conservative
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US-10-774-721-25
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US-10-774-721-24/C

US-10-774-721-24/C

Sequence 24, Application US/10774721

Sequence 24, Application No. US2005009042A1

SEQUENT COUTUMER, Cyril

APPLICANT: COUTUMER, Cyril

APPLICANT: UHLMANN, Eugen

TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction

TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction

TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor

FILE REPERENCE: TAAV2003/0005 US NP

CURRENT FILING DATE: 2004-02-09

PRIOR FILING DATE: 2003-04-07

PRIOR PELING DATE: 2003-02-10

NUMBER OF SEQ ID NOS: 47

SOFURARE: Patentin version 3.1

SEQ ID NO 24

LEVENTY BOOK APPLICATION NUMBER: OF SEQ ID NO 24

LEVENTY BOOK APPLICATION NUMBER: OF SEQ ID NO 24

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Sequence 25, Application US/10774721

Publication No. US20050009042A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: COUTURIER, Cyril

APPLICANT: UHLMANN, Eugen
TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor FILE REFERENCE: FRAV2003/0005 US NP
FILE REFERENCE: ERAV2003/0005 US NP
CURRENT APPLICATION NUMBER: US/10/774,721
CURRENT FILING DATE: 2004-02-09
PRIOR FILING DATE: 2003-04-07
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58;
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100.0%; Pred. No. 58;
Live 0; Mismatches
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PRIOR FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
LENGTH: 20
                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.C
Matches 20; Conservative
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US-10-774-721-23
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US-10-774-721-25/c
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RESULT 88
US-10-774-721-30/C
Sequence 30, Application US/1074721
Sequence 30, Application US/1074721
Sequence 30, Application US/10774721
Sequence 30, Application VIS2050009042A1
GENERAL INFORMATION:
APPLICANT: COUTUMER:
ATTILE OF INVENTION: Olignoclectides Which inhibit Expression of the OB-RGRP Protein of TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor;
TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor;
FILE REPRENCE: FRAV2003/0005 US NP
CURRENT APPLICATION NUMBER: 60/461,005
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 47
SOCTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 20
LENGTH: 20
LENGTH: 20
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; Sequence 31, Application US/2005009042A1
; Publication No. US2005009042A1
; GENERAL INFORMATION:
APPLICANT: JOCKERS, Ralf
APPLICANT: COUTURIER, Cyril
APPLICANT: UHLMANN, ENgen
TITLE OF INVENTION: Olignocleotides Which inhibit Expression of the OB-RGRP Protein
TITLE OF INVENTION: Olignocleotides which inhibit Expression of the CB-RGRP Protein
TITLE OF INVENTION: Olignocleotides of the OB-RGRP Protein
TITLE OF INVENTION: Between Proteins of the OB-RGRP Family And The Leptin Receptor
TITLE OF INVENTION: Between Proteins of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRAV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
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Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: 60/461,005
PRIOR FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: 0301543
PRIOR FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 47
SOGTWARE: PATENTIN VERSION 3.1
SEQ ID NO 29
: LENGTH: 20
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ORGANISM: Artificial Sequence
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COTHER INFORMATION: ASOB
US-10-774-721-29
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US-10-774-21-28/C

US-10-774-21-28/C

Sequence 28, Application US/10774721

Sequence 28, Application US/10774721

Sequence 28, Application US/205009042A1

SEMBRAL INFORMATION:

APPLICANT: COUTURIER, CYII

APPLICANT: COUTURIER, CYII

APPLICANT: UNIMANN, Eugen

TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction

TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction

TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction

TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction

TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction

TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction

TITLE OF INVENTION NUMBER: 60/461,005

PRIOR FILING DATE: 2003-02-09

PRIOR FILING DATE: 2003-02-10

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 28

LANGTH: 20

LANGTH: 20
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Sequence 29, Application US/2006009042A1
Publication No. US20050009042A1
Publication No. US20050009042A1
APPLICANT: OCUTUMIER, Cyril
APPLICANT: UHLMANN, EUGEN
TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
TITLE OF INVENTION: Between Proteins of the OB-RGRP Family And The Leptin Receptor FILE REFERENCE: FRAV2003/0005 US NP
CURRENT APPLICATION NUMBER: US/10/774,721
CURRENT FILING DATE: 2004-02-09
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1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels
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                           PRIOR FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: 0301543
PRIOR FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 47
SOFWARE: Patentin version 3.1
SEQ ID NO 27
LENGTH: 20
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 20; Conservative
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US-10-774-721-27
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US-10-774-721-29/c
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APPLICANT: JOCKERS, Ralf

APPLICANT: COUTURIER, Cyril

APPLICANT: COUTURIER, Cyril

APPLICANT: COUTURIER, Cyril

APPLICANT: COUTURIER, Cyril

TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction

TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction

TITLE OF INVENTION: Between Proteins of the OB-RGRP Family And The Leptin Receptor

FILE REFERENCE: FRANZO03/0005 US NP

CURRENT APPLICATION NUMBER: US/10/774,721

CURRENT PILING DATE: 2003-02-09

PRIOR FILING DATE: 2003-04-07

PRIOR FILING DATE: 2003-02-10

NUMBER OF SEQ ID NOS: 47

SEQ ID NOS: 47

LENGTH: 21

LENGTH: 21
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Patent No. US20020146678A1
GENERAL INFORMATION:
APPLICANT: Benvenisty, Nissim
TITLE OF INVENTION: Directed Differention of Embryonic Stem
TITLE OF INVENTION: Cells
FILE REPERENCE: 1822/113
CURRENT APPLICATION NUMBER: US/09/918,702
CURRENT PILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 20;
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100.0%; Pred. No. 65;
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1.8%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/10/774,721
CURRENT FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: 60/461,005
PRIOR APPLICATION NUMBER: 0301543
PRIOR PILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin version 3.1
SOFTWARE: 20
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US-10-774-721-38/c
Sequence 38, Application US/10774721
Publication No. US20050009042A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370 CCTTGTGTTGGCAGGCAATG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 AGTGCCTGTCGGGAACTGGC 279
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Best Local Similarity 100.0
Matches 20, Conservative
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US-10-774-721-34
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APPLICANT: JOCKERS, Ralf

APPLICANT: COUTURER, Crril

APPLICANT: OLINGARIA, Bugen

TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction

TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction

TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor

FILE REFERENCE: FRANZO03/0005 US NP

CURRENT APPLICATION NUMBER: 60/461,005

PRIOR FILING DATE: 2003-04-07

PRIOR FILING DATE: 2003-02-10

PRIOR FILING DATE: 2003-02-10

NUMBER OF SEQ ID NOS: 47

SSOFTWARE: PRIOR FILING DATE: 2003-02-10

SSOTTWARE: PRIOR FILING DATE: 2003-02-10

LENGTH: 20

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APPLICANT: JOCKERS, Ralf
APPLICANT: COUTURIER, Cyril
APPLICANT: COUTURIER, Cyril
APPLICANT: UHLWANN, Eugen
TITLE OF INVENTION: Olignocleotides Which inhibit Expression of the OB-RGRP Protein
TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
FILE REFERENCE: FRAV2003/0005 US NP
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58;
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1.8%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.8%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 58; Matches 20; Conservative 0; Mismatches
CURRENT FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: 60/461,005
PRIOR PILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: 0301543
PRIOR FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 20
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US-10-774-721-34/c
Sequence 34, Application US/10774721
Publication No. US2005009042A1
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US-10-774-721-33
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                                                                                                                                                                                                                                                 TYPE: DNA
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US-10-719-956-445813
US-10-719-956-445813
Sequence 445813. Application US/10719956
; Publication No. US20040146910A1
; GENDRAL INFORMATION:
APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILER REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2002 11.20
; PRIOR FILING DATE: 2002 11.20
; PRIOR FILING DATE: 2002 11.20
; NUMBER: OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; ERNOTH: 25
; TENDRAL: 25
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US-10-719-956-48484
is Sequence 48484, Application US/10719956
j Publication No. US20040146910A1
j GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
j TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.
CURRENT APPLICATION NUMBER: US/10/719,956
j CURRENT FILING DATE: 2003-11-20
pRIOR FILING DATE: 2002-11 20
pRIOR FILING DATE: 2002-11 20
j NUMBER OF SEQ ID NOS: 699466
j SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
j SEQ ID NO 48484
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1.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 25;
                                                            Score 19.4; DB 1; Length 21; Pred. No. 76;
                                                                                                                Indels
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1.7%; Score 19.2; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 3;
                                                                                                                     4; Mismatches
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US-10-719-956-456462
; Sequence 456462, Application US/10719956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    379 GGCAGGCAATGCAGTCATTTCCT 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AAGGGTCACCTATGACTCGGACGC 24
                                                                                                                                                                261 GIGCCIGICGGGAACTGGCAT 281
                                                                                                                                                                                                1 GUGCCUGUCGGGAACUGGCTT 21
                                                                 Hest Local Similarity 76.2%;
Matches 16; Conservative
, OTHER INFORMATION: Artificial US-10-774-721-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Rattus norvegicus
US-10-719-956-445813
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| Sequence 37, Application US/10774721
| Sequence 37, Application No. US2005000942A1
| Publication No. US2005000942A1
| Publication No. US2005000942A1
| Publication No. US2005000942A1
| GENERAL INFORMATION:
| APPLICANT: JOCKERS, Raif
| APPLICANT: COUTURIER, Cyril
| APPLICANT: USIMANN, Eugen
| TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
| TITLE OF INVENTION: Between Proteins of the OB-RGRP Family And The Leptin Receptor TITLE OF INVENTION NUMBER: US/10/774,721
| CURRENT APPLICATION NUMBER: 607461,005 |
| PRIOR FILING DATE: 2003-04-07 |
| PRIOR APPLICATION NUMBER: 607461,005 |
| PRIOR FILING DATE: 2003-02-10 |
| NUMBER OF SEQ ID NOS: 47 |
| SOFTWARE: Patentin version 3.1
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; Sequence 178975. Application US/10719956
; Publication No. US20040146910A1
; Publication No. US20040146910A1
; GENERAL INFORMATION:
    APPLICANT: Xue Methods of Genetic Analysis of Rat
    TITLE OF INVENTION: Methods of Genetic Analysis of Rat
    TITLE OF INVENTION: WHORER: US/10/719,956
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR PILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002-11-20
; NUMBER: OF SEQ ID NOS: 699466
; SOFTWARE: MACACOARTAY Probe Sequence Listing Generator V 1.1
; SEQ ID NO 178975
; LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 91.3%; Score 19.8; DB 1; Length 25; Similarity 91.3%; Pred. No. 97; 21; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                Query Match
1.8%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 97;
Matches 21; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                     ; OTHER INFORMATION: 3' primer of Parathyroid Hormone
US-09-918-702-59
                 NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 59
LENGTH: 25
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Rattus norvegicus
US-10-719-956-178975
                                                                                                                     TYPE: DNA
ORGANISM: Homo sapien
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Best Local
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             GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
ITILE OF INVENTION: Methods of Genetic Analysis of Rat
ITILE OF INVENTION: Methods of Genetic Analysis of Rat
FILER REPERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 456462
LENGTH: 25
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Fublication No. US20040146910A1
GENERAL INPORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
FRIOR FILING DATE: 2003-11-20
FRIOR FILING DATE: 2003-11-20
FRIOR APPLICATION NUMBER: 60/427,836
FRIOR FILING DATE: 2003-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
FERROR DATE: 2004-11-20
NUMBER OF SEQ ID NOS: 699466
SEQ ID NOS: 699466
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87.5%; Pred. No. 1.1e+02;
tive 0; Mismatches 3; Indels
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Publication No. US20050048531A1
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Lockhart
APPLICANT: David Nochart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
CURRENT APPLICATION WUMBER: US/09/396,196
PRIOR APPLICATION NUMBER: US/09/396,196
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
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Publication No. US20040146910A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-511569
                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-456462
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Best Local Similarity 87.5-
Thes 21; Conservative
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US-10-719-956-511569/c
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Woulds, William
APPLICANT: Mounts, William
APPLICANT: Mounts, William
APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUBBER: US/10/956,157
CURRENT FILING DATE: 2004-110-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 97217
LENGTH: 25
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Sequence 97220, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounts, William

APPLICANT: Wounts, WILLEC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION WUMBER: US/10/956,157

CURRENT APPLICATION WUMBER: US/10/956,157

CURRENT PILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: Patentin version 3.2

SEQ ID NO 97220
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1larity 90.9%; Pred. No. 1.3e+02;
Conservative 0; Mismatches 2; Indels
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Pred. No. 1.3e+02;
0; Mismatches 2; Indel8
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Pred. No. 1.3e+02;
0; Mismatches 2;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 107033
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                            US-10-956-157-97217/c
; Sequence 97217, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                           626 GITTIATICICAGCAAATAGAC 647
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US-10-956-157-97220
                                                                                       ORGANISM: mus musculus
US-10-809-189-107033
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Best Local Similarity
Matches 20; Conserv
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Best Local Similarity
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Best Local S
                                                                TYPE: DNA
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1.7%; Score 18.6; DB 1;
84.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 4;
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APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Might Signature
APPLICANT: Might Signature
FILE PEFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 12/806
SEQ ID NOS: 12/806
SEQ ID NOS: 12/806
SEQ ID NOS 12/806
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                                                                                                                                                                                                                       874 ATGCTATTAAAAGTGTGGCCCACAG 898
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Best Local Similarity 84.0
Matches 21; Conservative
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CRGANISM: mus musculus
US-10-809-189-125800
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US-10-719-900-464383
                      LENGTH: 25
TYPE: DNA
CRGANISM: Mus musculus
US-10-719-900-262562
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US-10-719-900-464383
SEQ ID NO 262562
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Best Local
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; Sequence 262562, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; AFPLICATI XE Med Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: 00/427,808
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; PRIOR FILING DATE: 2002.11.20
; WHISER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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US-10-098-263B-110792

y Sequence 110792, Application US/10098263B

y Publication No. US20030104410A1

y Publicant: Mittman, Michael

y TITE OF INVENTION: Human Microarray

FILE REFRENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098,263B

CURRENT FILING DATE: 2001-09

PRIOR FILING DATE: 2001-01-06

PRIOR FILING DATE: 2001-01-06

NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25

"LENGTH: 25
               US-010-103
US-10-79-956-553897
US-10-719-956
Sequence 553897, Application US/10719956
Sequence 553897, Application US/10719956
Sequence 553897, Application US/10719956
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Sequence Listing Generator V 1.1
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Best Local Similarity 84.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels
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90.9%; Pred. No. 1.3e+02;
tive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-553897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.9
Matches 20; Conservative
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US-10-719-900-262562
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; Sequence 464383, Application US/10719900
; Publication No. US2050026164A1
; GENERAL INFORMATION:
    APPLICANT: Xue Mei Zhou
    TITLE OF INVENTION: Methods of Genetic Analysis of Mouse;
    TITLE PREFERENCE: 3528.1
    CURRENT FILING DATE: 2003-11-20
    PRIOR PILING DATE: 2003-11-20
    PRIOR PILING DATE: 2002-11
    NUMBER OF SEQ ID NOS: 982914
    SEQ ID NO 464383
    LENGTH: 25

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Similarity 84.0%; Pred. No. 1.3e+02;
21; Conservative 0; Mismatches 4; Indels
Query Match 1.7%; Score 18.6; DB 1; Length 25; Best Local Similarity 84.0%; Pred. No. 1.3e+02; Matches 21; Conservative 0; Mismatches 4; Indels
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; Publication No. US20040146910A1
; General Information.
; TTLE OF UNIVERTION:
; APPLICANT: Xue Mei Zhou
; TTLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.116.20
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR APPLICATION NUMBER: 60/427,836
; RIUNG DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 133888
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Sequence 231988, Application US/10719956

Publication No. US20040146910A1

GENERAL INFORMATION:

TITLE OF INVENTION: Methods of Genetic Analysis of Rat

FILE REFERENCE: 3527.1

CURRENT FILING DATE: 2003-11-20

PRIOR PILING DATE: 2003-11-20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 231988
                                                                                                                                                                                                                                            Query Match
1.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels
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PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 16448
LENGTH: 25
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US-10-719-956-16848
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; ORGANISM: Rattus norvegicus
US-10-719-956-133888
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US-10-719-956-231988
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APPLICANT: Wounts, William
APPLICANT: Wounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERRNCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARET: Patentin version 3.2
SEQ ID NO 97213
LENGTH: 25
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TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FIRE REPREBNCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SEQ ID NO 314866
LENGTH: 25
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TITLE OF INVEXTION: Methods of Genetic Analysis of Rat
FILE REPERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
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     864 GITGIAGICCAIGCIAITAAAAGIG 888
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Publication No. US20050118625A1
GENERAL INFORMATION:
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; Publication No. US20040146910A1
; GENERAL INFORMATION:
                                      1 GCTGTACTTCATGCTGTTAAAAGTG
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Best Local Similarity 84.0%;
Matches 21; Conservative (
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US-10-956-157-97213
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; ORGANISM: Probe Sequence
US-10-956-157-314866
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Best Local 8
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673 AAATTATGTTACTTGTTTGGCTG 695
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20; Conservative
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CORGANISM: Mus musculus
US-10-719-900-18782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus
US-10-719-900-707
                                                                   TYPE: DNA
CRGANISM: Homo sapien
US-10-098-263B-63072
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Publication No. US20040146910A1

Publication No. US20040146910A1

GENERAL INFORMATION:

TITLE OF INVENTION: Methods of Genetic Analysis of Rat

TITLE REFERENCE: 3527.1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT FILING DATE: 2003-11-20

PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 255221

LENGTH: 25
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Best Local Similarity 84.0%; Pred. No. 1.38+02;
Matches 21; Conservative 0; Mismatches 4; Indels
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US-10-098-263B-63072/c
US-10-098-263B-63072, Application US/10098263B
; Sequence 63072, Application US/10098263B
; Publication No. US20030104410A1
GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TILE REFERENCE: 3118.1
; CURRENT APPLICATION UNDERR: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               440 GAIGAITITAGCIGGGAGCAGIGGI 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                363 CCTGCGGCCTTGTGTTGGCAGGCAA 387
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TYPE: DNA
CRGANISM: Rattus norvegicus
US-10-719-956-365165
                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Rattus norvegicus
US-10-719-956-255221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 114
US-10-719-956-365165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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US-10-719-900-18782

19-10-719-900-18782

1 Sequence 18782, Application US/10719900

2 Sequence 18782, Application US/20050026164A1

3 GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
TITLE REFERENCE: 3528.1

3 FILE REFERENCE: 3208.11-20
CURRENT APPLICATION NUMBER: 05/427,808
PRIOR PILING DATE: 2002.11.20
NUMBER OF SEQ ID NOS: 982914

3 SOFTHARE: Microarray Probe Sequence Listing Generator V 1.1

5 SEQ ID NO 19782

LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 707, Application US/10719900
; Sequence 707, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; TITLE OF INVERTION: Methods of Genetic Analysis of Mouse;
; TILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR PILING DATE: 2003-11-20
; RIOR PILING DATE: 2003-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; TENGRATION OF 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 87.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.6%; Score 18.2; DB 1; Length 25; 87.0%; Pred. No. 1.5e+02; ative 0; Mismatches 3; Indels
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 63072
LENGTH: 25
                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                  Query Match
Best Local Similarity 87.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    377 TTGGCAGGCAATGCAGTCATTTT 399
                                                                                                                                                                                                                                                                                                                     271 GGAACTGGCATATTTCTTCACTA 293
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
HILLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT FILING DATE: 2003-11-20
PRIOR RPPLICATION NUMBER: 05/427,836
PRIOR FILING DATE: 2002-11-20
PRIOR FILING DATE: 2002-11-20
PRIOR FILING DATE: 2002-11-20
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 178976
LENGTH: 25
LENGTH: 25
                                                                                                                                                                                                                                                                 Query Match 1.6%; Score 18.2; DB 1; Length 25; Best Local Similarity 87.0%; Pred. No. 1.5e+02; Matches 20; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.6%; Score 18.2; DB 1; Length 25; Best Local Similarity 87.0%; Pred. No. 1.5e+02; Matches 20; Conservative 0; Mismatches 3; Indels
PRIOR APPLICATION NUMBER: 60/469,545
PRIOR FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 238196
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 233408
LENGTH: 25
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Publication No. US20020193571A1

GENERAL INFORMATION:

APPLICANT: Carter, Paul J.

APPLICANT: Kyung, Jin Kim

APPLICANT: Matthews, William

APPLICANT: Matthews, Maxia L.

TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.5 inch, 1.44 Mb floppy disk
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                      2 cccacagaccaagagcarcgaga 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Rattus norvegicus US-10-719-956-178976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WinPatin (Ge CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 incl
                                                                                                                                                                                    ; ORGANISM: SARS Virus
US-10-843-527-233408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-779-457-30/c
                                                                                                                                                                  TYPE: DNA
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US-10-956-157-250112/
Sequence 250112, Application US/10956157
Sequence 250112, Application US/10956157
Sequence 250112, Application US/10956157
Sequence 250112, Application US/10956157
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION WHORE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: ParentIn version 3.2
SEQ ID NO 250112
LENGTH: 25
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US-10-843-527-4769/c

Sequence 4769, Application US/10843527

Publication No. US20050136395A1

GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: Exic Schell

TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
FILE REFERENCE: 3602.1

CURRENT FILING DATE: 2004-05-10

PRIOR APPLICATION NUMBER: 60/469,545

PRIOR APPLICATION NUMBER: 60/469,545

PRIOR PRIUG DATE: 2003-05-08

NUMBER OF SEQ ID NOS: 238196

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

FEASOFT APPLICATION OF 9
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Publication No. US20050136395A1
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: Exic Schell
TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
PILE REPERENCE: 3602.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.6%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.6%; Score 18.2; DB 1; Length 25; 87.0%; Pred. No. 1.5e+02; tive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 TTCAGTGGGGCTATTGGACTGAC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 TTCAGTGGGAGTATTGGTCTGAC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 CCCACAGACCAAGAGCATCGAGA 2
               AAAGTTTGTTCCTTGTTTGGCTG
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Best Local Similarity 87.07
East Local Similarity 87.07
East 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-250112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-4769
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US-10-843-527-233408
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                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                  Length 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTER: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,802
FILING DATE: 06-Aug-2002
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/780,562
FILING DATE: «UNKNOWN-
PILING DATE: «UNKNOWN-
APPLICATION NUMBER: 08/585005
FILING DATE: «UNKNOWN-
APPLICATION NUMBER: 60/
FILING DATE: 08-Jan-97
ATTORNEY/AGENT INPORMATION:
MATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                     DB 1;
82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Matthews, William
APPLICANT: Matthews, William
Bennett, Brian
TITLE OF INVENTION: WSX RECEPTOR
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P0986R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                     Query Match 1.6%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 82; Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 30, Application US/10214802
publication No. US20030004109A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                  136 GCTGGGATGTGCCTTAGA 153
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TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEK: 910/371-7168
INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARRACTERISTICS: LENGTH: 18 base pairs TENGTH: 18 base pairs STRANDENESS: Single STRANDENESS: Single TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-214-802-30/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-214-802-30
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US-00-779-457-31
Sequence 31, Application US/08779457
Sequence 31, Application US/08779457
Septican No. US20020193571A1
SEMERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Kyung, Jin Kin
APPLICANT: Matthews, William
APPLICANT: Matthews, William
APPLICANT: Matthews, William
APPLICANT: Matthews, William
APPLICANT: ACTIQUES. S1
CORRESPONDENCES: 51
CORRESPONDENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94080

ZIP: 94080

COMPUTER READBLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: 1BM PC compatible

COMPUTER: 1BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winbatin (Genentech)

CURRENT APPLICATION DATA: US/08/779,457
                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667197
FILING DATE: 06/20/96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/96
ATTORNEY/ACENT INFORMATION:
NAME: Lee, Wendy M. 40,378
REGISTRATION NUMBER: P0986P2
TELEPHONE: 415/25-9881
TELEPHONE: 415/25-9881
TELEX: 910/311-7168
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LEMCTH: 18 base pairs
TYPE: NUCLeic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986P2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667197
FILING DATE: 06/20/96
PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/585005
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
                        APPLICATION NUMBER: US/08/779,457 PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 GCTGGGATGTGCCTTAGA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 GCTGGGATGTGCCTTAGA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: Linear
US-08-779-457-30
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Sequence 31, Application US/10921710

Dublication No. US20050019325A1

Sequence 31, Application US/10921710

Publication No. US20050019325A1

SERBEAL INPORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Chiang, Nancy Y.
APPLICANT: Chiang, Nancy Y.
TITLE OF INVENTION: METHODS FOR IDENTIFYING ANTIBODIES THAT

TITLE OF INVENTION: METHODS FOR IDENTIFYING ANTIBODIES THAT

TITLE OF INVENTION: OBECEA ANIMAL
TITLE OF INVENTION: OBECEA ANIMAL
FILE REFERENCE: GENENT.53CP2C1

CURRENT APPLICATION NUMBER: 08/10/921,710

CURRENT FILING DATE: 1997-01-07

PRIOR FILING DATE: 1996-01-08

PRIOR PELLOR OFFEE 1996-01-08

PRIOR FILING DATE: 1996-01-08

PRIOR PRIOR PRIOR DATE: 1996-01-08

PRIOR PRIOR PRIOR DATE: 1996-01-08

PRIOR PRIOR PRIOR DATE: 1996-01-08

PRIOR PRIOR DATE: 1996-01-08

PRIOR PRIOR PRIOR DATE: 1996-01-08

PRIOR PRIOR
DECREASE BODY WEIGHT, FAT-DEPOT WEIGHT OR FOOD INTAKE IN AN OBESE ANIMAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Synthetic oligonucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
1.6%; Score 18; DB 1;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.6%; Score 18; DB 1; Best Local Similarity 100.0%; Pred. No. 82; Matches 18; Conservative 0; Mismatches
        TITLE OF INVENTION: DECREASE BODY WEIGHT, FP
TITLE OF INVENTION: OBESE ANIMAL
FILE REPERENCE: GENENT. 33CP2C1
CURRENT APPLICATION NUMBER: US/10/921,710
CURRENT FILING DATE: 2004-08-18
FRIOR FILING DATE: 1997-01-07
PRIOR PELING DATE: 1996-01-08
PRIOR FILING DATE: 1996-01-08
SPRIOR FILING DATE: 1996-01-08
PRIOR PRILING DATE: 1996-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 GCTGGGATGTGCCTTAGA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GCTGGGATGTGCCTTAGA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-921-710-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 18;
82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,802
FILING DATE: 06-Aug-2002
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/780,562
FILING DATE: UNKNOWN>
APPLICATION NUMBER: 08/585005
FILING DATE: 08-Jan-97
APPLICATION NUMBER: 08/585005
FILING DATE: 08-Jan-97
APPLICATION NUMBER: 08/585005
FILING DATE: 08-Jan-97
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
RESISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: 40,378
REFERENCE/DOCKET NUMBER: 40,378
REFERENCE/DOCKET NUMBER: 101604
                                                                                                                                                                                                                                                                                     Sequence 31, Application US/10214802
Publication No. US2003000410941
GENERAL INPORMATION:
APPLICANT: Matthews, William
Bennett, Brian
TITLE OF INVENTION: WSX RECEPTOR
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 18 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.6%; Score 18;
100.0%; Pred. No.
:ive 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 415/225-1994
                         136 GCTGGGATGTGCCTTAGA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUDIICACION NO. 05.005.001935.5A.
PUDIICANT. Carter, Paul J.
APPLICANT: Carter, Paul J.
APPLICANT: Chiang, Nancy Y.
APPLICANT: Kim, Kyung Jin
APPLICANT: Matthews, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 18; Conservative
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US-10-719-956-152720
US-10-719-956-152720, Application US/10719956
Sequence 152720, Application US/10719956
GENERAL INFORMATION:
APPLICANT: KUE Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
TITLE OF INVENTION: Wethods of Genetic Analysis of Rat
CURRENT APPLICATION UNMBER: US/10/719,956
CURRENT APPLICATION NUMBER: 05/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 979209, Application US/10719900
| Sequence 979209, Application US/10719900
| Publication No. US20050026164A1
| GENERAL INPORMATION:
| APPLICANT: Xue Mei Zhou
| TITLE OF INVERTION: Methods of Genetic Analysis of Mouse
| TITLE OF INVERTION: Methods of Genetic Analysis of Mouse
| TITLE OF INVERTION: Methods of Genetic Analysis of Mouse
| TITLE OF INVERTION: MOUSER: US/10/719,900
| CURRENT FILING DATE: 2003-11-20
| PRIOR APPLICATION NUMBER: 60/427,808
| PRIOR FILING DATE: 2002-11 20
| NUMBER OF SEQ ID NOS: 982914
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| SEQ ID NO 979209
| LENGTH: 25
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1.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels
                                                                                                                                   1.6%; Score 17.8; DB 1; Length 25; 90.5%; Pred. No. 1.7e+02; ive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                299 ATTGTTGTTTCTGCCTTTGGA 319
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                                                                                                                                                                                                                                                                                                 2 Arrercerracrecerries 22
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                                                                                                                                                      Query Match
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Mus musculus US-10-719-900-979209
                     LENGTH: 25
TYPE: DNA
CRGANISM: Mus musculus
US-10-719-900-793561
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Best Local Similarity
Matches 19; Conserv
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SEQ ID NO 793561
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; Sequence 793561, Application US/10719900
; Sequence 793561, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Kue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TITLE OF INVENTION: MUMBER: US/10/719,900
; CURRENT APPLICATION NUMBER: 60/427,808
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR PILING DATE: 2002 11 20
; PRIOR FILING DATE: 2002 11 20
; RUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 129
US-10-719-900-708562
US-10-719-900-708562, Application US/10719900

; Bequence 708562, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
    APPLICANT: Xue Mei Zhou
    TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TITLE REPERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002-11-20
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
; TENGTH: 25
                                                                         Sequence 300059, Application US/10719900

Sequence 300059, Application US/10719900

Publication No. US20050026164A1

GENERAL INFORMATION:
APPLICANT: Xue Met Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse;
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR FILING DATE: 2003-11-20
PRIOR FILING DATE: 2002-11 20
NUMBER: OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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1.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      888 GTGGCCCACAGACCAAGAGCC 908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Mus musculus
US-10-719-900-300059
                                                      RESULT 128
US-10-719-900-300059
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US-10-719-956-356718/c

j Sequence 356718 Application US/10719956

j Sequence 356718 Application US/10719956

j Publication No. US20040146910A1

j GENERAL INFORMATION:
 j APPLICANT: Xue Mei Zhou

j TITLE OF INVERTON: Methods of Genetic Analysis of Rat
 FILE REPERENCE: 3527.1

j CURRENT APPLICATION NUMBER: US/10/719,956

j CURRENT APPLICATION NUMBER: 60/427,836

j PRIOR APPLICATION NUMBER: 60/427,836

j RIOR FILING DATE: 2002 11 20

j NUMBER OF SEQ ID NOS: 699466

j SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

j LENGTH: 25
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; Publication No. US20040146910A1
; GENERAL INPORMATION:
; APPLICANT: Xue Mei Zhou
; FILE REFRENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT PILING DATE: 2003-11-20
; PRIOR FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.6%; Score 17.8; DB 1; Length 25; 90.5%; Pred. No. 1.7e+02; ive 0; Mismatches 2; Indels
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90.5%; Pred. No. 1.7e+02;
tive 0; Mismatches 2; Indels
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 571667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 571667, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION UNBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR PILING DATE: 2003-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1019 CATCATCATAGAGAAGTAAAC 1039
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                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-356718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Rattus norvegicus US-10-719-956-427749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 90.5
Matches 19; Conservative
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Matches 19; Conservative
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US-10-719-956-427749/c
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US-10-719-956-571667
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APPLICANT: Ranagan, Laura
APPLICANT: Ranagan, Laura
APPLICANT: Nasif, Nadine
TITLE OF INVENTION: DIAGNOSIS OF TUMORS
FILE REFERENCE: 16026-9267
CURRENT APPLICATION NUMBER: US/09/841,366A
CURRENT PILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 68
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 60
LENGTH: 24
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; Publication No. US2003009200941
; GENERAL INFORMATION:
    APPLICANT: Raia Palm
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
; TITLE OF INVENTION: UNMER: 10S/09/992,665
; CURRENT FILING DATE: 2001-11-13
    PRIOR APPLICATION NUMBER: 60/249,508
; RIOR AILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NOS: 380
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                                                                                               Query Match
1.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                    US-09-841.366A-60/c.
Sequence 60, Application US/09841366A
Patent No. US20020058265A1
GENERAL INFORMATION:
APPLICANT: Bacher, Jeffery W.
                                                                                                                                                                                                      299 ATTGTTGTTTCTGCCTTTGGA 319
                                                                                                                                                                                                                                   2 ATTGTCGTTACTGCCTTTGGA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: BAT-25 primer US-09-841-366A-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-571667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Probe US-09-992-665-263
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ORGANISM: Homo sapiens
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Best Local Similarity
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Matches

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Sequence 266991/C

Sequence 26691/Application US/10719900

Publication No. US20050026164A1

Publication No. US20050026164A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

FILER REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT APPLICATION NUMBER: 05/427,808

PRIOR FILING DATE: 2003-11-20

PRIOR FILING DATE: 2003-11-20

NUMBER OF SEQ ID NOS: 982914

SOFFWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 266991

LENGTH: 25
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US-10-719-900-217495, Application US/10719900
Sequence 217495, Application US/10719900
Sequence 217495, Application US/20050026164A1
CHAPLICANI: NO US20050026164A1
GENERAL INPORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT PILLIGATION NUMBER: US/10/719,900
CURRENT FILLING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR PILLING DATE: 2003-11-20
NUMBER OF SEQ ID NOS: 982214
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 211495
Sequence 143190.

Sequence 143190.

Sequence 143190.

Publication No. US20050026164A1

Publication No. US20050026164A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REPERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

FILE REPERENCE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2002 11 20

PRIOR FILING DATE: 2002 11 20

FRIOR FILING DATE: 2002 11 20

NUMBER: OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 143190

LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17.6; DB 1; Length 25;
Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 GAATTGTTGTTTCTGCCTTTGGAT 320
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Best Local Similarity 83.3%;
Matches 20; Conservative (
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CORGANISM: Mus musculus
US-10-719-900-217495
                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Mus musculus
US-10-719-900-143190
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Best Local S
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US-10-314-810-60/c

is Sequence 60, Application US/10314810

is Sequence 60, Application WS.030030180758A1

is GENERAL INFORMATION:

APPLICANT: Bandgan, Laura

APPLICANT: Bandgan, Laura

TITLE OF INVENTION: DIRECTION OF WICKOSATELLITE INSTABILITY AND ITS USE IN

TITLE OF INVENTION: DIAGNOSIS OF TUMORS

PRIOR FILING DATE: 2002-12-09

PRIOR FILING DATE: 2000-09-15

NUMBER OF SEQ ID NOS: 68

SOFTWARE PATELING DATE: 2000-09-15

NUMBER OF SEQ ID NOS: 68

SEQ ID NO 60

LENGTH: 24
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US-10-098-263B-87092/C
Sequence 87092, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Mitchan, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR PILING DATE: 2003-01-08
PRIOR FILING DATE: 2010-01-08
SOFIUM OF SEQ ID NOS: 131066
SOFIWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 87092
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Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels
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                     Indels
                        4,
                          0; Mismatches
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                                                                        834 CCAGGAAGGCCGGGGTGGATCCCT 857
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                                                                                                                        1 ccagrarddccdddarddaraccr 24
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CTHER INFORMATION: BAT-25 primer
US-10-314-810-60
                             20; Conservative
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US-10-098-263B-87092
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Best Local Similarity
Matches 20; Conserv
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RESULT 140

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RESULT 146
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
    APPLICANT: Xue Mei Zhou
    TITLE OF INVENTION:
    FILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
    PRIOR FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 646382
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US-10-719-900-685910
US-210-719-900-685910
Sequence 685910, Application US/10719900
Sequence 685910, Application US/10719900
Sequence 685910, Application US/10719900
TITLE NEPRENCE: 3528.1
TITLE OF INVENTION: METHODS of Genetic Analysis of Mouse FILE REPERENCE: 3528.1
CURRENT PRILIC DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
FRIOR PILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 685910
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.6%; Score 17.6; DB 1; Length 25; Best Local Similarity 83.3%; Pred. No. 1.7e+02; Matches 20; Conservative 0; Mismatches 4; Indels
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1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels
                                                                                    Length 25;
                                                                                                                           4; Indels
                                                                                Query Match
1.6%; Score 17.6; DB 1;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4;
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                                                                                                                                                                  813 CTGAAGCAGGCCTCTCATGACCCA 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         750 TGCCACCTTATGCAGTGCATCGAA 773
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CRGANISM: Mus musculus
US-10-719-900-646382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-685910
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-266991
                                                                                                                                                                                                                                                                   RESULT 143
US-10-719-900-646382
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RESULT 145 US-10-719-900-718042

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| Publication NO. US20050026164A1
| CENERAL INFORMATION:
| APPLICANT: Kue Mei Zhou
| TITLE OF INVENTION: Methods of Genetic Analysis of Mouse:
| TITLE OF INVENTION: Methods of Genetic Analysis of Mouse:
| CURRENT APPLICATION NUMBER: US/10/719,900
| CURRENT FILING DATE: 2003-11-20
| PRIOR FILING DATE: 2002 11-20
| WUMBER OF SEQ ID NOS: 982914
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| LENGTH: 25
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Sequence 767443

Sequence 767443

Sequence 767443

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
CURRENT FILING DATE: 2003.11-20

PRIOR FILING DATE: 2003.11-20

PRIOR FILING DATE: 2002.11 20

PRIOR FILING DATE: 2002.11 20

NUMBER: OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

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                                                                   TITLE OF INVENTION: Methods of Genetic Analysis of Mouse TITLE OF INVENTION: Methods of Genetic Analysis of Mouse CURRENT APPLICATION NUMBER: US/10/719,900 CURRENT PILING DATE: 2003-11-20 PRIOR APPLICATION NUMBER: 00/427,808 PRIOR PILING DATE: 2002 11 20 NUMBER OF SEQ ID NOS: 982914 SOFFWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 718042
Sequence 718042, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       589 IGITCACTITAAGAAAGACTICAT 612
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Best Local Similarity 83.3<sup>1</sup>
Matches 20; Conservative
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Best Local Similarity 83.3
Matches 20; Conservative
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US-10-719-900-718042
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US-10-719-900-762876
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                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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1.6%
Query Match
Best Local Similarity 83.3%
Matches 20; Conservative
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US-10-809-189-20048
                                                                                                                                                                              TYPE: DNA
CRGANISM: Mus musculus
US-10-719-900-899808
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US-10-809-189-20048/c
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US-10-719-900-884508
US-10-719-900-884508
Sequence 884508, Application US/10719900
Sequence 884508, Application US/10719900
Sequence 884508, Application US/10719900
SENERAL INFORMATION:
TITLE OF INFORMATION:
TITLE OF INFORMATION WITHOUS US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR PILING DATE: 2003-11-20
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
TIRMOTHL...
SEQ ID NO 884508
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                                                                                                                                                                      / Match 1.6%; Score 17.6; DB 1; Length 25; Local Similarity 83.3%; Pred. No. 1.7e+02; res 20; Conservative 0; Mismatches 4; Indels
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                                 Query Match
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels
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US-10-719-900-899808/c
; Sequence 899808, Application US/10719900
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Best Local Similarity 83.3
Matches 20; Conservative
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CORGANISM: Mus musculus
US-10-719-900-884508
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; ORGANISM: Mus musculus
US-10-719-900-767443
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RESULT 152

US-10-956-157-97212/c
US-10-97212/c
US-10-97
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITIE OF INVENTION: Methods of Genetic Analysis of Mouse
TITIE OF INVENTION: Methods of Genetic Analysis of Mouse
TITIE REPERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20048, Application US/10809189
; Sequence 20048, Application US/10809189
; Publication No. US20050048531A1
GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affwertix, Inc.
; APPLICANT: Affwertix, Inc.
; TILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT APPLICATION NUMBER: US/09/396,196
; PRIOR APPLICATION NUMBER: 10S/09/396,196
; PRIOR PILING DATE: 1998-09-15
; PRIOR PILING DATE: 1998-09-15
; RUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FRASESQ for Windows Version 4.0
; SEQ ID NO 20048
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Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           957 TCTGGACCCAGGACATTTTGATGA 980
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APPLICANT: Mounts, William
TITLE OF INVENTION: HUMAN OSTEOARTHRITS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 316449
LENGTH: 25
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; Sequence 8674, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
    APPLICANT: Michael Mittmann
; APPLICANT: Mittmann
; TILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SEQ ID NO 8674
; LENGTH: 25
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Sequence 105776, Application US/10843527

Publicaction No. US20050136395A1

Sequence 105776, Application US/10843527

SEQUENCE INFORMATION:

APPLICANT: Michael Mittmann

APPLICANT: Michael Mittmann

TILE OF INVENTION Methods of Genetic Analysis of SARS Virus

FILE REFERENCE: 3602.1

CURRENT APPLICATION NUMBER: US/10/843,527

CURRENT FILING DATE: 2004-05-10

PRIOR FILING DATE: 2003-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.6%; Score 17.6; DB 1; Length 25; 83.3%; Pred. No. 1.7e+02; tive 0; Mismatches 4; Indel8
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1.6%; Score 17.6; DB 1;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4;
                                                                Sequence 316449, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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Best Local Similarity
Matches 20; Conserv
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Sublication No. US20050118625A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William
TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 155162
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROFEASES
TITLE OF INVENTION: 10180-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SEQ ID NO 9718
LENGTH: 25
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ilarity 83.3%; Pred. No. 1.7e
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                             922 GAGCCTTATTAGAAATGCAGAATC 945
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; Sequence 97218, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
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SOFTWARE: Patentin version 3.2
SEQ ID NO 97212
LENGTH: 25
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; ORGANISM: Probe Sequence
US-10-956-157-97218
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; ORGANISM: Probe Sequence
US-10-956-157-155162
                                                                                                  ; ORGANISM: Probe Sequence
US-10-956-157-97212
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Best Local Similarity
Matches 20; Conserv
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hes 20; Conserv
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Matches 20
                                                                           TYPE: DNA
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RESULT 162
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; Sequence 132401, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; CURRENT TILING DATE: 2004-05-10
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR PELING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 132401
; LENGTH: 25
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US-10-843-527-229503/C
US-10-843-527-229503/C
US-10-843-527-229503/C
US-20-8603/C
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1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels
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NUMBER OF SEQ ID NOS: 238196
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 105776
LENGTH: 25
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Best Local Similarity 83.33
Matches 20; Conservative
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CRGANISM: SARS Virus
US-10-843-527-229503
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US-10-843-527-132401
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CRGANISM: SARS Virus
US-10-843-527-105776
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Gaps
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APPLICANT: Met, Rui,
APPLICANT: Shen, Mei, Mei,
APPLICANT: Shen, Mei-Mei
APPLICANT: Shen, Mei-Mei
APPLICANT: Shen, Methode for Genotyping Polymorphisms in Humans
TITLE OF INVENTION: Methode for Genotyping Polymorphisms in Humans
FILE REFERENCE: 352.2
CURRENT APPLICATION NUMBER: US/10/681,773
CURRENT FILING DATE: 2003-10-07
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: 60/417,190
PRIOR PILING DATE: 2002-10-08
NUMBER OF SEO ID NOS: 124031
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
                                                                                                                                                                                                                                                                          APPLICANT: Met, Rui,
APPLICANT: Shen, Wei, Rui,
APPLICANT: Shen, Wei, Rui,
APPLICANT: Shen, Wei, Rui,
APPLICANT: Shen, Wei, Rui,
APPLICANT: Kennedy, Giulia
TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
FILE REFERENCE: 352.2
CURRENT APPLICATION NUMBER: US/10/681,773
CURRENT FILING DATE: 2002-06-10-07
PRIOR APPLICATION NUMBER: 60/470,475
PRIOR FILING DATE: 2002-05-14
PRIOR PILING DATE: 2002-06-10-08
NUMBER OF SEQ ID NOS: 124031
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 16943
LENGTH: 25
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1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels
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Pred. No. 1.7e+02;
0; Mismatches 4; Indel8
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; Sequence 16944, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
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                                                                                                                                                               Sequence 16943, Application US/10681773; Publication No. US20040146890A1; GENERAL INFORMATION: APPLICANT: Matsuzaki, Hajime
24 TAAAGACTTGTTAGTAATGCAGAA 1
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Best Local Similarity 83.3%;
Matches 20; Conservative (
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ORGANISM: Homo sapien
US-10-681-773-16944
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CORGANISM: Homo sapien
US-10-681-773-16943
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                                                                                          APPLICANT: Matsuzaki, Hajime
APPLICANT: Kennedy, Giulia
TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
FILE OF INVENTION: WUMBER: US/10/681,773
CURRENT APPLICATION NUMBER: US/10/681,773
CURRENT FILING DATE: 2003-10-07
PRIOR APPLICATION NUMBER: 60/470,475
PRIOR APPLICATION NUMBER: 60/417,190
PRIOR APPLICATION NUMBER: 60/417,190
PRIOR APPLICATION NUMBER: 60/417,190
ANDMBER OF SEQ ID NOS: 124031
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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| Publication No. US20040146910A1
| GENERAL INFORMATION:
| APPLICANT: Kue Mei Zhou
| TITLE OF INVENTION: Methods of Genetic Analysis of Rat
| FILE REFERENCE: 3527.1
| CURRENT APPLICATION NUMBER: 60/427,836
| PRIOR PILING DATE: 2003-11-20
| PRIOR PILING DATE: 2002 11 20
| NUMBER OF SEQ ID NOS: 699466
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| LENGTH: 25
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1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels
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Publication No. US20040146910A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REPERENCE: 3527.1
CURRENT APPLICATION UNDER: US/10/719,956
CURRENT PLING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
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US-10-681-773-103264/c
; Sequence 103264, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
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, ORGANISM: Rattus norvegicus
US-10-719-956-48483
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Best Local Similarity 83.3
Matches 20; Conservative
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US-10-681-773-103264
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US-10-719-956-649616/C
US-10-719-956-649616/C

Sequence 649616, Application US/10719956

Publication No. US20040146910A1

GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REPERENCE: 357-1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT APPLICATION NUMBER: 0503-11-20

PRIOR PILING DATE: 2002-11-20

PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 699466

SOPTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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APPLICANT: You Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REPERENCE: 357.1

CURRENT APPLICATION WUMBER: US/10/719,956

CURRENT FILING DATE: 2003-11-20

PRIOR PELLING DATE: 2002-11-20

PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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83.3%; Pred. No. 1.7e+02;
ative 0; Mismatches 4; Indels
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PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 276484
LENGTH: 25
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1.6%; Score 17.6; DB 1;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4;
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; Sequence 357405, Application US/10719956
; Publication No. US20040146910A1
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                                                                                                                            ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-276484
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US-10-719-956-649616
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Best Local Similarity 83.3
Matches 20; Conservative
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GENERAL INCOMMATION:

APPLICANT: Ballodeau, Pierre
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Colutuow, Anna M.G.
APPLICANT: Louo, Ming.
APPLICANT: Louo, Ming.
APPLICANT: Dennis, Elizabeth S.
APPLICANT: Dennis, Elizabeth S.
APPLICANT: Dennis, Elizabeth S.
APPLICANT: Dennis, Ming.
TITLE OF INVENTION: Method for inducing seed development by down-regulating
TITLE OF INVENTION: Method for inducing seed development by down-regulating
TITLE OF INVENTION: More Elizabeth S.
TITLE OF INVENTION: WINGER: 09/198, 237
FRIOR APPLICATION NUMBER: 00/101,184
FRIOR FILING DATE: 1998-09-20
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1999-07-01
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Sequence 68551. Application US/10719956

Sequence 68551. Application No. US20040146910A1

Sequence 68551. Application No. US20040146910A1

SEQUENCE OF INVENTION: Methods of Genetic Analysis of Rat

TITLE OF INVENTION: Methods of Genetic Analysis of Rat

TITLE OF INVENTION: WHERE: US/10/719,956

CURRENT FILING DATE: 2003-11-20

PRIOR PILING DATE: 2003-11-20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25

LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              874 ATGCTATTAAAAGTGTGGCCCACA 897
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Sequence 208, Application US/10231778
Publication No. US20030126647A1
GENERAL INFORMATION:
25 TTTAGCTGACAGCAAAGGTAGCAC 2
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ORGANISM: Artificial Sequence
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ORGANISM: Rattus norvegicus
US-10-719-956-685651
                                                                                                               RESULT 167
US-10-719-956-685651/c
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; Bublication Wo. US20050009182A1
; Bublication Wo. US20050009182A1
; GENERAL INFORMATION:
APPLICANT: OW, DAVID
; TITLE OF INVENTION: BTRACKING OF DNA IN EUKARYOTIC GENOMES
; TITLE OF INVENTION: STRACKING OF DNA IN EUKARYOTIC GENOMES
; TITLE OF INVENTION: STRACKING OF DNA IN EUKARYOTIC GENOMES
; TITLE OF INVENTION: STRACKING OF DNA IN EUKARYOTIC GENOMES
; TITLE OF INVENTION: STRACKING OF DNA IN EUKARYOTIC GENOMES
; FILE REFERENCE: 16313-0052
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US/09/911,088
; PRIOR FILING DATE: 2000-07-21
; RIOR FILING DATE: 2000-07-21
; SEQ ID NO 1
; SEQ ID NO 1
; LENGHARE: PATENTING VET: 2.1
                                                                                                                                                                                                                                                Sequence 1, Application US/09911088
; Sequence 1, Application US/09911088
; Patent No. US2002012145A1
; GENERAL INFORMATION:
    APPLICANT: OW, DAVID
; TITLE OF INVENTION: METHODS FOR THE REPLACEMENT, TRANSLOCATION, AND
; TITLE OF INVENTION: STACKING OF DNA IN BUKARYOTIC GENOMES
; TITLE OF INVENTION: STACKING OF DNA IN BUKARYOTIC GENOMES
; FILE REFERENCE: 16313-0052
; CURRENT FILING DATE: 2001-07-23
; PRIOR PILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTION VINSER: 60/220,062
; SOFTWARE: PATENTION VINSER: 60/220,11
; SEQ ID NO 1
; LENGTH: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE: PEATURE: OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-911-088-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.5%; Score 16.8; DB 1; Length 24; Best Local Similarity 90.0%; Pred. No. 2e+02; Matches 18; Conservative 0; Mismatches 2; Indels
1.5%; Score 16.8; DB 1; Length 21; 90.0%; Pred. No. 1.5e+02; ive 0; Mismatches 2; Indels
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ilarity 90.0%; Pred. No. 2e+02;
Conservative 0; Mismatches 2;
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                                                                                                       606 ACTICATAAGTAGGAGAIGA 625
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ORGANISM: Artificial Sequence
                 Query Match
Best Local Similarity 90.0%
Matches 18; Conservative
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TYPE: DNA
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Sequence 44458, Application US/10751736

Publication No. US20040265230A1

GENERAL INFORMATION:

APPLICANT: Martinez, Robert

APPLICANT: Brown, Eugene

APPLICANT: Brown, Eugene

APPLICANT: Liu, Wei

TITLE OF INVENTION: CANCESS

TITLE OF INVENTION: CANCESS

TITLE APPLICATION NUMBER: US/10/751,736

CURRENT APPLICATION NUMBER: US/10/751,736

CURRENT APPLICATION NUMBER: US/2003-01-06

FILE REFERENCE: A003-01-06

PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000

PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000

SOFTWARE PARENTE: 2003-01-06

NUMBER OF SEQ ID NOS: 54873

SOFTWARE PARENTE: 2013-01-06

LENGTH: 21
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          Sequence 4596, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION
APPLICANT: Terry, Roemer D.
APPLICANT: Terry, Roemer D.
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT PILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 4596
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85.7%; Pred. No. 1.8e+02;
tive 0; Mismatches 3; Indels
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Publication No. US20030027252A1
GENERAL INFORMATION:
APPLICANT: Tian, Hui
APPLICANT: Zhao, Jiagang
APPLICANT: Chen, Jin-Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 TCTTTCTTCAACACTGGAATT 1
                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-4596
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Matches 18; Conservative
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ORGANISM: homo sapiens
US-10-032-585-4596/c
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US-09-990-940-23/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: TGR342Right PCR ; OTHER INFORMATION: expression profiling primer US-09-990-940-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-681-199-23
Sequence 23, Application US/10681199
Sequence 23, Application US/10681199
Sequence 23, Application US/10681199
Sequence 23, Application US/10681199
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLEXIA
TITLE OF INVENTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLEXIA
TITLE OF INVENTION: UNMERS: US/10/681,199
CURRENT PILING DATE: 2003-10-09
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
LENGTH: 23
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         APPLICANT: Gupte, Jamila 3.
APPLICANT: Tularik Inc.
TITLE OF INTENTION: No. US20030027252A1e1 Receptors
TITLE OF INTENTION: No. US20030027252A1e1 Receptors
FILE REPERENCE: 018781-007410US
CURRENT APPLICATION NUMBER: US/09/990,940
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/252,841
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-03-28
PRIOR PILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 23
FROWTH OF SEQ ID NOS: 54
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1.5%; Score 16.2; DB 1;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 3;
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US-10-681-199-23
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; Sequence 633, Application US/10913280
; Publication No. US2050089894A1
; GENERAL INFORMATION:
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Gupte, Jamila S.
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117 TIGGACTGACTITICITATGC 137
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: TGR342Right PCR
OTHER INFORMATION: expression profiling primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.5%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels
APPLICANT: Ginns, Edward I.
APPLICANT: Galdzicka, Marzena
TITLE OF INVENTION: SYSTEMS AND METHODS FOR ANALYZING
TITLE OF INVENTION: SYSTEMS AND METHODS FOR ANALYZING
TITLE OF INVENTION: WICLEIC ACID SEQUENCES
FILE REFERENCE: 07917-23801
CURRENT APPLICATION NUMBER: US /10/913,280
CURRENT FILING DATE: 2004-08-06
PRIOR APPLICATION NUMBER: US 60/493,238
PRIOR PILING DATE: 2003-08-06
PRIOR PELING DATE: 2003-08-06
PRIOR FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 920
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 633
LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/11038360

Sequence 23, Application US/11038360

Publication No. US20050170397A1

GENERAL INFORMATION:
APPLICANT: Than, Hui
APPLICANT: Chen, Jin-Long
APPLICANT: Tularik Inc.
TITLE OF INVENTION: Novel Receptors
FILE OF INVENTION: Novel Receptors
FILE OF INVENTION: Novel Receptors
FILE OF INVENTION: NOVER: US/09/990,940
PRIOR APPLICATION NUMBER: US/09/990,940
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: US 60/257,636
PRIOR FILING DATE: 2000-11-22
PRIOR PELING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 60/257,636
PRIOR FILING DATE: 2000-10-22
PRIOR APPLICATION NUMBER: US 60/257,636
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN VET. 2.1
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Sequence 45, Application US/10774721
; Sequence 45, Application US/10774721
; Publication No. US2005009042A1
; Publication No. US2005009042A1
; Publication No. US2005009042A1
; GENERAL INFORMATION:
    APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
APPLICANT: UHLMANN, Bugen
; TITLE OF INVENTION: Olignocleotides Which inhibit Expression of the OB-RGRP Frotein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; TITLE OF INVENTION NUMBER: G0/461,005
; CURRENT FILING DATE: 2004-02-09
; PRIOR FILING DATE: 2003-04-07
; PRIOR FILING DATE: 2003-04-07
; PRIOR PILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 45
; LENGTH: 16
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| Sequence 47, Application US/10339793
| Publication No. US20030180764A1
| Publication No. US20030180764A1
| Publication No. US20030180764A1
| Publication No. US20030180764A1
| GENERAL INPORMATION:
| APPLICANT: Shang, Jin
| APPLICANT: Shang, Jin
| TITLE OF INVENTION: GENES AFFECTED BY CHOLESTEROL TREATMENT AND DURING ADIPOGENESIS
| FILE REPERENCE: 37-000310US
| CURRENT APPLICATION WUMBER: US/10/339,793
| CURRENT APPLICATION WUMBER: 2003-01-08
| NUMBER OF SEQ ID NOS: 443
| SOFTWARE: Patentin version 3.1
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1.4%; Score 16; DB
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 16; Conservative 0; Mismatches
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Best Local Similarity 100.0
Matches 16; Conservative
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Chatterjee, Aurobindo
De Jong, Pieter J.
Li, Shanru
Li, Xia
Ohmen, Jeffrey D
Reed, Danielle R.
Ross, David
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Best Local Similarity 100.0
Matches 16; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, TITLE OF INVENTION: HGRBMY30 FILE REPERBACKE: D0169NP CURRENT APPLICATION NUMBER: US/10/159,339 CURRENT FILING DATE: 2002-05-30 PRIOR PLICATION NUMBER: US 60/294,411 PRIOR PLICATION NUMBER: 2001-05-30 NUMBER OF SEQ ID NOS: 94 SOFTWARE: PARENT NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Li, SHELLANI:
APPLICANT: Li, SHELLANI:
APPLICANT: Chimen, Jeffrey D
APPLICANT: Reed, Danielle R.
APPLICANT: Reed, Danielle R.
APPLICANT: Reed, Danielle R.
APPLICANT: Reed, Danielle R.
APPLICANT: Reed, David
APPLICANT: Tordoff, Michael G.
TITLE OF INVENTION: GENE AND SEQUENCE VARIATION ASSOCIATED WITH SENSING
TITLE OF INVENTION: CARBOHYDRATE COMPOUNDS AND OTHER SWEETNERS
TITLE OF INVENTION: CARBOHYDRATE COMPOUNDS AND OTHER SWEETNERS
TILE REFERENCE: PC18306A
CURRENT FILING DATE: 2002-10-25
PRIOR PLILOG DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 652
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 284
LENGTH: 20
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100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0; Indels
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US-10-280-183A-286/c
Sequence 286, Application US/10280183A
; Publication No. US20040081964A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 284, Application US/10280183A; Publication No. US20040081964A1; GENERAL INFORMATION:
Sequence 21, Application US/10159339; Publication No. US20030166540A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Pfizer Inc. APPLICANT: Bachmanov, Alexander A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beauchamp, Gary K.
Chatterjee, Aurobindo
De Jong, Pieter J.
Li, Shanru
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Matches 16; Conservative
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ORGANISM: Homo sapiens
US-10-280-183A-284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
US-10-159-339-21
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US-10-280-183A-284/c
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APPLICANT: Basacham Gary Kall
APPLICANT: De Jong, Pieter J.
APPLICANT: ORGEN DATE SENDENCE VARIATION ASSOCIATED WITH SENSING
ITILE OF INVENTION: CARGONITRANTE COMPOUNDS AND OTHER SWEETERS
AND APPLICANT: 2000-10.25
FRACTOR PRILING DATE: 2000-10.25
FRACTOR PRILING DATE: 2000-10.25
FRACTOR PRILING DATE: 2000-10.25
FRACTOR SWEETER SWEETER SWEETER SWEETERS
AND APPLICANT: APPLICATION WARREN: 60/20.79
FRACTOR PRILING DATE: 2000-10.25
FRACTOR SWEETER SWEETER SWEETER SWEETERS
AND APPLICANT: APPLICATION WARRANTE SWEETER SWEETERS
AND APPLICANT: APPLICATION WARRANTE SWEETER SWEETERS
APPLICANT: BASIGNATION AND APPLICANTION WARRANTE APPLICANTE SWEETER SWEETERS
APPLICANT: BASIGNATION AND APPLICANTION WARRANTE SWEETERS
APPLICANT: BASIGNATION AND APPLICANTION WARRANTE SWEETERS
APPLICANT: BASIGNATION WARRANTE SWEETERS
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US-10-655-847-48

is Sequence 48, Application US/10655847

j Publication No. US20040063129A1

j GENERAL INFORMATION:
 j APPLICANT: William Garde

j APPLICANT: Susan M. Freier

APPLICANT: Andrew T. Watt

j TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION

j TITLE OF INVENTION: NUMBER: US/10/655,847

CURRENT PILING DATE: 2003-09-05

j PRIOR PILING DATE: 2003-09-05

j PRIOR FILING DATE: 2003-09-05

j NUMBER: OF SEQ ID NOS: 296
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SGRERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: William Garde
APPLICANT: Andrew T. Watt
TITLE OF INVENTION ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION
FILE REPERENCE: RTS-0189
CURRENT APPLICATION NUMBER: US/10/160,807
CURRENT PILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 296
SEQ ID NO 196
APPLICANT: William Gaarde
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Andra M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION
FILE REFERENCE: RTS-0189
FURBENT APPLICATION NUMBER: US/10/160,807
CURRENT PILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 296
SEQ ID NO 48
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.4%; Score 15.8; DB 1;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2;
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Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 185
US-10-160-807-196/c
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LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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Sequence 805, Application US/10923516
Publication No. US2005017602541
Sequence 805, Application No. US2005017602541
Sequence 805, Application No. US2005017602541
GENERAL INFORMATION:
APPLICANT: Sithar Therapeutic, Inc.
APPLICANT: Sithar Therapeutic, Inc.
APPLICANT: Sithar Therapeutic, James
APPLICANTION: USA Inceference Mediated Inhibition of B-Cell CLL/Lymphoma-2
ITILE OF INVENTION: MAN Inceference Expression Using Short Interfering Nucleic Acid (sin)
FILE REPERENCE: 400/1/3 (MH802-14.F)
CURRENT FILING DATE: 2004-06-24
PRIOR PRILING DATE: 2003-02-18
PRIOR PRILING DATE: 2003-02-18
PRIOR PRILING DATE: 2003-05-24
PRIOR PRILING DATE: 2003-05-24
PRIOR PRILING DATE: 2003-05-24
PRIOR PLILING DATE: 2003-02-20
PRIOR PLILING DATE: 2003-03-03-23
                                                                                                                                      . OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense US-10-923-516-391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region US-10-923-516-805
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1.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 47.4%; Pred. No. 1.7e+02;
Matches 9; Conservative 8; Mismatches 2;
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US-10-160-807-48
Sequence 48, Application US/10160807
; Publication No. US20030224514A1
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ORGANISM: Artificial Sequence
                                                                       TYPE: RNA
ORGANISM: Artificial Sequence
                                           LENGTH: 19
                                                                                                                                   FEATURE:
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Query Match
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                                                                                                                                                                                                                                                                                   Sequence 196, Application US/10655847

Publication No. US2004006312941

GERREAL INFORMATION:

APPLICANT: William Gaarde

APPLICANT: Andrew T. Watt

ITILE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION

FILE REFERENCE: RTS-0189

CURRENT APPLICATION NUMBER: US/10/160,807

PRIOR APPLICATION NUMBER: US/10/160,807

PRIOR FILING DATE: 2003-09-05

PRIOR FILING DATE: 2003-09-05

NUMBER OF SEQ ID NOS: 296

SEQ ID NO 196

LENGTH: 20
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                                                                                        1.4%; Score 15.8; DB 1; Length 20;
89.5%; Pred. No. 1.8e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15.8; DB 1; Length 20; Pred. No. 1.8e+02;
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2e+02;
~hea 2; Indels
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; Publication No. US20030027136A1
; GENERAL INFORMATION:
    APPLICANT: Geroray, Jorg J.
    TITLE OF INVENTION: RHEUMATOID ARTHRITIS MARKERS; FILE REFERENCE: 07039-221001
; CURRENT APPLICANTON INWER: US/09/816,814
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 23
; SOTWARE: PASELSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 21
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89.5%; Pred. No. ...
0; Mismatches
                 FEATURE:

COTHER INFORMATION: Antisense Oligonucleotide
US-10-655-847-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: primer for PCR US-09-816-814-7
                                                                                                                                                              783 TTGGGGATGTGCTTGGAGA 801
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ORGANISM: Artificial Sequence
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Best Local Similarity 89.53
Matches 17; Conservative
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Matches 17, Conservative
                                                                                                           Best Local Similarity 89.5
Matches 17; Conservative
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                                                                                                                                                                                                                                                                          US-10-655-847-196/c
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                                                                                         Query Match
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APPLICANT: Martinez, Robert
APPLICANT: Martinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM100927 (031896-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
PRIOR FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
SOFTWARE: PatentIn version 3.2
SEQ ID NO 45418
LIENGTH: 21
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0; Mismatches
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APPLICANT: Terry, Roemer D., APPLICANT: Charles, Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                        932 AGAAATGCAGAATCTGAAG 950
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                                                                                                                                                                                                                                                                                                ; TYPE: RNA
; ORGANISM: RNAi-sense strand
US-10-786-720-15221
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Matches 17; Conservative
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CORGANISM: homo sapiens
US-10-751-736-45418
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US-10-263-594-29
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TITLE OF INVENTOR Gene Disruption Methodologies for Drug Target Discovery FILE REFERENCE: 10182-065-999; CURRENT FILIAN DATE: 2001-12-20; CURRENT FILIAN DATE: 2001-12-20; NUMBER OF SEQ ID NOS: 8000 SOFTWARE: PatentIn version 3.1 SEQ ID NO 4031 LENGTH: 22 TYPE: TYPE: A 12 TYPE: TYPE
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| Sequence 29, Application US/10035978A
| Publication No. US20030165860A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Outlower Common PROBES, METHODS AND KITS FOR DETECTION
| TITLE OF INVENTION: BIOLOGICAL SAMPLES
| TITLE OF INVENTION: BIOLOGICAL SAMPLES
| FILE REFERENCE: INNOG2.001C1
| CURRENT APPLICATION NUMBER: US/10/035,978A
| CURRENT FILING DATE: 2001-12-21
| PRIOR FILING DATE: 1999-04-16
| PRIOR FILING DATE: 1999-04-16
| PRIOR APPLICATION NUMBER: EP 97870133.2
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1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels
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US-10-035-978A-29
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LENGTH: 22
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COMPUTER KEALABLE FORM:

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/263,594

FILING DATE: 0-0ct-2002

APPLICATION NUMBER: EP96/870131.8

FILING DATE: 16-0cT-1997

ATTORNEY AGENT INFORMATION:

NAME: 10-0cT-1997

ATTORNEY AGENT INFORMATION:

REGISTRATION NUMBER: 34,115

REGISTRATION NUMBER: 34,115

REGISTRATION NUMBER: 34,115

REGISTRATION NUMBER: 10-0cT-1997

ATTORNEY AGENT INFORMATION:

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: INNOG2.001APC

TELEPHONE: (949) 760-0404
                                                                                                                                                                                                                                                                    Query Match
1.4%; Score 15.6; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 15; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 280
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: P481 vacA-derived probe
US-10-035-978A-29
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ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
PRIOR FILING DATE: 1997-09-09
PRIOR APPLICATION NUMBER: EP 96870131.8
PRIOR FILING DATE: 1996-10-16
NUMBER OF SEQ ID NOS: 280
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 20
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TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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COUNTRY: USA
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Fri Aug 19 11:00:02 2005
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TYPE: DNA
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US-10-797-333A-95

US-10-797-333A-95

Sequence 95, Application US/10797333A

Publication No. US2004020929A1

GENERAL INFORMATION:

APPLICANT: RURIHARA, TAKAO

APPLICANT: SLEPTSOVA, IRINA

APPLICANT: SLEPTSOVA, IRINA

APPLICANT: BRUENING, ERIC EGON

APPLICANT: BRUENING, ERIC EGON

APPLICANT: MAKAROV, VLADIMIR L.

TITLE OF INVENTION: INVIRO DNA IMMORTALIZATION AND WHOLE GENOME

TITLE OF INVENTION: FRAGMENTED DNA

TITLE OF INVENTION: FRAGMENTED DNA

TITLE OF INVENTION: BAPLICATION USING LIBRARIES GENERATED FROM RANDOMLY

TITLE OF INVENTION: BAPLICATION UNDERS: 0504-03-08

CURRENT APPLICATION NUMBER: 60/453,071

FRIOR FILING DATE: 2004-03-08

NUMBER OF SEQ ID NOS: 145

SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SON, INC.
APPLICANT: SON, INC.
APPLICANT: PINTER, JONATHON H.
APPLICANT: PINTER, JONATHON H.
APPLICANT: SLEPTSON, IRINA
APPLICANT: MAKARO, TAKKO
APPLICANT: MAKAROV, VLADIMIR L.
ITILE OF INVENTION: AMPLIPICATION AND ANALYSIS OF WHOLE GENOME AND WHOLE
ITILE OF INVENTION: TRANSCRIPTOME LIBRARIES GENERATED BY A DNA
ITILE OF INVENTION: POLYMERIZATION PROCESS
ITILE REPERENCE: RUBC. 10210-103-08
CURRENT FILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: 66/453,060
PRIOR PILING DATE: 2003-0-07
NUMBER OF SEQ ID NOS: 127
SOFTHARE: PALENTIN Ver. 2.1
SEG ID NO 93
LENGTH: 22
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                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Query Match 1.4%; Score 15.6; DB 1; Length 20; Best Local Similarity 83.3%; Pred. No. 1.9e+02; Matches 15; Conservative 2; Mismatches 1; Indels
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1.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels
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Sequence 93, Application US/10795667
Publication No. US20040209298A1
GENERAL INFORMATION:
APPLICANT: KAMBEROV, EMMANUEL
                                                                                                103 CTTCAGTGGGCTATTGG 120
                                                                                                                             2 CTTTAGTRGGGYTATTGG 19
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LENGTH: 22
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Sequence 11660, Application US/10349143

Publication No. US20040005584A1

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE: GENSET.020CP1

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US/10/349,143

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US 09/298,850

PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21

PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

WHMBER OF SEQ ID NOS: 11796

LENGTH: 18
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, OTHER INFORMATION: downstream amplification primer 99-21246 for SEQ 3795, in complem
US-10-349-143-11660
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APPLICANT: LOBUGILO, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
TITLE OF INVENTION: PACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER TITLE OF INVENTION: AGENTS
FILE REFERENCE: 21085.0029U6
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                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic;; OTHER INFORMATION: Primer
US-10-797-333A-95
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; Publication No. US2030133932A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
                                                                                                                                                                                                                                                                                                         297 GAATTGTTGTTTCTGCCTTTGG 318
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Ichkawa, Kimihisa ·
Kimberly, Robert P.
Koopman, William J.
Oshumi, Jun
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 94.1
Matches 16; Conservative
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APPLICANT:
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APPLICANT:
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; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637Ale = Synthe US-10-286-132A-9
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085.0029U7
CURRENT APPLICATION NUMBER: US 10/286,132A
CURRENT PILING DATE: 2001-01-22
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR PLILOR DATE: 2001-05-02
PRIOR PLILOR DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
SOFTWARE: PATCHIN VERSION 3.0
SEQ ID NOS: 102
SEQ ID NOS: 102
SEQ ID NOS: 102
SEQ ID NOS: 103
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US-10-688-706-2397

Sequence 2397, Application US/10688706

Sequence 2397, Application US/10688706

Publication No. US20040102412A1

GENERAL INFORMATION:

APPLICANT: Broschat, Kay

TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION

TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION

FILE REFERENCE: 01393/1

CURRENT APPLICATION NUMBER: US/10/688,706

CURRENT PILING DATE: 2002-10-17

PRIOR APPLICATION NUMBER: 60/419,268

PRIOR APPLICATION NUMBER: 60/419,268

PRIOR APPLICATION NUMBER: 60/419,268

SEQ ID NO 2397

LENGTH: 20
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Pred. No. 2e+02;
0; Mismatches 1; Indels
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US-10-688-706-2465
Sequence 2465, Application US/10688706
Publication No. US20040102412A1
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Broschat, Kay,
TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
FILE REPERENCE: 01393/1
CURRENT APPLICATION NUMBER: US/10/688,706
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1.4%; Score 15.4; DB 1;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1;
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1.4%;
Best Local Similarity 94.1%;
Matches 16; Conservative (
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Sequence 9, Application US/10275180A
Publication No. US20030190687A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: The UAB Research Foundation
APPLICANT: The UAB Research Foundation
APPLICANT: Chikawa, Kinihisa
APPLICANT: Kimberly, Robert P.
APPLICANT: Kimberly, Robert P.
APPLICANT: NUMBRICON: INDUCING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085.0029U5
CURRENT APPLICATION NUMBER: US/10/275,180A
CURRENT FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthe US-10-281-479A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687Ale = , OTHER INFORMATION: Synthetic Construct US-10-275-180A-9
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1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 1.4%; Score 15.4; DB 1; Length 20; Local Similarity 94.1%; Pred. No. 2e+02; les 16; Conservative 0; Mismatches 1; Indels
                             Sequence 9, Application US/10286132A
Publication No. US20030198637A1
GENERAL INFORMATION:
APPLICANT: Zhou, Tong
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: LoBuglio, Albert S.
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                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: artificial sequence
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US-10-286-132A-9
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Matches
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Query Match
Best Local Similarity 85.0°
Matches 17; Conservative
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Best Local Similarity 85.0
Matches 17; Conservative
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; TYPE: DNA
; ORGANISM: Human
US-09-817-913-33
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LENGTH: 20
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; Publication No. US20040102412A1
; GENERAL INFORMATION:
    APPLICANT: Pharmacia Corp.
; APPLICANT: Pharmacia Corp.
; APPLICANT: Pharmacia Corp.
; APPLICANT: PARSCHALE, Kay
; TILLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; PILE REPERENCE: 01393/1;
; CURRENT PILING DATE: 2003-10-17
; PRIOR PAPLICATION NUMBER: 60/419,268
; PRIOR PAPLICATION NUMBER: 60/419,268
; PRIOR APPLICATION NUMBER: 50/419,268
; ROTHWARE: Patentin version 3.2
; SEQ ID NO 2639
; LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2492, Application US/10688706

Publication No. US20040102412A1

GENERAL INFORMATION:

APPLICANT: Pharmacia Corp.

TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION

TITLE OF INVENTION: ANTISENSE NOULATION OF GFAT EXPRESSION

FILE REFERENCE: 0193/1

CURRENT FILING DATE: 2003-10-17

PRIOR FILING DATE: 2002-10-17

NUMBER OF SEQ ID NOS: 3071

SOFTWARE: Patentin version 3.2

LENGTH: 20
                                                                                                                                                                                                                                                                                 Query Match 1.4%; Score 15.4; DB 1; Length 20; Best Local Similarity 94.1%; Pred. No. 2e+02; Matches 16; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                    ) OTHER INFORMATION: human GFAT antisense US-10-688-706-2465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: human GFAT antisense
US-10-688-706-2492
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: 60/419,268
PRIOR FILING DATE: 2002-10-17
                                                                                                                                                                                                                                                                                                                                                                         553 TTAATATGCTGGGTTTT 569
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                                                               NUMBER OF SEQ ID NOS: 3071
SOFTWARE: Patentin version 3.2
SEQ ID NO 2465
LENCTH: 20
                                                                                                                                                         TYPE: DNA ORGANISM: artificial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 203
US-10-688-706-2492
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US-10-688-706-2639
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                                                                                                                                                                                             FEATURE:
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Sequence 33, Application US/09817538

Sequence 33, Application US/09817538

Patent No. US20020137162A1

GENERAL INFORMATION:

APPLICANT: Li, Zuomei

APPLICANT: Benefils, Claire

TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone

TITLE OF INVENTION: Deacetylase Isoforms

FILE REFERENCE: 106101.144

CURRENT APPLICATION NUMBER: US/09/817,538

CURRENT APPLICATION NUMBER: US 60/192,157

PRIOR APPLICATION NUMBER: US 60/192,157

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: L. Zuomei
APPLICANT: Bonfils, Claire
APPLICANT: Bonfils, Claire
APPLICANT: Bonfils, Claire
APPLICANT: Benefils, Claire
APPLICANT: Benefils, Claire
APPLICANT: Descreman, Jeffrey
TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
FILE REFERENCE: 106101.145
CURRENT APPLICATION NUMBER: US/09/817,913
CURRENT FILING DATE: 2001-03-26
PRIOR PILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
SEQ ID NO 33
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85.0%; Pred. No. 2.1e+02;
Ative 0; Mismatches 3; Indels
                                                                                 Query Match 1.4%; Score 15.4; DB 1; Length 20; Best Local Similarity 94.1%; Pred. No. 2e+02; Matches 16; Conservative 0; Mismatches 1; Indels
) OTHER INFORMATION: human GFAT antisense US-10-688-706-2639
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 33, Application US/09817913; Patent No. US20020061860A1; GENERAL INFORMATION:
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1 AGCCAGCTGCCACTTGATGC 20

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817 AGCAGGCCTCTCATGACCCA 836
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US-10-167-034-32/c
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APPLICANT: Bentils, Claire
APPLICANT: Lounei
APPLICANT: L. Zuomei
APPLICANT: Lounei
APPLICANT: Vaisburg, Arkadii
APPLICANT: Vaisburg, Arkadii
APPLICANT: Poirne, Daniel
APPLICANT: Fournel, Marielle
APPLICANT: Eavoie, Rico
APPLICANT: Fournel, Marielle
APPLICANT: Fournel, Marielle
APPLICANT: Fournel, Marielle
APPLICANT: Eavoie, Rico
APPLICANT: Lavoie, Rico
CURRENT EAPPLICATION NUMBER: US/10/051,819B
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US 60/261,674
PRIOR PLILING DATE: 2001-01-12
PRIOR PLILING DATE: 2001-01-12
SEQIPMARE: FastSEQ for Windows Version 4.0
SEQIPMARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                             APPLICANT: Lavoie, Rico
TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
FILE REFERENCE: MET-004USI
CURRENT APPLICATION NUMBER: US/10/052,390B
CURRENT FILING DATE: 2002-01-14
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 19
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 20
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1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.4%; Score 15.2; DB 1; Length 20; 85.0%; Pred. No. 2.1e+02;
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                                                                                             Sequence 18, Application US/10052390B Publication No. US20030148970A1 GENERAL INFORMATION:
APPLICANT: Besterman, Jeffery M. APPLICANT: Bonfils, Claire
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Woo, Soon H.
Vaisburg, Arkadii
Delorme, Daniel
Fournel, Marielle
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Best Local Similarity 85.0°
Matches 17; Conservative
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ORGANISM: Homo sapiens
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APPLICANT:
APPLICANT:
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APPLICANT:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
APPLICANT: KIM, Cheol Min
APPLICANT: KIM, Cheol Min
APPLICANT: KIM, Cheol Min
APPLICANT: PARK, Hee Kyung
ITILE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria
FILE REPERBNCE: PPO5020/PCT
CURRENT APPLICATION NUMBER: US/10/448,836
CURRENT APPLICATION NUMBER: KR 10-1999-0019631
PRIOR PLILING DATE: 1999-05-29
PRIOR FILING DATE: 1999-05-29
PRIOR FILING DATE: 1999-05-29
PRIOR PLILING DATE: 1999-05-29
PRIOR PLILING DATE: 1999-05-29
PRIOR PLILING DATE: 1999-05-29
PRIOR PPLICATION NUMBER: KR 10-1999-0019634
PRIOR PLILING DATE: 1999-05-29
PRIOR PLILING DATE: 1999-05-39
PRIOR PLILING DATE: 1990-05-39
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Sequence 32, Application WS/10167034

Publicatalion No. US20030228690A1

GRNERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: Kenneth W. Dobie
1TILE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-1 EXPRESS
1TILE REFERENCE: PTS-0003
FILE REFERENCE: PTS-00
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CRGANTSM: Artificial Sequence
PEATURE:
OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium
CTHER INFORMATION: diernhoferi
US-10-448-836-219
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1.4%; Score 15.2; DB 1;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3;
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Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Antisense Oligonucleotide US-10-167-034-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 998 TGCACATGAAAGTTTGAGAA 1017
Sequence 219, Application US/10448836
Publication No. US20030207313A1
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ORGANISM: Artificial Sequence
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US-10-289-762-6064/c

Sequence 6064, Application US/10289762

Sequence 6064, Application No. US-10-289162

Publication No. US-2040006218A1

GENERAL INFORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmenter
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preverant Reference: 9710-003-999

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/10/289,762

CURRENT FILING DATE: 2003-03-27

NUMBER OF SEQ ID NOS: 6849
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US-10-210-429-24/c
US-10-210-429-24/c
Sequence 24, Application US/10210429
Publication No. US20040023379A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HEPATOMA-DERIVED GROWTH FACTOR EXPRESSION
FILE REFERENCE: PTS-0048
CURRENT APPLICATION UNMBER: US/10/210,429
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 148
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Sequence 95, Application US/10210429
Publication No. US20040023379A1
Sequence 95, Application US/20210429
Publication No. US20040023379A1
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HEPATOMA-DERIVED GROWTH FACTOR EXPRESSION FILE REPERENCE: PTS-0048
CURRENT FILE OF THE OFFICE OFF
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illarity 85.0%; Pred. No. 2.1e+02;
Conservative 0; Mismatches 3;
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1.4%; Score 15.2; DB 1;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3;
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US-10-210-429-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 459 AGTGGTAGCACTTTATTCTG 478
           1 TGCACAACAACTTTGAGAA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 AGGCAGAAAACCCTGAAGGA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-6064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 24
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Sequence 219, Application US/10448914A

Sequence 219, Application US/10448914A

Bublication No. US20030235856A1

GENERAL INFORMATION:

APPLICANT: KIM, Oscip Joon; SJ HIGHTECH Co., Ltd.

APPLICANT: KIM, Checl Min

APPLICANT: KIM, Checl Min

APPLICANT: MIM, Checl Min

TITLE OF INVENTION OLIGORACEORIGE for detection and identification of Mycobacteria

FILE REFERENCE: PRO5020/PCT

CURRENT APPLICATION NUMBER: US/10/448,914A

CURRENT PILING DATE: 1999-05-29

FRIOR APPLICATION NUMBER: KR 10-1999-0019631

FRIOR APPLICATION NUMBER: KR 10-1999-0019634

FRIOR PELING DATE: 1999-05-29

FRIOR APPLICATION NUMBER: KR 10-1999-0019634

FRIOR APPLICATION NUMBER: KR 10-1999-0019634

FRIOR PELING DATE: 1999-05-29

FRIOR APPLICATION NUMBER: KR 10-1999-0019635

FRIOR APPLICATION NUMBER: KR 10-1999-0019635

FRIOR APPLICATION NUMBER: KR 10-1999-0019635

FRIOR PELING DATE: 1999-05-29

FRIOR FILING DATE: 1999-05-29

FRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 243

SOFTWARE: KOPATENTIN 1.71

SEQ ID NO 219

LENGTH: 20
                                                                                                                                                               Sequence 103, Application US/10167034

Publication No. US20030228690A1

GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: Suban M. Preier
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-1 EXPRESS
FILE REFERENCE: PTS-0003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.4%; Score 15.2; DB 1; Length 2
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/167,034
CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 142
SEQ ID NO 103
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20 AGGAGGCCTCCTATGACCCA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 212
US-10-448-914A-219
                                                                                                           RESULT 211
US-10-167-034-103
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US-10-870-587-33
US-10-870-587-33
US-10-870-587-33

Sequence 33, Application US/10870587

Publication No. US20040266718A1

GENERAL INFORMATION:
APPLICANT: Li, Zuomei
APPLICANT: Bonfils, Claire
APPLICANT: Besteram, Jeffrey
TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
FILE REFERENCE: 106101.145
CURRENT APPLICATION NUMBER: US/10/870,587
CURRENT FILING DATE: 2004-06-17
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Version 3.1
SEQ ID NO 33
LENGTH: 20
TWO 33
LENGTH: 20
TWO 33
TWO 34
TO 35
TEND 35
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Pred. No. 2.18+02;
0; Mismatches 3; Indels
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Sequence 249, Application US/10913280

Publication No. US20050089894A1

SEMERAL INFORMATION:
APPLICANT: Ginns, Edward I.
APPLICANT: Ginns, Edward I.
APPLICANT: Ginns, Edward I.
TITLE OF INVENTION: SYSTEMS AND METHODS FOR ANALYZING
CURRENT PLILIAG DATE: 2004-08-06
FRIOR PRILING DATE: 2003-08-06
FRIOR PRILING DATE: 2003-08-06
FRIOR PRILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 920
SOFTWARE: PSECE FOR WINGOWS VERSION 4.0
SEQ ID NOS: 920
SED INFORMATE: 2004-05-07
SEQ ID NOS: 920
SED INFORMATE: 2004-05-07
SEQ ID NOS: 920
SED INFORMATE: 2004-05-07
SED INFORMATE: PROSE FOR WINGOWS VERSION 4.0
Indels
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85.0%; Pred. No. 2.1e+02;
tive 0; Mismatches 3;
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       0; Mismatches
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                                                       608 TTCATAAGTAGGAGATGAGT 627
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ORGANISM: Artificial Sequence
                                                                                                            20 Trcccaagragcagargagr
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Best Local Similarity 85.0%;
Matches 17; Conservative
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Best Local Similarity 85.0
Matches 17; Conservative
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          17; Conservative
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US-10-870-587-33
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                  Matches
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US-10-189-818B-30

US-10-189-818B-30

Sequence 30, Application US/10189818B

Publication No. US20040072770&1

GENERAL INFORMATION:

APPLICANT: BESTERMAN, UEFFREY M.

APPLICANT: DELORME, DANIEL

APPLICANT: DELORME, DANIEL

APPLICANT: DELORME, DANIEL

APPLICANT: DELORME, DANIEL

APPLICANT: BONFILS, CLAIRE

TITLE OF INVENTION: METHODS FOR SPECIFICALLY INHIBITING HISTONE DEACTYLASE-7 AND 8

FILE REFERENCE: METHODS FOR SPECIFICALLY

CURRENT PILING DATE: 2002-07-03

NUMBER OF SEQ ID NOS: 41

SEQ ID NO 30

LENGTH: 20
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Sequence 9, Application US/10673886A
Publication No. US20040132139A1
GENERAL INFORMATION:
APPLICANT: GENODYSEE
TITLE OF INVENTION: New Polymucleotides and Polypeptides of the IFNalpha-21 Gene
FILE REFERENCE: BIF0022965 PCT
CURRENT APPLICATION NUMBER: US/10/673,886A
CURRENT APPLICATION NUMBER: FR 0 104 404
PRIOR APPLICATION NUMBER: FR 0 104 404
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 20
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US-10-189-818B-30
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1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
OTHER INFORMATION: Synthetic oligonucleotide
                                                                                                                                                                      Query Match
1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
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CRGANISM: Homo sapiens
US-10-673-886A-9
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Best Local Similarity
                                                            TYPE: DNA ORGANISM: H. sapiens
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                                                                                                                            ; FEATURE:
US-10-210-429-95
                                     LENGTH: 20
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; OTHER INFORMATION: Antisense compound US-10-831-901A-14585
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APPLICANT: Hofstadler, Steven A.
APPLICANT: Hofstadler, Steven A.
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Swayze, Eric
APPLICANT: Baker, Brenda F.
APPLICANT: Baker, C. Frank
TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
TILE OF INVENTION: Acute Respiratory Syndrome (SARS)
TILE OF INVENTION: Acute Respiratory Syndrome (SARS)
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
TILE OF INVENTION: Acute Respiratory Syndrome (SARS)
CURRENT FILING DATE: 2004-04-26
PRIOR PILING DATE: 2003-04-28
PRIOR PRILING DATE: 2003-04-30
PRIOR PILING DATE: 2003-04-30
PRIOR PILING DATE: 2003-04-30
PRIOR PILING DATE: 2003-06-10
PRIOR PILING DATE: 2003-06-27
NUMBER OF SEQ ID NOS: 30063
SECOIL NO 14 656
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                                                                                 Sequence 18, Application US/10498505A
Publication No. US20050090642A1
GENERAL INFORMATION:
APPLICANT: MYAMAKI, Atsushi
APPLICANT: MARASAWA, Satoshi
TITLE OF INVENTION: Fluorescent Protein
FILE REPERENCE: P25481
CURRENT APPLICATION NUMBER: US/10/498,505A
CURRENT APPLICATION NUMBER: PCT/JP02/13363
PRIOR FILING DATE: 2004-06-18
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.3
SEQ ID NO 18
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Publication No. US20050100885A1
GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
APPLICANT: Sampath, Rangarajan
APPLICANT: Freier, Susan M.
APPLICANT: Massire, Christian
APPLICANT: Hofstadler, Steven A.
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Swayze, Eric
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ORGANISM: Artificial Sequence
PEATURE:
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ORGANISM: Artificial
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LENGTH: 20
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### APPLICANT: Fretaer, Christian APPLICANT: Fretaer, Christian APPLICANT: Hoferadler, Christian APPLICANT: Hoferadler, Steven A.
#### APPLICANT: Howery, Kristin Sannes
#### APPLICANT: Baker, Eric
#### APPLICANT: Baker, Brenda F.
### APPLICANT: Composition And Methods For The Treatment Of Severe
### TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
### FILING DATE: 2004-04-26
### PRIOR APPLICATION NUMBER: 60/466,426
### PRIOR APPLICATION NUMBER: 60/466,562
### PRIOR APPLICATION NUMBER: 60/469,562
### PRIOR PRIING DATE: 2003-05-06
### PRIOR PRIING DATE: 2003-06-10
### PRIOR PRIO
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1.4%; Score 15.2; DB 1; Length 20;
85.0%; Pred. No. 2.1e+02;
ative 0; Mismatches 3; Indel8
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; Sequence 15629, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14586, Application US/10811901A Publication No. US20050100885A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Crooke, Stanley T.
APPLICANT: Excer, David J.
APPLICANT: Sampath, Rangarajan
APPLICANT: Freier, Susan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
         Query Match
Best Local Similarity 85.0°
Matches 17; Conservative
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TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                      FEATURE:
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APPLICANT: Crooke, Stanley T.
APPLICANT: Crooke, Stanley T.
APPLICANT: Ecker, David J.
APPLICANT: Sampath, Rangarajan
APPLICANT: Sampath, Rangarajan
APPLICANT: Massire, Christian
APPLICANT: Hofstadler, Steven A.
APPLICANT: Hofstadler, Steven A.
APPLICANT: Hofstadler, Steven A.
APPLICANT: Baker, Brenda F.
APPLICANT: Baker, Brenda F.
APPLICANT: Baker, Brenda F.
APPLICANT: Baker, Brenda F.
APPLICANT: Bannet. C. Frank
APPLICANT: Baker, Brenda F.
APPLICANT: Bannet. C. Frank
APPLICANT: Bannet. 2003-04-06
PRIOR FILING DATE: 2003-04-07
PRIOR APPLICANTION NUMBER: 60/468,627
PRIOR APPLICANTION NUMBER: 60/468,627
PRIOR APPLICANTION NUMBER: 60/477,637
PRIOR APPLICANTION NUMBER: 60/477,637
PRIOR FILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-10
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APPLICANT: Hofstadler, Steven A.
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Swayze, Eric
APPLICANT: Baker, Brenda F.
APPLICANT: Baker, Brenda F.
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
FILE REFERENCE: ISISO083-100 (BIOL0008US)
CURRENT APPLICATION NUMBER: US/10/831,901A
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                                                                                                                                                                                                                                                                                       CUKKENT FILING DATE: 2004-04-26

PRIOR APPLICATION NUMBER: 60/466,426

PRIOR PILING DATE: 2003-04-28

PRIOR PILING DATE: 2003-04-28

PRIOR PILING DATE: 2003-05-06

PRIOR PILING DATE: 2003-05-06

PRIOR PILING DATE: 2003-06-07

PRIOR PILING DATE: 2003-06-07

PRIOR PILING DATE: 2003-06-07

PRIOR PLING DATE: 2003-06-07

PRIOR PLING DATE: 2003-06-10

PRIOR PLING DATE: 2003-06-10

PRIOR PLING DATE: 2003-06-10

PRIOR PLING DATE: 2003-06-10

PRIOR PLING DATE: 2003-06-17

PRIOR PLING DATE: 2003-06-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Antisense compound US-10-831-901A-15629
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ORGANISM: Artificial Sequence
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Best Local Similarity
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GENERAL INFORMATION:

APPLICANT: Crooke, Stanley T.
APPLICANT: Ecker, David J.
APPLICANT: Sampath, Rangarajan
APPLICANT: Sampath, Rangarajan
APPLICANT: Sampath, Rangarajan
APPLICANT: Herier, Susan M.
APPLICANT: Herier, Christian Sannes
APPLICANT: Hofstadler, Steven A.
APPLICANT: Hofstadler, Steven A.
APPLICANT: Baker, Brenda F.
APPLICANTON TOWNER: US/10/831,901A
CURRENT APPLICATION NUMBER: 60/466,426
PRIOR PLING DATE: 2003-04-26
PRIOR PLING DATE: 2003-04-26
PRIOR APPLICATION NUMBER: 60/468,527
PRIOR PLING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/468,537
PRIOR PLING DATE: 2003-06-10
PRIOR APPLICATION NUMBER: 60/483,579
PRIOR PRIUNG DATE: 2003-06-10
PRIOR APPLICATION NUMBER: 60/483,579
PRIOR PRIUNG DATE: 2003-06-10
PRIOR APPLICATION NUMBER: 60/483,579
PRIOR PRIUNG DATE: 2003-06-27
NUMBER PRIUNG DATE: 2003-06-27
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                                                                                                                                                                                                                                                                                          Query Match 1.4%; Score 15.2; DB 1; Length 20; Best Local Similarity 85.0%; Pred. No. 2.1e+02; Matches 17; Conservative 0; Mismatches 3; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26186
LENGTH: 20
NUMBER OF SEQ ID NOS: 30063
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26184
LENGTH: 20
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US-10-831-901A-26187/c
; Sequence 26187, Application US/10831901A
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                                                                                                                                                                                                         ; OTHER INFORMATION: Antisense compound US-10-831-901A-26184
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ORGANISM: Artificial Sequence
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TYPE: DNA
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                                                                                                                APPLICANT: ECKET, UBYLD U.

APPLICANT: ECKET, SUBBATH, RANGBATAJAN
APPLICANT: Freier, Suban M.
APPLICANT: Massire, Christian
APPLICANT: Massire, Christian
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Swayze, Eric
APPLICANT: Swayze, Eric
APPLICANT: Bennett, C. Frank
ITILE OF INVENTION: Compositions And Methods For The Treatment Of Severe
ITILE OF INVENTION: Compositions And Methods For The Treatment Of Severe
ITILE OF INVENTION: Compositions And Methods For The Treatment Of Severe
ITILE OF INVENTION: Compositions And Methods For The Treatment Of Severe
ITILE OF INVENTION: Acute Respiratory Syndrome (SARS)
ITILE OF INVENTION NUMBER: U8/10/831,901A
CURRENT PILING DATE: 2003-04-26
PRIOR PILING DATE: 2003-04-26
PRIOR PPLICATION NUMBER: 60/466,426
PRIOR APPLICATION NUMBER: 60/466,57
PRIOR PPLICATION NUMBER: 60/466,627
PRIOR APPLICATION NUMBER: 60/468,627
PRIOR PILING DATE: 2003-06-10
PRIOR PLING DATE: 2003-06-10
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Sequence 26489, Application US/10831901A

Publication No. US20050100885A1

GENERAL INFORMATION:

APPLICANT: Crooke, Stanley T.

APPLICANT: Sampath, Rangarajan

APPLICANT: Freier, Susan M.

APPLICANT: Hofstadler, Steven A.

APPLICANT: Hofstadler, Steven A.

APPLICANT: Hofstadler, Steven A.

APPLICANT: Baker, Bric

APPLICANT: Baker, Bric

APPLICANT: Compositions And Methods For The Treatment Of Severe

TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe

TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe

TITLE REFERENCE: ISISO083-100 (BIOL0008US)

CURRENT APPLICATION NUMBER: US/10/831,901A

CURRENT FILING DATE: 2004-04-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Antisense compound US-10-831-901A-26187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/466,426
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: 60/468,562
PRIOR FLILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/467,770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 TTCCTGTTATTCTTGCTCGT 340
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Publication No. US20050100885A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-831-901A-26489/c
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Sequence 4773, Application US/10257158A

Bublication No. US20050142543A1

GENERAL INFORMATION.

APPLICANT: Zirvi, Monib

APPLICANT: Zirvi, Monib

APPLICANT: Zirvi, Monib

APPLICANT: Eavis, Reyna

APPLICANT: Favis, Reyna

APPLICANT: Kliman, Richard

ITLE OF INVENTION: SEQUENCE DIFFERENCES USING LIGASE DETECTION OF NUCLBIC AC

ITLE OF INVENTION: SEQUENCE DIFFERENCES USING LIGASE DETECTION REACTION

FILE REFERENCE: 19603/2834

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: PCT/US01/10958

FRIOR FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 9544

SEQ ID NO 4773

LENGTH: 20

LENGTH: 2
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Sequence 7299, Application US/10786720

Publication No. US20040191818A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Weth

APPLICANT: Liu, Wei

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
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PRIOR APPLICATION NUMBER: 60/468,627
PRIOR FILING DATE: 2003-05-06
PRIOR PILING DATE: 2003-05-06
PRIOR PILING DATE: 2003-06-10
PRIOR PILING DATE: 2003-06-10
PRIOR PILING DATE: 2003-06-27
NUMBER OF SEQ ID NOS: 30063
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 26489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Antisense compound US-10-831-901A-26489
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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Best Local Similarity 85.09
Matches 17; Conservative
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DEBLECANT: Wyeth APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: O'Toole, Margot APPLICANT: O'Toole, Margot APPLICANT: O'Toole, Margot TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE TITLE OF INVENTION: DISEASES FILE REFERENCE: 031896-023000 (AM101331L) CURRENT APPLICATION NUMBER: US/10/786,720 CURRENT FILING DATE: 2004-02-26 NUMBER OF SEQ ID NOS: 21135 SOFTWARE: PATENTIN OF SEQ ID NOS: 21135 SOFTWARE: PATENTIN OF SEQ ID NOS: 21135 LENGTH: 21
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Pred. No. 2.38+02;
5; Mismatches 3; Indels
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85.0%; Pred. No. 2.3e+02;
iive 0; Mismatches 3;
Best Local Similarity 85.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 3
                                                                                                                                                                                                                                                                           ; Sequence 15111, Application US/10786720
; Publication No. US20040191818A1
; GENERAL INFORMATION:
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                                                                                        927 TTATTAGAAATGCAGAATCT 946
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                                                                                                                                                21 Tracaágacargcagaarcr 2
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Best Local Similarity 60.0%;
Matches 12; Conservative
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Best Local Similarity 85.0°
Matches 17; Conservative
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; ORGANISM: RNAi
US-10-751-736-44459
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US-10-913-280-632/c
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Publication No. US20040191818A1
GENERAL INFORMATION:
APPLICANT: Week
APPLICANT: O'TOOle, Wargot
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
TITLE OF INVENTION: DISEASES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOUTHWARE: Patentin version 3.2
SEQ ID NO 15:109
LENGTH: 2109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9567, Application US/10786720

Sequence 9567, Application No. US20040191818A1

SERVERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: O'TOOLE, Margot
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1.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 9; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                              1.4%; Score 15.2; DB 1; Length 21;
40.0%; Pred. No. 2.3e+02;
tive 9; Mismatches 3; Indels
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                          ; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: 031896-023000 (AM101331L)
; CURRENT APPLICATION NUMBER: US/10/786,720
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 21135
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7299
; LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                678 ATGTTACTTGTTTGGCTGTT 697
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CRGANISM: RNAi-antisense strand
US-10-786-720-9567
                                                                                                                                                                                                                                                          TYPE: RNA CRGANISM: RNAi-antisense strand US-10-786-720-7299
                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.49
Best Local Similarity 40.09
Matches 8; Conservative
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US-10-786-720-9567
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Query Match

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JOS-193-79-703-6
Sequence 6, Application US/09749709
Sequence 6, Application US/09749709
Sequence 6, Application No. US20010032340A1
GENERAL INFORMATION:
APPLICANT: LIU, CHENGYU
APPLICANT: WANG, JIN
TITLE OF INVENTION: TRANSGENES ONTO THE SEX CHROMOSOMES
TITLE OF INVENTION: TRANSGENES ONTO THE SEX CHROMOSOMES
TITLE OF INVENTION: TRANSGENES ONTO THE SEX CHROMOSOMES
CURRENT APPLICATION NUMBER: US/09/749,709
CURRENT FILING DATE: 2000-12-27
PRIOR PELIGN DATE: 1999-12-27
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
1.3%; Score 15; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-838-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-751-736-26321
; Sequence 26321, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1079 CTTAACCTCTCTGGG 1093
                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 TGGCTGTGATCAAAT 356
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
ORGANISM: RNAi
                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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APPLICANT: Wyeth
APPLICANT: Be, Xiaobing
APPLICANT: Be, Xiaobing
APPLICANT: Blui, Weth
APPLICANT: Slonim, Donna
APPLICANT: Howes, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
FILE REFERENCE: 031896-026000 (AMI01264)
CURRENT APPLICATION NUMBER: US/10/847,918
FRIOR APPLICATION NUMBER: US 60/471,729
PRIOR APPLICATION NUMBER: US 60/471,729
PRIOR PLING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 14937
SOFTWARE: Patentin version 3.2
LENGTH: 21

LENGTH: 21
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                                                               APPLICANT: Galdaicka, Marzena
APPLICANT: Galdaicka, Marzena
TITLE OF INVENTION: SYSTEMS AND METHODS FOR ANALYZING
TITLE OF INVENTION: SYSTEMS AND METHODS FOR ANALYZING
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES
FILE REPERENCE: 07917-238001
CURRENT FAPLICATION NUMBER: US 60/493,238
FRIOR APPLICATION NUMBER: US 60/493,238
FRIOR APPLICATION NUMBER: US 60/566,956
FRIOR APPLICATION NUMBER: US 60/566,956
FRIOR APPLICATION NUMBER: US 60/566,956
FRIOR FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 920
SEQ ID NO 632
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 8793, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
Sequence 632, Application US/10913280 Publication No. US20050089894A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-210-838-82/c
Sequence 82, Application US/10210838
Fublication No. US/20040023905A1
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Sanjay Bhanot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 GTGGCATTATCCTTCAGTGG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: RNA
; ORGANISM: RNAi-antisense strand
US-10-847-918-8793
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Primer
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Matches 10; Conserva
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APPLICANT: Wyeth

APPLICANT: Watch

APPLICANT: Martinez, Robert

APPLICANT: Brown, Eugene

APPLICANT: Liu, Wei

TITLE OF INVENTION: CANCERS

FILE OF INVENTION: CANCERS

FILE REFERENCE: AMIO927 (031896-002000)

CURRENT APPLICATION NUMBER: US/10/751,736

CURRENT APPLICATION NUMBER: US/10/751,736

FILE OF INVENTION: CANCERS

FILE REFERENCE: AMIO927 (031896-002000)

CURRENT APPLICATION NUMBER: US/10/751,736

FILE REPERENCE: AMIO937 (031896-002000)

CURRENT APPLICATION NUMBER: US/10/751,736

FRIOR FILING DATE: 2003-01-06

PRIOR FILING DATE: 2003-01-06

NUMBER OF SEQ ID NOS: 54873

SOFTWARE: PALENTIN VERSION 3.2

SEQ ID NO 26321 Gaps ö ö APPLICANT: Kenneth W. Dobie
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF LAR EXPRESSION
FILE REPERENCE: PTS-0013
CURRENT APPLICATION NUMBER: US/10/210,838
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 198
SEQ ID NO 82
LENGTH: 20 0; Indels Length 20; 1.3%; Score 15; DB 1; Length 21; 66.7%; Pred. No. 2.5e+02;

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RESULT 236

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Sequence 9, Application US/09858152A

Sequence 9, Application US/09858152A

Publication NO. US20030044419A1

GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: Marchetti, Antonio
APPLICANT: Smith, Gilbert H.
APPLICANT: Smith, Gilbert H.
APPLICANT: Callahan, Robert
APPLICANT: Callahan, Robert
APPLICANT: SMITH SPECENTE: 4239-59122
CURRENT APPLICATION NUMBER: US/09/858,152A
CURRENT FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 32
CURRENT PRICES PATENTIN VERSION 3.1
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                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic US-09-800-629A-152
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US-10-002-974-52/C
Sequence 52, Application US/10002974
Sequence 52, Application US/10002974
Publication No. US20020197616A1
GENERAL INFORMATION:
APPLICANT: Numez, Gabriel
APPLICANT: Inchara, Nachiro
APPLICANT: Cho, Judy
APPLICANT: Cho, Judy
APPLICANT: Bonen, Danise
TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
FILE REPRENCE: UM-06646
CURRENT APPLICATION NUMBER: US/10/002,974
CURRENT APPLICATION NUMBER: 2001-10-26
NUMBER OF SEQ ID NOS: 99
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.3%; Score 14.8; DB 1;
88.9%; Pred. No. 2.4e+02;
tive 0; Mismatches 2;
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Best Local Similarity 88.9%; Pred. No. 2.46+02;
Matches 16; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Oligonucleotide primer US-09-858-152A-9
PRIOR APPLICATION NUMBER: 09/280,799
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 152
LENGTH: 20
                                                                                                                                                                                                                                                                                                            1050 ACTICCTTATCTTTCCAG 1067
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                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 88.9
Matches 16; Conservative
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LENGTH: 20
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; Sequence 152. Application US/09800629A
; Patent No. US20020128216A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Wicholas M.
; APPLICANT: MCKAY, ROBERT
; APPLICANT: MANOBAREN, Muthiah
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
; TITLE OF INVENTION: TRANSDUCTION
; TILE REFERENCE: ISPH-0537
; CURRENT APPLICATION NUMBER: US/09/800,629A
; CURRENT FILING DATE: 2001-03-07
; FRIOR FILING DATE: 2000-03-17
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1.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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Pred. No. 2.4e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/09734847A Patent No. US20020049173Al GENERAL INFORMATION: APPLICANT: Bennett, C. Frank APPLICANT: Crooke, Stanley T. APPLICANT: Manoharan, Muthiah APPLICANT: Manoharan, Muthiah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1050 ACTICCTTATCTTTCCAG 1067
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Best Local Similarity 88.9%;
Matches 16; Conservative (
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                    SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 6
                                                                             TYPE: DNA
CORGANISM: Mus musculus
US-09-749-709-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 240
US-09-800-629A-152
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US-09-734-847A-16
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US-10-462-691-67/c
US-10-444-206-314
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15 Sequence 68, Application US/10012984
15 Publication No. US20030118561A1
15 GENERAL INFORMATION:
16 APPLICANT: Kenneth W. Dobie
17 TITLE OF INVENTION: ANTI-SENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE 4 EXPRESSION
17 FILE REPERENCE: RTS-0334
18 CURRENT APPLICATION NUMBER: US/10/012,984
19 CURRENT FILING DATE: 2001-12-04
19 SEQ ID NOS: 92
10 ENGTH: 20
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Sequence 314, Application US/1044206

Publication No. US20040023917A1

GENERAL INFORMATION:

APPLICANT: Bennett, Clarence Frank
APPLICANT: Wickers, Timothy A.

APPLICANT: Wickers, Timothy A.

TITLE OF INVENTION: Modulation of the Expression of B7 Protein
FILE REPERBRECE:

CURRENT APPLICATION NUMBER: US/10/444,206

CURRENT FILING DATE: 2003-05-23

PRIOR PLILOM DATE: 2003-05-23

PRIOR PLILOM DATE: 2000-05-05

PRIOR PLILOM DATE: 2000-05-05

PRIOR APPLICATION NUMBER: PCT/US00/14471

PRIOR PLILOM DATE: 1999-06-04

PRIOR PLILOM DATE: 1999-06-04

PRIOR PLILOM DATE: 1999-06-04

PRIOR PLILOM DATE: 1999-12 31

NUMBER OF SEQ ID NOS: 444

SOFTWARE PLEATION VUMBER: 08/777,266

PRIOR PLING DATE: 1990-06-04

PRIOR PLING DATE: 1990-06-04

PRIOR PLING DATE: 1990-06-04

PRIOR PLING DATE: 1990-12 31

NUMBER OF SEQ ID NOS: 444

SOFTWARE PLEATION VUMBER: 08/05-04

SEQ ID NO 314

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                                                                                                                                                              Query Match 1.3%; Score 14.8; DB 1; Length 20; Best Local Similarity 88.9%; Pred. No. 2.4e+02; Matches 16; Conservative 0; Mismatches 2; Indels
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88.9%; Pred. No. 2.4e+02;
iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Antisense Oligonucleotide US-10-012-984-68
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                                                                                                                                                                                                                                                              784 TGGGGATGTGCTTGGAGA 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 418 TTTCCTTATATTTGGAAG 435
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                    TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                                        ; OTHER INFORMATION: Synthetic US-10-002-974-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Matches 16; Conserv
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                                                                      FEATURE:
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Sequence 67, Application US/10462691
Publication No. US20040053306A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VSABININGH HAYASHIZAKI
APPLICANT: Mamoru KAMIYA
ITILE OF INVENTION: Polynucleotides encoding short polypeptides, polypeptides encoded
ITILE OF INVENTION: and methods of use thereof
ITILE OF INVENTION: and methods of use thereof
CURRENT APPLICATION NUMBER: US/10/462,691
CURRENT FILING DATE: 2003-06-17
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.1
IENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 68. Application US/10673523
Sequence 68. Application US/10673523
Publication No. US20040110713A1
GENERAL INFORMATION
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE 4 EXPRESSION
CURRENT APPLICATION NUMBER: US/10/673,523
CURRENT PILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US/10/012,984
PRIOR PILING DATE: 2001-12-04
NUMBER 0F SEQ ID NOS: 92
SEQ ID NO 68
LENGTH: 20
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                                              Gaps
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US-10-462-691-67
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88.9%; Pred. No. 2.4e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.3%; Score 14.8; DB 1; Length 20;
88.9%; Pred. No. 2.4e+02;
tive 0; Mismatches 2; Indels
                                              Indels
1.3%; Score 14.8; DB 1; 88.9%; Pred. No. 2.4e+02;
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                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 418 TTTCCTTATATTTGGAAG 435
                                                                                        640 AAATAGACCTGTCAAATT 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 CCCAGTTCGGGAGACATG 73
                                                                                                                        20 AAATAGACCTCTCAATTT 3
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Query Match 1.39
Best Local Similarity 88.99
Matches 16; Conservative
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Best Local Similarity 88.9°
Matches 16; Conservative
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Matches 16; Conservative
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US-10-783-415-9
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; Sequence 15.2 Application WS/10679532
; Publication No. US20040121376A1
; Publication No. US20040121376A1
; GENERAL INFORMATION:
; APPLICANT: Rarray, Robert
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: ARTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
; TITLE OF INVENTION: TRANSDUCTION
; FILE REPRENCE: ISPH-0537
; CURRENT APPLICATION NUMBER: US/10/679,532
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: PCT/US00/629A
; PRIOR APPLICATION NUMBER: PCT/US00/07318
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Sequence 40, Application US/10317478

Sequence 40, Application US/10317478

Publication No. US20040115636A1

GENERAL INFORMATION:

APPLICANT: Brenda F. Baker

APPLICANT: Renneth W. Dobie

TITLE OF INVENTION: MODULATION OF INTERLEUKIN 18 EXPRESSION

FILE REFERENCE: PTS-0025

CURRENT APPLICATION NUMBER: US/10/317,478

CURRENT PILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 130

LENGTH: 20
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1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.40+02;
Matches 16; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
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1 Sequence 96, Application US/10317478

2 Sequence 96, Application US/10317478

3 Fublication No. US20040115636A1

3 Fublication No. US20040115636A1

3 Fublication No. US20040115636A1

3 APPLICANT: Kenneth W. Dobie

3 TITLE OF INVENTION: WODULATION OF INTERLEUKIN 18 EXPRESSION

7 TITLE OF INVENTION: WOUNDER: US/10/317,478

5 CURRENT APPLICATION UNDBER: US/10/317,478

5 CURRENT FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2: Indels
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1.3%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Antisense Oligonucleotide US-10-317-478-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          748 GCTGCCACCTTATGCAGT 765
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US-10-679-532-152
     US-10-317-478-40/c
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LENGTH: 20
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US-10-783-415-9/C

Sequence 9, Application US/10783415

Publication No. US20040141918A1

Publication No. US20040141918A1

Publication No. US20040141918A1

Publication No. US20040141918A1

APPLICANT: THE GOVERNAMENT OF THE UNITED STATES OF AMERICA AS

APPLICANT: HUMAN SERVICES

APPLICANT: Marchetti, Antonio

APPLICANT: Mattita, Fiamma

APPLICANT: Mutitata, Fiamma

APPLICANT: Smith, Gilbert H.

APPLICANT: Smith, Gilbert H.

APPLICANT: Scotta Solvente AND DEDUCED AMINO ACID SEQUENCES OF TUMOR GENE INT6

FILE REFERENCE: 4239-59122

CURRENT APPLICATION NUMBER: US/10/783,415

CURRENT FILING DATE: 2004-05-19

PRIOR FILING DATE: 2001-05-14

PRIOR FILING DATE: 2001-05-14

SEQ ID NO 9

LENGTH: 20

LENGTH: 20

FILENCE AND PARTICATION NUMBER: US/10/783,415

PRIOR FILING DATE: 2001-05-14

SEQ ID NO 9

LENGTH: 20

FILENCE AND 10 NO 9

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                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-10-679-532-152
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1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.3%; Score 14.8; DB 1; Length 20; Best Local Similarity 88.9%; Pred. No. 2.4e+02; Matches 16; Conservative 0; Mismatches 2; Indels
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Sequence 1118, Application US/10619739

Publication No. US20040175719A1

GENERAL INFORMATION:

TITLE OF INVENTION: Synthetic Tag Genes

FILE REFERENCE: 3502.1

CURRENT APPLICATION NUMBER: US/10/619,739

CURRENT FILING DATE: 2003-07-14

PRIOR APPLICATION NUMBER: 60/395,530

PRIOR FILING DATE: 2002-07-12

PRIOR FILING DATE: 2002-07-12

NUMBER OF SEQ ID NOS: 2068

SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THER INFORMATION: Oligonucleotide primer
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 09/280,799
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 152
LENGTH: 20
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JAPELICANT: Crooke, Stanley T.
APPLICANT: Ecker, David J.
APPLICANT: Ecker, David J.
APPLICANT: Freier, Sampath, Rangarajan
APPLICANT: Freier, Susan M.
APPLICANT: Massire, Christian
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Baker, Brenda F.
APPLICANT: Baker, Brenda F.
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
TITLE OF INVENTION: Compositions and Methods For The Treatment Of Severe
TITLE OF INVENTION: Compositions and Methods For The Treatment Of Severe
TITLE OF INVENTION: Compositions and Methods For The Treatment Of Severe
TITLE OF INVENTION: Compositions and Methods For The Treatment Of Severe
TITLE OF INVENTION: Compositions and Methods For The Treatment Of Severe
TITLE OF THE PRESENCE: ISSO083-100 (BIOLOGOBUS)
CURRENT APPLICATION NUMBER: US/10/831,901A
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TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3

TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3

TITLE OF INVENTION: Expression

FILE REFERENCE: ISPH-082

CURRENT APPLICATION NUMBER: US/10/773,678

CURRENT APPLICATION NUMBER: US/10/73,139

PRIOR APPLICATION NUMBER: 01/713,139

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2001-01-11

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 1099-04-08

PRIOR FILING DATE: 1999-04-08

PRIOR FILING DATE: 1999-04-08

NUMBER OF SEQ ID NOS: 402

SOFTWARE: PATENTION VET: 2.1

SEQ ID NO 222

LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2004-04-26
PRIOR APPLICATION NUMBER: 60/466,426
PRIOR PILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: 60/466,562
PRIOR PILING DATE: 2003-05-06
PRIOR PILING DATE: 2003-06-06
PRIOR PILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: 60/468,627
PRIOR APPLICATION NUMBER: 60/468,627
PRIOR PILING DATE: 2003-05-06
PRIOR PILING DATE: 2003-05-06
                                                                                                                                                                                      US-10-773-678-222/c
: Sequence 222, Application US/10773678
: Publication No. US20050074879A1
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     548 GAAATTTAATATGCTGGG 565
      640 AAATAGACCTGTCAAATT 657
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Matches 16; Conservative
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Sequence 47, Application US/10659473

Sequence 47, Application US/10659473

Sequence 47, Application O. US20040197966A1

Sequence 47, Application No. US2004019796A1

SEQUENCE INFORMATION:

APPLICANT: Bact P. Monia

APPLICANT: Bactuline Wyatt

TITLE OF INVENTION: ANTISENSE MODULATION OF PKA REGULATORY SUBUNIT RII BETA EXPRESSIC

TITLE OF INVENTION: ANTISENSE MODULATION OF PKA REGULATORY SUBUNIT RII BETA EXPRESSIC

CURRENT APPLICATION NUMBER: US/0659,473

CURRENT PILING DATE: 2003-09-100

PRIOR FILING DATE: 2001-07-25

NUMBER OF SEQ ID NOS: 83

LENGTH: 20
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TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
TITLE OF INVENTION: Oligonucleotide Compositions of B7 Protein
FILE REPERENCE: 30566/39578
FILE REPERENCE: 30566/39578
CURRENT APPLICATION NUMBER: US/10/641,962
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 444
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 314
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1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                     ; OTHER INFORMATION: Synthetic Oligonucleotide US-10-619-739-1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-659-473-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 663 TATGTTACTCAAATTATG 680
                                                                                                                                                                                                                                                                                                                                                                               697 TCATGTAGTCACGGTGCT 714
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                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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; SEQ ID NO 1118
; LENGTH: 20
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US-10-81-901A-16531

Sequence 15631, Application US/10831901A

Publication No. US20050100895A1

Publication No. US20050100895A1

APPLICANT: Crooke, Stanley T.

APPLICANT: Sampath, Rangarajan

APPLICANT: Becker, David J.

APPLICANT: Massire, Christian

APPLICANT: Massire, Christian

APPLICANT: Massire, Christian

APPLICANT: Benner, Steven A.

APPLICANT: Benner, C. Prank

APPLICANT: BROOS: 1004-04-26

PRIOR FILING DATE: 2003-04-26

PRIOR PRILNG DATE: 2003-05-06

PRIOR PLILNG DATE: 2003-05-06

PRIOR FILING DATE: 2003-06-10

PRIOR FILING DATE: PRESED for Windows Version 4.0

SEQ ID NO 15631

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                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
PRIOR APPLICATION NUMBER: 60/483,579
PRIOR FILING DATE: 2003-06-27
NUMBER OF SEQ ID NOS: 30063
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15630
LENGTH: 20
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; OTHER INFORMATION: Antisense compound US-10-831-901A-15631
                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: Antisense compound US-10-831-901A-15630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGAATCATCATGGAGAA
                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -10-831-901A-15631
                                                                                                                                                                                                                                              FEATURE:
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RESULT 257

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APPLICANT: Sampath, Rangarajan
APPLICANT: Sampath, Rangarajan
APPLICANT: Freier, Susan M.
APPLICANT: Hassirer, Christian
APPLICANT: Hofstadler, Steven A.
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Sawaye, Eric
APPLICANT: Baker, Brenda F.
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
FILE REFERENCE: ISISO0083-100 (BIOL0008US)
CURRENT FILING DATE: 2004-04-26
                                                                                GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
APPLICANT: Ecker, David J.
APPLICANT: Ecker, David J.
APPLICANT: Ecker, David J.
APPLICANT: Enger, Sugard M.
APPLICANT: Freier, Sugard M.
APPLICANT: Freier, Sugard M.
APPLICANT: Massire, Christian
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Baker, Brenda F.
APPLICANT: Baker, Brenda F.
APPLICANT: Baker, Eric
APPLICANT: Baker, Brenda F.
APPLICANT: 2003-6-10
PRIOR FILING DATE: 2003-6-10
PRIOR PLILNG DATE: 2003-6-27
PRIOR APPLICATION NUMBER: 60/468,562
PRIOR PLILNG DATE: 2003-6-27
PRIOR APPLICATION NUMBER: 60/468,527
PRIOR APPLICATION NUMBER: 60/468,562
PRIOR PLILNG DATE: 2003-6-27
NUMBER OF SEQ ID NOS: 30663
SEQ ID NO 25596
ILENGTH: 20
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88.9%; Pred. No. 2.4e+02;
tive 0; Mismatches 2;
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Sequence 25596, Application US/10831901A publication No. US20050100885A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Antisense compound US-10-831-901A-25596
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PRIOR APPLICATION NUMBER: 60/466,426
PRIOR APPLICATION NUMBER: 60/468,562
PRIOR APPLICATION NUMBER: 60/468,562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     718 AGAAATATATTAACGCA 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.9
Matches 16; Conservative
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US-10-831-901A-25597
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GENERAL INCORANTION

JAPPIICANT: Crooke, Stanley T.

APPLICANT: Ecker, David J.

APPLICANT: Ecker, David J.

APPLICANT: Ecker, David J.

APPLICANT: Expert, Sugarajan

APPLICANT: Freier, Sugarajan

APPLICANT: Massire, Christian

APPLICANT: Massire, Christian

APPLICANT: Howery, Kristian

APPLICANT: Baker, Brends F.

APPLICANTON NUMBER: 2004-04-26

PRIOR APPLICATION NUMBER: 60/468,562

PRIOR APPLICATION NUMBER: 60/469,562

PRIOR APPLICATION NUMBER: 60/467,770

PRIOR PILING DATE: 2003-06-10

PRIOR PILING DATE: 2003-06-10

PRIOR PILING DATE: 2003-06-10

PRIOR APPLICATION NUMBER: 60/483,579

PRIOR APPLICATION NUMBER: 60/483,579

PRIOR PILING DATE: 2003-06-27

NUMBER OF SEQ ID NOS: 30063

SOFTWARE: FastesQ for Windows Version 4.0

SEQ ID NO 26089

LENGTH: 20
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APPLICANT: Hoferadler, Steven A.
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Swayze, Eric
APPLICANT: Baker, Brenda F.
APPLICANT: Baker, Brenda F.
APPLICANT: Bennett, C. Frank
IITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.3%; Score 14.8; DB 1; Length 20;
88.9%; Pred. No. 2.4e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                           US-10-831-901A-26089/c; Sequence 26089, Application US/10831901A; Publication No. US20050100885A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Antisense compound US-10-831-901A-26089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   993 TIGTATGCACATGAAAGT 1010
                                                          718 AGAAATATATTAACGCA 735
                                                                                                                     3 AGAAATATATCAAGGCA 20
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APPLICANT: Secret, David J.
APPLICANT: Sampath, Rangarajan
APPLICANT: Freier, Susan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 TTGTAAGCACAAGAAGT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.9<sup>1</sup>
Matches 16; Conservative
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APPLICANT
APPLICANT
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APPLICANT: ECKET, David J.
APPLICANT: Sampath, Rangarajan
APPLICANT: Massire, Christian
APPLICANT: Massire, Christian
APPLICANT: Hofstadler, Steven A.
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Baker, Eric
APPLICANT: Baker, Chrank
TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
TITLE OF INVENTION: Compositions And Methods For The Treatment
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
TILLE REFERENCE: 12080-40-26
TILLE REFERENCE: 12080-40-26
PRIOR PLILING DATE: 2003-04-26
PRIOR PILING DATE: 2003-05-06
PRIOR PLILING DATE: 2003-05-06
PRIOR PLILING DATE: 2003-06-10
PRIOR PLILING DATE: 2003-06-10
PRIOR PLILING DATE: 2003-06-10
PRIOR PLILING DATE: 2003-06-10
PRIOR PLILING DATE: 2003-06-27
PRIOR PLILING DATE: 2003-06-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.3%; Score 14.8; DB 1; Length 20; 88.9%; Pred. No. 2.4e+02; rive 0; Mismatches 2; Indels
PRIOR FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/467,770
PRIOR FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: 60/468,627
PRIOR PLING DATE: 2003-05-06
PRIOR PLING DATE: 2003-06-10
PRIOR PLING DATE: 2003-06-10
PRIOR PLING DATE: 2003-06-10
PRIOR PLING DATE: 2003-06-27
NUMBER OF SEQ ID NOS: 30063
SQOTWARE: FRSEESC for Windows Version 4.0
SEQ ID NO 25597
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Sequence 25598, Application US/10831901A
Publication No. US20050100885A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Antisense compound US-10-831-901A-25598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Antisense compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      718 AGAAAATATATAACGCA 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Crooke, Stanley T. APPLICANT: Ecker, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-831-901A-25597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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Gaps

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RESULT 264
US-10-831-901A-26490/c
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    FEATURE:
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APPLICANT: Sampath, Rangarajan
APPLICANT: Sampath, Rangarajan
APPLICANT: Massire, Christian
APPLICANT: Massire, Christian
APPLICANT: Massire, Christian
APPLICANT: Moffetaler, Steven A.
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Swayze, Eric
APPLICANT: Benett, C. Frank
TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
FILE REFERENCE: ISISO083-100 (BIOLOGO8899)
CURRENT APPLICATION NUMBER: US/10/831,901A
CURRENT FILING DATE: 2003-04-26
PRIOR FILING DATE: 2003-04-28
PRIOR FILING DATE: 2003-04-66
PRIOR PILING DATE: 2003-04-66
PRIOR APPLICATION NUMBER: 60/466,426
PRIOR APPLICATION NUMBER: 60/466,770
PRIOR APPLICATION NUMBER: 60/466,770
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-06-10
PRIOR APPLICATION NUMBER: 60/4763,779
PRIOR FILING DATE: 2003-06-10
PRIOR APPLICATION NUMBER: 60/4763,779
PRIOR APPLICATION NUMBER: 60/483,579
PRIOR APPLICATION NUMBER: 60/464
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TITLE OF INVENTION: Acute Respiratory Syndrome (SARS); FILE REFERENCE: ISISO083-100 (BIOLO008US); CURRENT PEPLICATION NUMBER: US/10/831,901A CURRENT FILING DATE: 2004-04-26; PRIOR PELICATION NUMBER: 60/466,426; PRIOR PELICATION NUMBER: 60/466,426; PRIOR PELICATION NUMBER: 60/466,562; PRIOR PELICATION NUMBER: 60/467,770; PRIOR FILING DATE: 2003-05-06; PRIOR FILING DATE: 2003-04-30; PRIOR FILING DATE: 2003-06-10; PRIOR PELICATION NUMBER: 60/468,627; PRIOR APPLICATION NUMBER: 60/469,677; PRIOR APPLICATION NUMBER: 60/469,579; PRIOR PLICATION NUMBER: 60/483,579; PRIOR PLICATION NUMBER: 60/483,579; PRIOR PLING DATE: 2003-06-27; NUMBER: PRIOR PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 30063
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26091
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Antisense compound US-10-831-901A-26090
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 88.9°
Matches 16; Conservative
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US-10-831-901A-26091/c
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UG-10-831-901A-26185/c

UG-10-831-901A-26185/c

Sequence 26185, Application US/10831901A

Publication No. US2050100895A1

SEQUENCE 26185, Application US/10831901A

SEQUENCE CORORGE STATE STATE
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Pred. No. 2.48+02;
0; Mismatches 2; Indels
                                                                                                        1.3%; Score 14.8; DB 1; Length 20; 88.9%; Pred. No. 2.4e+02; tive 0; Mismatches 2; Indels
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Publication No. US20050100885A1
GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
APPLICANT: Ecker, David J.
APPLICANT: Sampath, Rangarajan
APPLICANT: Freier, Susan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Antisense compound US-10-831-901A-26185
OTHER INFORMATION: Antisense compound US-10-831-901A-26091
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                                                                                                                                                                                                                                                                         993 TTGTATGCACATGAAAGT 1010
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Local Similarity 88.9%;
Les 16; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.9
Matches 16; Conservative
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Grooke, Stanley T.
APPLICANT: Ecker, David J.
APPLICANT: Sampath, Rangarajan
APPLICANT: Sampath, Rangarajan
APPLICANT: Freier, Susan M.
APPLICANT: Hofstadler, Steven A.
APPLICANT: Hofstadler, Steven A.
APPLICANT: Baker, Kristin Sannes
APPLICANT: Baker, Brenda F.
APPLICANT: Bannett, C. Frant
APPLICANT
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                                                                                  APPLICANT: LOWETY, Kristin Sannes
APPLICANT: LOWETY, Kristin Sannes
APPLICANT: Swayze, Eric
APPLICANT: Swayze, Eric
APPLICANT: Barker, Erenda F.
APPLICANT: Barker, Erenda F.
APPLICANT: Barker, Erenda F.
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
TITLE OF INVENTION: 2003-04-26
FILE REFERENCE: 1215003-04-26
FRIOR APPLICATION NUMBER: 60/466,426
FRIOR APPLICATION NUMBER: 60/466,426
FRIOR FILING DATE: 2003-04-26
FRIOR PILING DATE: 2003-06-06
FRIOR APPLICATION NUMBER: 60/467,770
FRIOR FILING DATE: 2003-06-06
FRIOR APPLICATION NUMBER: 60/467,770
FRIOR PILING DATE: 2003-06-06
FRIOR APPLICATION NUMBER: 60/467,730
FRIOR FILING DATE: 2003-06-06
FRIOR APPLICATION NUMBER: 60/476,537
FRIOR FILING DATE: 2003-06-10
FRIOR APPLICATION NUMBER: 60/473,579
FRIOR FILING DATE: 2003-06-10
FRIOR APPLICATION NUMBER: 60/473,579
FRIOR FILING DATE: 2003-06-27
FRIOR APPLICATION NUMBER: 60/473,579
FRIOR FILING DATE: 2003-06-27
FRIOR APPLICATION NUMBER: 60/473,579
FRIOR FILING DATE: 2003-06-27
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FRIOR APPLICATION NUMBER: 60/473,579
FRIOR FILING DATE: 2003-06-27
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; Sequence 26491, Application US/10831901A
; Publication No. US20050100885A1
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Massire, Christian
Hofstadler, Steven A.
Lowery, Kristin Sannes
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Best Local Similarity 88.9
Matches 16; Conservative
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APPLICANT: Beliman, Merav
APPLICANT: Beliman, Merav
APPLICANT: Beliman, Merav
APPLICANT: Beliman, Merav
APPLICANT: Bahel, Dani
APPLICANT: Bahel, Dani
APPLICANT: Braitsky, Kinneret
APPLICANT: Braitsky, Kinneret
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ErbB-2 POLYPEPTIDES AND KITS AND
TITLE OF INVENTION: METHODS USING SAME
FILE REFERENCE: 28399
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.2
SEQ ID NO 29
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Publication No. US20040161768A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOFFMEYER, SVEN
TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
TILLE OF INVENTION: US-1004
CURRENT APPLICATION NUMBER: US/10/627,253A
CURRENT FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: PCT/FP02/00796
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                                                                                                                                                                                                                                                                   Score 14.8; DB 1; Length 20;
Pred. No. 2.4e+02;
0; Mismatches 2; Indels
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PRIOR FILING DATE: 2003-06-27
NUMBER OF SEQ ID NOS: 30063
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26491
LENGTH: 20
                                                                                                                                                                       FRATURE:
OTHER INFORMATION: Antisense compound US-10-831-901A-26491
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Rocman, Galit
Sela-Tavor, Osnat
Walach, Shira
Sameah-Greenwald, Shirley
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                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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88.9%;
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Best Local Similarity 88.99
Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserv
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APPLICANT:
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Sequence 302, Application US/10627253A

Sequence 302, Application US/20616168A1

Publication No. US20040161768A1

GENERAL INFORMATION:

APPLICANT: HOFPENEYER, SVEN

APPLICANT: HOFPENEYER, SVEN

APPLICANT: MORNHINWEG, ESTHER

TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS

TITLE OF INVENTION: PERSONAL SOURCE AND THERAPEUTIC APPLICATION NUMBER: US/10/627,253A

CURRENT APPLICATION NUMBER: EPT/FEP02/00796

PRIOR PILING DATE: 2002-01-25

PRIOR PLING DATE: 2001-01-26

NUMBER OF SEQ ID NOS: 406

SOFTWARE PATENTIAL VERSONAL SOURCE AND SEQ ID NO 302

LENGTH: 21

LENGTH: 21
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US-10-627-253A-302
                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide US-10-627-253A-301
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1.3%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2;
PRIOR APPLICATION NUMBER: PCT/ED02/00796
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: EP 01101651.6
NUMBER OF SEQ ID NOS: 406
SOFTWARE: Patentin version 3.2
LENGTH: 21.
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ORGANISM: Artificial Sequence
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US-10-627-233A-300/C

Sequence 300, Application US/10627253A

Sequence 300, Application US/10627253A

PUBLICATION NO. US20040161768A1

SEGUENCE TINFORMATION:

APPLICANT: HOFPMEYER, SVEN

APPLICANT: HOFPMEYER, SVEN

APPLICANT: MORNHINNEG, ESTHER

APPLICANT: MORNHINNEG, ESTHER

TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG

TITLE OF INVENTION: RESISTANCE-ASSOCIATED PROTEIN 1 (MRP-1) AND THEIR USE IN

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS

FILE REFERENCE: VOS-42 CON

CURRENT APPLICATION NUMBER: US/10/627,253A

CURRENT FILING DATE: 2003-07-24

PRIOR FILING DATE: 2003-07-24

PRIOR FILING DATE: 2001-01-26

NUMBER OF SEQ ID NOS: 406

SEQ ID NO 300

LENGTH: 21
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US-10-627-253A-300
                                                                                                                                                                                                                                                                                                                                                                                              THER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide US-10-627-253A-299
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US-10-627-253A-301
US-10-627-253A-301
Sequence 301, Application US/10627253A
Sequence 301, Application US/10627253A
Publication No. US2004016176BA1
GENERAL INPORMATION:
APPLICANT: HOFFMEYER, SVEN
APPLICANT: HOFFMEYER, SVEN
TITLE OF INVENTION: POLYWORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
TITLE OF INVENTION: RESISTANCE-ASSOCIATED PROTEIN 1 (MRP-1) AND THEIR USE IN
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
TITLE REPERENCE: VOS-42 CON
TURBENT APPLICATION NUMBER: US/10/627,253A
CURRENT FILING DATE: 2003-07-24
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1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
                                          PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: EP 01101651.6
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 406
SSOFTWARE: Patentin version 3.2
SSQ ID NO 299
LENGTH: 21
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Best Local Similarity 88.9<sup>3</sup>
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                TYPE: DNA
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APPLICANT: 0'Toole, Margot
APPLICANT: 0'Toole, Margot
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
TITLE OF INVENTION: DISBASES
FILE REFERENCE: 031896-022000 (AM101331L)
CURRENT APPLICATION NUMBER: 105/10/786,720
CURRENT PILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
LENGTH: 21
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Publication No. US20040265230A1

GENERAL INFORMATION:

APPLICANT: Weather, Robert

APPLICANT: Brown, Eugene

APPLICANT: Liu, Wei

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON

TITLE OF INVENTION: CANCERS

FILE REFERENCE: AM100927 (031896-002000)

CURRENT APPLICANTION NUMBER: US/10/751,736

CURRENT APPLICATION NUMBER: US/10/751,736

FILE REPRESENCE: AM100927 (031896-002000)

CURRENT APPLICATION NUMBER: US/2010-06

PRIOR PHILING DATE: 2003-01-06

PRIOR PHILING DATE: 2003-01-06

PRIOR APPLICATION DATE: 2003-01-06

PRIOR PHILING DATE: 2003-01-06
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                                                                                                                                                                                                                                                                                                                                      Query Match
1.3%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15222, Application US/10786720 Publication No. US20040191818A1 GENERAL INFORMATION:
APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                933 GAAATGCAGAATCTGAAG 950
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CRGANISM: RNAi-antisense strand
US-10-786-720-15222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GACATGCAGAATCTCAAG 4
   CURRENT FILING DATE: 2004-02-2
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: PatentIn version 3.2
SEQ ID NO 15220
LENGTH: 21
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SOFTWARE: Patentin version 3.2
SEQ ID NO 29451
LENGTH: 21
                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
US-10-786-720-15220
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US-10-786-720-15222
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US-10-751-736-29451
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10s-10-786-720-15220/c

1 Sequence 15220, Application US/10786720

2 Publication No. US20040191818A1

3 GENERAL INFORMATION:

4 APPLICANT: Wyeth

5 APPLICANT: Wyeth

7 APPLICANT: Liu, Wei

8 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE

7 TITLE OF INVENTION: DISEASES

8 FILE REFERENCE: 031896-023000 (AM101331L)

5 CURRENT APPLICATION NUMBER: US/10/786,720
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1 Sequence 304, Application US/10627253A

1 Publication No. US20040161768A1

1 GENERAL INFORMATION:

APPLICANT: BRINKWANN, ULRICH

APPLICANT: HOFFMETRE, SETHER

1 TITLE OF INVENTION: RESISTANCE-ASSOCIATED PROTEIN 1 (MRP-1) AND THEIR USE IN

1 TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS

2 TITLE APPLICATION INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS

2 TITLE APPLICATION INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide US-10-627-253A-303
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CURRENT FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: PCT/EP02/00796
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 406
SOFTWARE: Patentin version 3.2
LENGTH: 21
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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Sequence 293, Application US/10484577
; Sequence 293, Application US/10484577
; Publication No. US20550032724A1
; GENERAL INFORMATION:
    APPLICANT: EPIDAUROS Biotechnologie Aktiengesellschaft
    APPLICANT: EPIDAUROS Biotechnologie Aktiengesellschaft
    APPLICANT: EPIDAUROS Biotechnologie Aktiengesellschaft
    APPLICANT: EPIDAUROS Biotechnologie Aktiengesellschaft
    FILE REFERENCE: F2265FCT-1
    CURRENT APPLICATION UNMERR: US/10/484,577
    CURRENT APPLICATION NUMBER: EP 02/08220
    PRIOR FILING DATE: 2002-07-23
    PRIOR FILING DATE: 2001-07-23
    PRIOR PILING DATE: 2002-05-24
    NUMBER OF ES UD NOS: 683
    SEQ ID NOS: 683
    SEQ ID NOS: 683
    SEQ ID NOS: 683
    COFTWARE: PatentIn version 3.1
    CONTWARE: PatentIn version 3.1
    CONTWARE: PatentIN VOICE CONTWARE: PATENTING DATE: 2002-05-24
    NUMBER OF SEQ ID NOS: 683
    CONTWARE: PATENTING DATE: 2002-05-24
    NUMBER OF SEQ ID NOS: 683
    CONTWARE: PATENTING DATE: 2002-05-24
    NUMBER OF SEQ ID NOS: 683
    CONTWARE: PATENTING DATE: 2002-05-24
    NUMBER OF SEQ ID NOS: 683
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Sequence 294, Application US/10484577

Publication No. US20050032724A1

GENERAL INFORMATION:
TITLE OF INVENTION: Means and methods for improved treatment of cancer based on UGT1.
TITLE REPERENCE: F2285CT-1

CURRENT APPLICATION NUMBER: US/10/484,577

CURRENT APPLICATION NUMBER: PCT/EP 02/08220

PRIOR APPLICATION NUMBER: EP 01 11 7608.8

PRIOR FILING DATE: 2002-07-23

PRIOR FILING DATE: 2002-07-23

PRIOR PRILING DATE: 2002-07-23

PRIOR PILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 688

SEQ ID NOS: 689

SEQ ID NOS: 689

SEQ ID NO 294

TENNOMEL PATENTION OF SEQ ID NOS: 689

SEQ ID NO 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.3%; Score 14.8; DB 1; Length 21;
88.9%; Pred. No. 2.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.3%; Score 14.8; DB 1;
88.9%; Pred. No. 2.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1074 AACCACTTAACCTCTCTG 1091
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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CRGANISM: Homo sapiens
US-10-484-577-294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-10-484-577-293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 279
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Sequence 31083, Application No. US20040265230A1

Sequence 31083, Application No. US20040265230A1

GENERAL INFORMATION:
APPLICANT: Watther, Robert
APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
TITLE OF INVENTION: CANCERS
TITLE 
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| Sequence 45419, Application US/10751736
| Sequence 45419, Application US/10751736
| Sequence 45419, Application US/00565230A1
| Sequence 45419, Application No. US20040265230A1
| GENERAL INFORMATION:
| APPLICANT: Wyeth
| APPLICANT: Brown, Eugene
| APPLICANT: Liu, Wel
| APPLICANT: Liu, Wel
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
| TITLE OF INVENTION: CANCERS
| FILE REFERENCE: AMIO027 (031896-002000)
| CURRENT FILING DATE: 2003-01-06
| PRIOR FILING DATE: 2003-01-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3%; Score 14.8; DB 1; Length 21; 88.9%; Pred. No. 2.6e+02;
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                               2; Indels
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. 2.6e+02;
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44.4%; Pred. No. 2.6e+02; ive 8; Mismatches 2
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                                                                                                     495 TTTCTTAGAACTCATACT 512
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1 UUUCUUAGAUCUCUUACU 18
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SOFWARE: Patentin version 3.2
SEQ ID NO 45419
LENGTH: 21
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Best Local Similarity 88.9
Matches 16; Conservative
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Matches 16; Conservative
   Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                 RESULT 276
US-10-751-736-31083/c
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US-10-751-736-45419
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US-10-751-736-31083
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Sequence 6, Application US/10451805
; Sequence 6, Application US/10451805
; Publication No. US20040248099A1
; CENDERAL INPORMATION:
; APPLICANT: Alzabimer, Christian
; APPLICANT: Alzabimer, Christian
; APPLICANT: Kagel, Heid;
; TITLE OF INVENTION: Descassium Channels and Modulators For Diagnosing and
; TITLE OF INVENTION: Potassium Channels and Modulators For Diagnosing and
; TITLE OF INVENTION: Potassium Channels and Modulators For Diagnosing and
; TITLE OF INVENTION: Treating Diseases Having Disturbed Keratinocyte Activity
; FILE REFERENCE: 50125/080001
; CURRENT APPLICATION NUMBER: US/10/451,805
; CURRENT FILING DATE: 2001-12-27
; PRIOR FILING DATE: 2001-13-20
; PRIOR FILING DATE: 2001-03-20
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6.
                                          APPLICANT: Liu, Wei
APPLICANT: Slonim, Donna
APPLICANT: Slonim, Donna
APPLICANT: Slonim, Donna
APPLICANT: Howes, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
FILE REFERENCE: 031896-026000 (AM101264)
CURRENT APPLICATION NUMBER: US/10/847,918
PRIOR APPLICATION NUMBER: US 60/471,729
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 14937
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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Sequence 2565, Application US/09866108
Factor No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GI, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 TICTICACTACTGGAATT 301
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Best Local Similarity 93.8
Matches 15; Conservative
                          Be, Xiaobing
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US-10-451-805-6
  Wyeth
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
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Sequence 296, Application US/10484577

Publication No. US2005033724A1

GENERAL INFORMATION:

TITLE OF INVENTION: Means and methods for improved treatment of cancer based on UGTLA

TITLE OF INVENTION: Means and methods for improved treatment of cancer based on UGTLA

TITLE OF INVENTION: MOMBER: US/10/484,577

CURRENT APPLICATION NUMBER: PC/22

PRIOR APPLICATION NUMBER: PC/22

PRIOR PLING DATE: 2002-01-23

PRIOR PLING DATE: 2001-07-23

PRIOR PLING DATE: 2001-07-23

PRIOR PLING DATE: 2001-05-05-44

NUMBER OF SEQ ID NOS: 683

SEQ ID NOS: 683

SEQ ID NO 296

LINGTH: 21
TITLE OF INVENTION: Means and methods for improved treatment of cancer based on UGTIA
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Pred. No. 2.6e+02;
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Pred. No. 2.6e+02;
0; Mismatches 2;
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                  FILE REFERENCE: F2285FCT-1
CURRENT APPLICATION NUMBER: US/10/484,577
CURRENT APPLICATION NUMBER: US/10/6820
PRIOR PLING DATE: 2004-01-23
PRIOR PLING DATE: 2002-07-23
PRIOR PLING DATE: 2001-07-23
PRIOR PLING DATE: 2001-07-23
PRIOR PLING DATE: 2001-07-23
PRIOR PLING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 693
SOFTWARE: PatentIn version 3.1
SENGTH: 21
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US-10-847-918-4920
S. Sequence 4920, Application US/10847918
Publication No. US20050119210A1
GENERAL INFORMATION:
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88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.3%;
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
| IOCATION: (11)...(11)
| OTHER INFORMATION: m=a or c
US-10-484-577-295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) NAME/KEY: misc feature
) LOCATION: (11)...(11)
; OTHER INFORMATION: k=g or t
US-10-484-577-296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.95
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 2566, Application US/09866108

Patent No. US20020048800A1

GENERAL INFORMATION:
APPLICANT: UI, Yonggang
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
CURRENT: APLICANTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
CURRENT APPLICATION WUMBER: 2001-05-25
CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26
                                                        APPLICANY: RANK, DAVIG K.
APPLICANY: SHANKON, MATK
TITLE OF INVENTION, MATK
TITLE OF INVENTION, MATK
TITLE OF INVENTION, MATK
TITLE OF INVENTION, MATK
TITLE OF INVENTION WINDER: US/09/066,108
CURRENT APPLICATION NUMBER: US/09/066,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US/06/236,359
PRIOR APPLICATION NUMBER: US/06/236,359
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR PILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-01-0-0
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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SOFTWARE: Acomica Sequence Listing Engine SEQ ID NO 2565
LENGTH: 17
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HANZEL, David K.
RANK, David R.
CHEN, Wensheng
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US-09-866-108-2565
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APPLICANT: Draper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
FILE REPERENCE: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REPERENCE: Method and Reagent for Inhibiting Hepatitis B Virus Replicanton
FILE OF INVENTION: WUMBER: US/09/877, 478
CURRENT APPLICATION NUMBER: US 07/882, 712
PRIOR FILING DATE: 1992-05-14
PRIOR FILING DATE: 2000-03-20
FRIOR FILING DATE: 2000-03-20
FRIOR FILING DATE: 2000-10-24
FRIOR PILING DATE: 2000-10-24
FRIOR FILING DATE: 2000-10-24
FRIOR FILING DATE: 1994-02-07
FRIOR FILING DATE: 1994-02-07
FRIOR FILING DATE: 1995-05-04
FRIOR FILING DATE: 1995-05-04
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 2566
LENGTH: 17
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Publication No. US20030068301A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
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APPLICATION NUMBER: US 08/434,504
FILING DATE: 1995-05-04
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US-09-745-237A-1012/c
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Sequence 478, Application US/09930423
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
TILE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REPERENCE: MBH800, 918-A 400/027
CURRENT APPLICATION NUMBER: US/09/930,423
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 4553
SEQ TWARE: Patentin version 3.0
SEQ ID NO 478
LENGTH: 17
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; Sequence 1012, Application US/09930423
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTYON: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: MBHB00, 918-A 400/027
CURRENT FILING DATE: 2001-08-15
CURRENT FILING DATE: 2001-08-15
SOFTWARE: Patentin version 3.0
SEQ ID NO 1012
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PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6586
SCFTWARE: PatentIn version 3.0
SEQ ID NO 948
LENGTH: 17
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                                                                                                                                                          ; ORGANISM: Hepatitis B virus US-09-877-478-948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: RNA
ORGANISM: Homo Sapiens
US-09-930-423-478
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; ORGANISM: Homo Sapiens
US-09-930-423-1012
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                                                                                                                                          TYPE: RNA
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APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
Sequence 478, Application US/09745237A
| Sequence 478, Application US/09745237A
| Publication No. US20030143708A1
| GENERAL INFORMATION:
| APPLICANT: Ribozyme Pharmaceuticals, Inc.
| APPLICANT: Blatt, Larry
| APPLICANT: McSwiggen, Jim
| TITLE OF INVENTION: McHand and Reagent for the Treatment of Alzheimer's Disease
| TILE REPERRING: 400/007 (MBHB00-918-A)
| CURRENT APPLICATION NUMBER: US/09/745,237A
| CURRENT FILMS DATE: 2002-04-15
| SOFTWARE: PatentIn version 3.0
| SOFTWARE: PatentIn version 3.0
| SOFTWARE: PatentIn version 3.0
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Publication No. US20030143708A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Machine Sequent for the Treatment of Alzheimer's Disease
TILE REFERENCE: 400/007 (MBHB00-918-A)
CURRENT APPLICANTION NUMBER: US/09/745,237A
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 4550
SOFTWARE Patentin version 3.0
SEQ ID NO 1012
LENGTH: 17
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; Publication No. US20040054156A1
; GENERAL INFORMATION:
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
CORGANISM: Homo sapiens
US-09-745-237A-478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-745-237A-1012
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**Levelicant: stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT APPLICATION NUMBER: US/10/287,949A

SOFTWARE: Patentin Version 3.0

SEQ ID NO 7395

LENGTH: 17
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APPLICANT: Panela, Pavora
APPLICANT: Panela, Pavora
APPLICANT: Patrice, Lee
APPLICANT: Patrice, Lee
APPLICANT: Remorth, Darger:
APPLICANT: Risabeth, Roberts
TITLE OF INVENTION: UIRCSNUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP;
TITLE OF INVENTION: UIRCSNUCLEOTIDE
TITLE OF INVENTION: UIRCSNUCLEOTIDE
TITLE OF INVENTION: US/10/669,841
CURRENT APPLICATION NUMBER: US/00/209-23
CURRENT APPLICATION NUMBER: US 60/296,876
PRIOR PILING DATE: 2001-06-08
PRIOR PILING DATE: 2001-024
PRIOR PILING DATE: 2001-10-24
PRIOR PILING DATE: 2001-10-24
PRIOR PILING DATE: 2001-10-24
PRIOR PLING DATE: 2001-10-34
PRIOR PLING DATE: 2001-10-36
PRIOR PLING DATE: 2001-10-36
PRIOR PLING DATE: 2001-10-36
PRIOR PPLING DATE: 2001-10-36
PRIOR PPLING DATE: 2001-10-36
PRIOR PPLING DATE: 2001-10-36
PRIOR PLING DATE: 2001-07-07
PRIOR PPLING DATE: 2000-07-07
PRIOR PPLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 16207
SOFTWARE: Patentin version 3.0
SEQ ID NO 948
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1.3%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1;
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US-10-669-841-948
i Sequence 948, Application US/10669841
j Publication No. US20040127446A1
j Publication No. US20040127446A1
j CENERAL INFORMATION:
j APPLICANT: Sirna Therapeutics, Inc.
j APPLICANT: Lawrence, Blatt
j APPLICANT: Dennis, Macejak
j APPLICANT: David, Morrissey
appLICANT: David, Morrissey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 626 GITITATICICAGCAA 641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 GTTTTATGCTCAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Barco, Pam
APPLICANT: Barco, Jaim
APPLICANT: Stinchcomb, Jaim
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 3955
TEXAMON: 17
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                                                                                                                                                                                                                          FILE REFERENCE: 400/075 (MBHB00-845-1)
CURRENT APPLICATION NUMBER: US/10/342,902
CURRENT FILING DATE: 2003-01-15.
PRIOR APPLICATION NUMBER: US 09/877,478
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-08-09
PRIOR FILING DATE: 2000-08-09
PRIOR PILING DATE: 2000-08-09
PRIOR PILING DATE: 2000-08-09
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 1994-02-07
PRIOR FILING DATE: 1994-02-07
PRIOR PILING DATE: 1995-05-14
PRIOR PILING DATE: 1995-05-14
PRIOR PILING DATE: 1995-05-14
PRIOR PILING DATE: 1995-01-08
NUMBER OF SEQ ID NOS: 6592
SEQ ID NO 948
PENDRY PARENTLY VETBION 3.2
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US-10-287-349A-7395/C
US-10-287-349A-7395, Application US/10287949A
; Sequence 7395, Application No. US20040102389A1
; GENERAL INFORMATION:
GAPLICANT: Ribozyme Pharmaceuticals, Inc.;
; APPLICANT: Pavco, Pam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 292
US-10-138-674-7395/c
Sequence 7395, Application US/10138674
Publication No. US20040077565A1
GENERAL INFORMATION:
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1 UUUAAUGCCUUUAUAU 16
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US-10-342-902-948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 93.8
Matches 15; Conservative
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ORGANISM: Homo sapiens
US-10-138-674-7395
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Best Local Similarity
Matches 6; Conserv
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APPLICANT: SHANNON, MAYK
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
FILE REFERENCE: PB0105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BavCo, Pamela

APPLICANT: Sandberg, Jennifer

APPLICANT: Sandberg, Jennifer

APPLICANT: Gordon, Gilad

APPLICANT: Gordon, Gilad

APPLICANT: Gordon, Gilad

APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACT

TITLE OF INVENTION: NUMBER: US /10/12,633

CURRENT APPLICATION NUMBER: US 60/005,974

PRIOR APPLICATION NUMBER: US 60/005,974

PRIOR APPLICATION NUMBER: US 09/31,772

PRIOR FILING DATE: 1999-08-10

PRIOR APPLICATION NUMBER: US 09/31,772

PRIOR APPLICATION NUMBER: US 09/31,772

PRIOR APPLICATION NUMBER: US 09/31,772

PRIOR APPLICATION NUMBER: US 09/710,161

PRIOR APPLICATION NUMBER: US 09/70,161
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                                                                                                                    FILE REFERENCE: PB0105
CURRENT PELICATION NUMBER: US/10/723,361
CURRENT FILING DATE: 2003-11-26
PRIOR PAPLICATION NUMBER: US 09/866,108
PRIOR PLILING DATE: 2001-05-25
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-03-27
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 2566
LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/334,461
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 10/138,674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2001-05-29
APPLICATION NUMBER: US 60/334,461
FILING DATE: 2001-11-30
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Publication No. US20040220128A1
GENERAL INFORMATION:
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Best Local Similarity 93.8
Matches 15; Conservative
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APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wark
TITLE OF INVENTION: HUMAN WYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
FILE REPERENCE: PBOIOS
CURRENT APPLICATION NUMBER: US 09/866,108
PRIOR APPLICATION NUMBER: US 09/866,108
PRIOR PILING DATE: 2000-05-25
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-27
PRIOR PLING DATE: 2000-05-27
PRIOR PLING DATE: 2000-05-27
PRIOR PLING DATE: 2000-10-04
PRIOR PILING DATE: 2001-10-04
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 20
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Query Match 1.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 37.5%; Pred. No. 1.9e+02; Matches 6; Conservative 9; Mismatches 1; Indels
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Pred. No. 1.9e+02;
0; Mismatches 1; Indels
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APPLICANT: GI, Yizhong
APPLICANT: PENN, Sharton G; APPLICANT: PENN, Sharton G; APPLICANT: PANXEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2565, Application US/10723361; Publication No. US20040137589A1; GENERAL INFORMATION:
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93.8%;
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 Similarity 93.8
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; ORGANISM: Homo sapiens
US-10-723-361-2565
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Best Local
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Matches
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 588 LENGTH: 19
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                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
US-10-477-238A-588
                                                                                               , ORGANISM: Homo sapiens
US-10-731-739-588
                                                                              TYPE: DNA
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JE-09-969-373-2494

Sequence 2494, Application US/09969373

Patent No. US20020133852A1

GENERAL INFORMATION:

APPLICANT: Effertz, Roger J.

APPLICANT: Hauge, Brian M.

TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping TITLE OF INVENTION: 100/100-02

FILE REFERENCE: 38-10(52679)A

CURRENT APPLICATION NUMBER: US/09/969,373

CURRENT FILING DATE: 2001-10-02

PRIOR APPLICATION NUMBER: US 09/754,853

PRIOR FILING DATE: 2001-01-05

PRIOR APPLICATION NUMBER: US 09/760,427

PRIOR APPLICATION NUMBER: US 09/805,768

PRIOR PILING DATE: 2001-01-13

PRIOR PILING DATE: 2001-01-13

SEQ ID NOS: 4593

SEQ ID NOS: 4593
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Sequence 588, Application US/10731739

Sequence 588, Application US/10731739

Publication No. US20040176582A1

GENERAL INFORMATION:
APPLICANT: Carulli, John P.
APPLICANT: Little, Randall D.
APPLICANT: Little, Randall D.
APPLICANT: Becker, Robert R.
APPLICANT: Bolmson, Mark L.
TITLE OF INVENTION: High bone mass gene of 11q13.3

FILE REFERENCE: 032796-013

CURRENT APPLICATION NUMBER: US/10/731,739

CURRENT APPLICATION NUMBER: US/09/544,398B

PRIOR APPLICATION NUMBER: US 09/229,319

PRIOR PLING DATE: 1999-01-13

PRIOR FILING DATE: 1999-01-13

PRIOR FILING DATE: 1999-01-13

PRIOR PILING DATE: 1999-01-13

PRIOR RILING DATE: 1999-01-13

PRIOR PILING DATE: 1998-10-23

NUMBER OF SEQ ID NOS: 641
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                     PRIOR FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 5989
SOFTWARE: PatentIn version 3.0
SEQ ID NO 347
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                         17 GTTTTATGCTCAGCAA 2
                                                                                                                                       TYPE: RNA
GRGANISM: Homo Sapiens
US-10-712-633-347
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CORGANISM: Glycine max
US-09-969-373-2494
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US-10-477-238A-588
; Sequence S88, Application US/10477238A
; Sequence S88, Application US/10477238A
; Publication No. US20040221326A1
; Publication No. US20040221326A1
; APPLICANT: Babi). Philip
; APPLICANT: Babi). Philip
; APPLICANT: Bex, Frederick J. III
APPLICANT: Bex, Frederick J. III
APPLICANT: Box, Frederick J. III
FILE REFERENCE: 032796-212
CURRENT FILING DATE: 1037196-110
PRIOR PILING DATE: 2001-05-11
PRIOR PLING DATE: 2001-05-17
PRIOR PLING DATE: 2001-05-17
PRIOR PLING DATE: 2001-05-17
PRIOR PLING DATE: 2002-02-01
PRIOR PLING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 812
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 588
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-680-287A-588

US-10-680-287A-588

Sequence 588, Application US/10680287A

Sequence 588, Application US/10680287A

Sequence 588, Application US/20040244069A1

Sequence 588, Application Sequence 588, Application 589, Application 589, Paul

APPLICANT: Bex, Frederick J. III

CURRENT Bex, Frederick J. III

PRIOR FILING DATE: 2003-10-08

PRIOR FILING DATE: 2003-05-13

PRIOR FILING DATE: 2001-05-11

PRIOR FILING DATE: 2001-05-17
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Query Match 1.3%; Score 14.4; DB 1; Length 19; Best Local Similarity 93.8%; Pred. No. 2.4e+02; Matches 15; Conservative 0; Mismatches 1; Indels
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APPLICANT: Waworsky, Paul
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.

** APPLICANT: Liu, Wei
TITLE OF INVENTION: HBM Variants that Modulate Bone Mass and Lipid Levels
FILE REFERENCE: 032796-135
CURRENT APPLICATION NUMBER: US 60/290,071
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2002-02-01
PRIOR FILING DATE: 2002-02-01
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 1086
SOFTWARE: FRASEE FOR Windows Version 4.0

SEQ ID NO 588

LENGTH: 19
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Publication No. US20050142617A1
GENERAL INPORMATION:
APPLICANT: Carulli, John P.
APPLICANT: Little, Randall D.
APPLICANT: Johnson, Mark L.
TITLE OF INVENTION: High bone mass gene of 11q13.3
FILE REFERENCE: 032796-014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 588, Application US/10477173
Publication No. US20050070699A1
GENERAL INFORMATION:
APPLICANT: Genome Therapeutics Corporation and APPLICANT: Allen, Kristina M.
PRIOR APPLICATION NUMBER: US 60/353,058
PRIOR FILING DATE: 2002-02-01
PRIOR PILING DATE: 2002-03-04
PRIOR PILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 812
SOFTWARE: FRAESEQ FOR Windows Version 4.0
SEQ ID NO 588
LENGTH: 19
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Best Local Similarity 93.8<sup>3</sup>
Matches 15; Conservative
                                                                                                                                                                                                                                                                                     Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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US-10-477-173-588
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US-10-834-377-588
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US-05-917-963-91/c

| Sequence 91, Application US/09917963 |
| Sequence 91, December 10 |
| Sequence 91, Sequ
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APPLICANT: Jacqueline Wyatt
APPLICANT: Jacqueline Wyatt
APPLICANT: Sugan M. Freier
APPLICANT: Brett P. Monia
APPLICANT: Madeline M. Butler
APPLICANT: Robert McKay
TITLE OF INVENTION: ANTISENSE MODULATION OF PTPIB EXPRESSION
FILE REFERENCE: ISPH-0576
CURRENT APPLICATION NUMBER: US/09/654,083
CURRENT APPLICATION NUMBER: US 09/629,644
PRIOR FILING DATE: 2000-07-31
PRIOR PILING DATE: 2000-07-31
PRIOR PILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 389
SEQ ID NO 297
LENGTH: 20
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Pred. No. 2.4e+02;
0; Mismatches 1;
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    CURRENT FILING DATE: 2004-04-29

PRIOR APPLICATION NUMBER: US/09/543,771B

PRIOR FILING DATE: 2000-04-05

PRIOR FILING DATE: 1999-01-13

PRIOR APPLICATION NUMBER: US 09/229,319

PRIOR APPLICATION NUMBER: US 00/071,449

PRIOR PILING DATE: 1998-01-13

PRIOR APPLICATION NUMBER: US 60/105,511

PRIOR FILING DATE: 1998-10-23

NUMBER OF SEQ ID NOS: 641

SOFTWARE: FASTEEQ for Windows Version 4.0

SEQ ID NO 588
CURRENT APPLICATION NUMBER: US/10/834,377
CURRENT FILING DATE: 2004-04-29
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ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGCTGTGATCAAAAGG 16
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Best Local Similarity 93.8'
Matches 15, Conservative
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Best Local Similarity 93.83
Matches 15; Conservative
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ORGANISM: Homo sapiens
US-10-834-377-588
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Sequence 37, Application US/10446373
Fublication NO US20030204076A1
Fublication NO US20030204076A1
FUBLICANT: C. Frank Bennett
APPLICANT: Andrew T. Watt
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPT
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0232
CURRENT APPLICATION NUMBER: US/10/446,373
CURRENT FILING DATE: 2003-05-28
PRIOR FILING DATE: 2001-09-13
NUMBER OF SEQ ID NOS: 154
SEQ ID NO 37
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APPLICANT: Jacqueline Wyatt
APPLICANT: Jacqueline Wyatt
APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Madeline M. Butler
APPLICANT: Madeline M. Butler
APPLICANT: Robert MCKAy
TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
CURRENT FILING DATE: 1091-077
PRIOR PELLING DATE: 2001-05-14
PRIOR FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 09/487,368
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
INWHERE OF SEQ ID NOS: 389
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1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                          Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; sequence 297, Application US/10360510; Publication No. US20030220282A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      626 GITITATICICAGCAA 641
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                         721 AAATATATTAACGCAG 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 GTTTTATGCTCAGCAA 19
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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-317
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US-10-360-510-297
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US-09-953-318-37
Sequence 37, Application US/09953318
Sequence 37, Application US/09953318
Sequence 37, Application US/09953318
Sequence 37, Application US/09953318
SERNERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: EXPRESSION
FILLE REFERENCE: RFS-023
CURRENT APPLICATION NUMBER: US/09/953,318
CURRENT PILING DATE: 2001-09-13
NUMBER OF SEQ ID NOS: 154
SEQ ID NO 37
LENGTH: 20
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Sequence 317, Application US/10085906

Publication No. US20030054371A1

GENERAL INFORMATION:

APPLICANT: Wu, Paul

APPLICANT: COSTINULATOR RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTINULATOR RECEPTOR LOCUS

CURRENT APPLICATION NUMBER: US/10/085,906

CURRENT FILING DATE: 2002-02-27

PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 545

SOFTWARE: FastEEQ for Windows Version 4.0

SEQ ID NO 317
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1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                              Query Match
1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Antisense Oligonucleotide US-09-953-318-37
                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence FEATURE: PEATURE: OTHER INFORMATION: Antisense Oligonucleotide US-09-917-963-91
                               CURRENT APPLICATION NUMBER: US/09/917,963
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 137
SEQ ID NO 91
LENGTH: 20
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                       FILE REFERENCE: ISPH-0591
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US-10-085-906-317
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US-10-455-229-23/C

US-10-455-229-23/C

Sequence 23, Application US/10455229

Publication No. US20040016030A1

GENERAL INFORMATION:

APPLICANT: CHOMET, PAUL

TITLE OF INVENTION: MITH INCREASED TRANSFORMABILITY

TITLE OF INVENTION: WITH INCREASED TRANSFORMABILITY

FILE REFERENCE: DEKM.195US

CURRENT APPLICATION NUMBER: US/10/455,229

CURRENT APPLICATION NUMBER: 60/386,522

PRIOR APPLICATION NUMBER: 60/386,522

PRIOR PILING DATE: 2002-06-06

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 23

LENGTH: 20
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Publication No. US20040092465A1
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION:
PILE REFERENCE: RTS-0432
CURRENT APPLICATION NUMBER: US/10/293,864
NUMBER OF SEQ ID NOS: 165
LENGTH: 20
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     Gaps
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1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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     Mismatches
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; Publication No. US20040092465A1
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                                                  287 TTCACTACTGGAATTG 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                19 Trcacracedeaarre 4
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     15; Conservative
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       Matches
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US-10-349-143-6795

Sequence 6795, Application US/10349143

Fublication No. US20040005584A1

GENERAL INFORMATION:

APPLICANT: Chumakov, Daniel

APPLICANT: Chumakov, Ilya

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE: GENSET.020CP1

CURRENT APPLICATION NUMBER: US/10/349,143

CURRENT PILING DATE: 1999-10-21

PRIOR APPLICATION NUMBER: US/09/422,978

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850

PRIOR PILING DATE: 1999-10-21

PRIOR PILING DATE: EARLIER FILING DATE: 1999-04-21

PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-33

PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-33

PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-35

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 6795

LENGTH: 20

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Faquence 1803, Application US/10289762

Fublication No: US20040006218A1

GENERAL INFORMATION:

APPLICANT: Griffals,

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering PILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/10/289,762

CURRENT FILING DATE: 2003-03-27

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 1803

LENGTH: 20
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; OTHER INFORMATION: upstream amplification primer 99-19464 for SEQ 2861,
US-10-349-143-6795
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                                                                      Query Match
1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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; OTHER INFORMATION: Antisense Oligonucleotide US-10-360-510-297
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; ORGANISM: Chlamydia pneumoniae
US-10-289-762-1803
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nes 15, Conservative
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ORGANISM: Homo Sapiens
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Best Local Similarity
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US-10-289-762-1803/c
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Best Local S
Matches 15
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Sequence 2537, Application US/10688706

| Sequence 2537, Application US/10688706
| Publication No. US20040102412A1
| GENERAL INFORMATION:
| APPLICANT: Pharmacia Corp.
| APPLICANT: Broschat, Kay
| TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
| FILE REFERENCE: 01393/1
| CURRENT APPLICATION NUMBER: US/10/688,706
| CURRENT PILING DATE: 2003-10-17
| PRIOR APPLICATION NUMBER: 60/419,268
| PRIOR FILING DATE: 2002-10-17
| NUMBER OF SEQ ID NOS: 3071
| SOFTWARE: PatentIn version 3.2
| SEQ ID NO 2537
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US-10-688-706-2670

$ Sequence 2670, Application US/10688706

$ Sequence 2670, Application US/10688706

$ Sequence 2670, Application US/10688706

$ Publication No. US20040102412A1

$ Publication No. US20040102412A1

$ APPLICANT: Pharmacia Corp.

$ APPLICANT: Pracechat, Kay

$ TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION

$ TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION

$ TITLE REFERENCE: 0193/110688,706

$ CURRENT PILLING DATE: 2003-10-17

$ PRIOR APPLICATION NUMBER: 60/419,268

$ PRIOR APPLICATION NUMBER: 60/419,268

$ PRIOR FILLING DATE: 2002-10-17

$ NUMBER OF SEQ ID NOS: 3071

$ SEQ ID NO 2670

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COTHER INFORMATION: human GFAT antisense
US-10-688-706-2670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: human GFAT antisense US-10-688-706-2537
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; Sequence 4408, Application US/10831901A
; Publication No. US20050100865A1
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813 CTGAAGCAGGCCTCTC 828
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Best Local Similarity 93.89
Matches 15; Conservative
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Best Local Similarity 93.8'
Matches 15; Conservative
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Sequence 121, Application US/10293864

Publication No. US20040092465A1

GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: MODULATION OF HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION FILE REFERENCE: RTS-04048R: US/10/293,864

CURRENT APPLICATION NUMBER: US/10/293,864

CURRENT FILING DATE: 2002-11-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 120, Application US/10293864

Publication No. US20040092465A1

GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF HUNTINGTIN INTERACTING PROTEIN I EXPRESSION
FILE REPRENCE: RTS-0432
CURRENT APPLICATION NUMBER: US/10/293,864
CURRENT FILING DATE: 2002-11-11
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 120
LENGTH: 20
             GENERAL INFORMATION:

APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION
FILE REFERENCE: RTS-0432
CURRENT APPLICATION NUMBER: US/10/293,864
CURRENT FILING DATE: 2002-11-11
NUMBER OF SEQ ID NOS: 165
LENGTH: 20
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1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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ORGANISM: H. sapiens
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ORGANISM: H. sapiens
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US-10-293-864-120
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APPLICATION NUMBER: 60/468,627
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                                                                                                                                                                                                      APPLICANT: Swayze, Eric
APPLICANT: Swayze, Eric
APPLICANT: Baker, Brenda F.
APPLICANT: Baker, Brenda F.
TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
FILE REPERENCE: ISISO083-100 (BIOLO008US)
CURRENT APPLICATION NUMBER: US/10/831,901A
CURRENT PILING DATE: 2003-04-26
PRIOR PPLICATION NUMBER: 60/466,426
PRIOR PPLICATION NUMBER: 60/468,562
PRIOR APPLICATION NUMBER: 60/467,770
PRIOR APPLICATION NUMBER: 60/467,770
PRIOR APPLICATION NUMBER: 60/467,770
PRIOR APPLICATION NUMBER: 60/477,637
PRIOR PILING DATE: 2003-05-06
PRIOR PILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/477,637
PRIOR APPLICATION NUMBER: 60/483,579
PRIOR APPLICATION NUMBER: 60/483,579
PRIOR APPLICATION NUMBER: 60/483,579
PRIOR APPLICATION NUMBER: 60/483,579
PRIOR PILING DATE: 2003-05-06-27
NUMBER OF SEQ ID NOS: 30063
SOFTWARE PREFERENCE
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APPLICANT: Hofstadler, Steven A.
APPLICANT: Hofstadler, Steven A.
APPLICANT: Baker, Exic
APPLICANT: Baker, Brenda F.
APPLICANT: Bannet, C. Franh
APPLICANT: Bannet, C. Franh
APPLICANT: Bannet, C. Franh
TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
CURRENT APPLICATION NUMBER: 60/466,426
PRIOR APPLICATION NUMBER: 60/466,562
PRIOR APPLICATION NUMBER: 60/468,562
PRIOR PILING DATE: 2003-04-28
PRIOR FILING DATE: 2003-04-30
PRIOR FILING DATE: 2003-04-30
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APPLICANT: Crooke, Stanley T. APPLICANT: Ecker, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Antisense compound US-10-831-901A-4408
                                                                       Sampath, Rangarajan
Freier, Susan M.
Massire, Christian
Hofstadler, Steven A.
Lowery, Kristin Sannes
Swayze, Eric
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Freder, Susan M.
Massire, Christian
Hofstadler, Steven A.
Lowery, Kristin Sannes
Swayze, Eric
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ORGANISM: Artificial Sequence
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                 cooke, Stanley T. Ecker, David J.
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LENGTH: 20
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APPLICANT:
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APPLICANT: Crooke, Stanley T.
APPLICANT: Ecker, David J.
APPLICANT: Sampath, Rangarajan
APPLICANT: Freier, Susan M.
APPLICANT: Freier, Susan M.
APPLICANT: Massire, Christian
APPLICANT: Lowery, Kristin Sames
APPLICANT: Swayze, Eric
APPLICANT: Baker, Brenda F.
APPLICANT: Baker, Brenda F.
APPLICANT: Bennett, C. Frank
ITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
ITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
TITLE OF INVENTION: Compositions and Methods For The Treatment Of Severe
TITLE OF INVENTION: Compositions and Methods For The Treatment Of Severe
TITLE OF INVENTION: Compositions and Methods For The Treatment Of Severe
TITLE OF INVENTION: Compositions and Methods For The Treatment Of Severe
TITLE OF INVENTION: Compositions and Methods For The Treatment Of Severe
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TITLE OF INVENTION: Compositions and Methods For The Treatment Of Severe
TITLE OF INVENTION: Compositions and Methods For The Treatment Of Severe
TITLE OF INVENTION: Compositions and Methods For The Treatment Of Severe
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Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1;
PRIOR FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/477,637
PRIOR FILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-27
NUMBER OF SEQ ID NOS: 30063
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4409
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PRIOR APPLICATION NUMBER: 60/466,426
PRIOR FILING DATE: 2003-04-28
PRIOR PILING DATE: 2003-04-28
PRIOR PILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-04-30
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-27
NUMBER OF SEQ ID NOS: 30063
SOFTWARE: PSESEQ for Windows Version 4.0
SEQ ID NO 4410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-831-901A-4410; Sequence 4410, Application US/10831901A; Publication No. US20050100885A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTHER INFORMATION: Antisense compound US-10-831-901A-4409
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ORGANISM: Artificial Sequence
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TTTTAATTCCTTTATA 18

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US-10-81-904-4411, Application US/10831901A

Sequence 4411, Application Wo. US20050100865A1

PUBLICANT: Crooke, Stanley T.

APPLICANT: Crooke, David J.

APPLICANT: Ecker, David J.

APPLICANT: Realer, David J.

APPLICANT: Realer, Sampath, Rangarajan

APPLICANT: Realer, Staven M.

APPLICANT: Massite, Christian

APPLICANT: Peaker, Staven M.

APPLICANT: Bender, Staven M.

APPLICANT: Bender, Staven M.

APPLICANT: Bender, Staven M.

APPLICANT: Bender, C. Frank

APPLICANT: Bender, Bender, C. Frank

APPLICANT: Bender, Bender, C. Frank

APPLICANT: Bender, C. Frank

APPLICANT: Bender, Bender, C. Frank

APPLICANT: Bender, B 1.3%; Score 14.4; DB 1; Length 20; 93.8%; Pred. No. 2.6e+02; tive 0; Mismatches 1; Indels FEATURE: COTHER INFORMATION: Antisense compound US-10-831-901A-4411 568 TITIAATACCITTATA 583 TYPE: DNA ORGANISM: Artificial Sequence 4 rrrraarrccrrrara 19 Query Match Best Local Similarity 93.8<sup>3</sup> Matches 15; Conservative ద ઠ

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Gaps ö

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APPLICANT: Jacqueline Wyatt
APPLICANT: Jacqueline Wyatt
APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Madeline M. Butler
APPLICANT: Robert MCKSy
TITLE OF INVENTION: ANTISENSE MODULATION OF PTPLE EXPRESSION
TITLE OF INVENTION: ANTISENSE WS/11/008,747
CURRENT PILING DATE: 2004-09-04
CURRENT FILING DATE: 2004-09-04
PRIOR FILING DATE: 2000-05-14
PRIOR APPLICATION NUMBER: US 09/629,644
PRIOR APPLICATION NUMBER: US 09/487,368
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
SEQ ID NO 297
LENGTH: 20
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Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1;
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CURRENT FILING DATE: 2004-04-26
PRIOR APPLICATION NUMBER: 60/466,426
PRIOR FILING DATE: 2003-04-28
PRIOR FILING DATE: 2003-04-28
PRIOR FILING DATE: 2003-05-06
PRIOR PELING DATE: 2003-05-06
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-06
PRIOR PILING DATE: 2003-06-10
PRIOR PILING DATE: 2003-06-10
PRIOR PILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-17
NUMBER OF SEQ ID NOS: 30063
SOFTWARE: FRAESEQ FOR WINDOWS VERSION 4.0
SOFTWARE: FARSESEQ FOR WINDOWS VERSION 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , OTHER INFORMATION: Antisense compound US-10-831-901A-4412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Publication No. US20050095710A1
; Publication No. US20050095710A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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RESULT 325 US-10-388-578-48

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Publication No. US20050059000A1

Publication No. US20050059000A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TIPLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/478,633A
CURRENT APPLICATION NUMBER: US/10/478,633A
CURRENT APPLICATION NUMBER: US/2001-11-25
PRIOR APPLICATION NUMBER: UP 2001-177737
PRIOR APPLICATION NUMBER: UP 2001-249689
PRIOR FILING DATE: 2001-06-12
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 173
TURE OF 177737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Designed oligonucleotide probe as Mycol70-probe to detect a DNA f; OTHER INFORMATION: amplifing a portion of ATPase operon from Mycoplasma pneumoniae. US-10-478-633A-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence-527, Application US/10783128
Publication No. US20050096284A1
Publication No. US20050096284A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Treatment of Polyglutamine (PolyQ) Repertitle OF INVENTION: RAPABLE APPLICANT: Expansion Diseases Using Short Interfering Nucleic Acid (sINA)
FILE REFERENCE: 04-105 (400.146)
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                     TITLE OF INVENTION: DELIGIBLE OF CARRACTIVE PROTEIN EXPRESSION FILE REPRENCE: BIOLO014US
FURENT PROPLICATION NUMBER: US/10/858,500
CURRENT FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 99/912,724
PRIOR APPLICATION NUMBER: US 60/475,272
PRIOR PILING DATE: 2001-07-25
PRIOR PILING DATE: 2003-06-02
PRIOR PILING DATE: 2003-06-02
PRIOR PILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 627
SEQ ID NO 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.3%; Score 14.2; DB 1; Length 19; 84.2%; Pred. No. 2.5e+02; tive 0; Mismatches 3; Indels
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84.2%; Pred. No. 2.5e+02;
iive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: Antisense Oligonucleotide US-10-858-500-599
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.2'
Matches 16; Conservative
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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APPLICANT: Stanton, Lawrence
APPLICANT: Stanton, Lawrence
APPLICANT: Stanton, Lawrence
APPLICANT: APPLICANT: Alph, Brandenberger
APPLICANT: John, Trving
APPLICANT: John, Trving
APPLICANT: Mandalam, Ramkumar
APPLICANT: Mok, Michael
TITLE OF INVENTION: A Marker System for Preparing and Characterizing High-Quality Hum
TITLE OF INVENTION: Mabbryonic Stem Cells
TITLE OF INVENTION: Embryonic Stem Cells
TITLE OF SEPTICANT: AND NUMBER: US/10/389,431
CURRENT FILING DATE: 2003-03-13
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.1
ENGTH: 19
                                                                                              APPLICANT: Stanton, Lawrence
APPLICANT: Stanton, Lawrence
APPLICANT: Stanton, Lawrence
APPLICANT: Stanton, Lawrence
APPLICANT: John, Irving
APPLICANT: Mandalam, Ramkumar
APPLICANT: Shelton, Dawne
TITLE OF INVENTION: Genes that are Up- or Down-Regulated During Differentiation of HU
FILE REFERENCE: 135/001
CURRENT APPLICATION NUMBER: US/10/388,578
CURRENT FILING DATE: 2003-03-13
NUMBER OF SEQ ID NOS: 139
SOFTWARE: CLASTOM
TEXAMOL 10
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84.2%; Pred. No. 2.5e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14.2; DB 1; Length 19;
Pred. No. 2.5e+02;
0; Mismatches 3; Indels
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; Sequence 599, Application US/10858500
; Publication No. US20050014257A1
; GRNERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
Sequence 48, Application US/10388578
Publication No. US20030224411A1
GENERAL INFORMATION:
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Publication No. US20040180347A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         827 TCATGACCCAGGAAGGCCG 845
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Best Local Similarity 84.2%;
Matches 16; Conservative (
                                                                                 APPLICANT: Geron Corporation
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Best Local Similarity 84.27
Marches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-389-431-48
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US-10-389-431-48
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GENERAL INFORMATION:
APPLICANT: BYORNATION:
APPLICANT: MCSWiggen, James
TITLE OF INVENTION: RNA Interference Mediated Treatment of Polyglutamine (PolyQ) RepC (PUNENTION: RNA Interference Mediated Treatment of Polyglutamine (PolyQ) RepC (TITLE OF INVENTION: RNA Interference Wediated Treatment of Polyglutamine (PolyQ) RepC (TITLE OF INVENTION: RNA INVENTION: RNA INVENTION: RAPABLICATION NUMBER: US/10/783,128
CURRENT FILING DATE: 2004-01-14
PRIOR PELING DATE: 2004-01-14
PRIOR PILING DATE: 2003-110-23
PRIOR PELING DATE: 2003-10-23
PRIOR PELING DATE: 2003-05-23
PRIOR PELING DATE: 2003-05-23
PRIOR PELING DATE: 2003-04-26
PRIOR PELING DATE: 2003-02-20
PRIOR PELING DATE: 2003-03-30
PRIOR PELING DATE: 2003-02-20
PRIOR PELING DATE: 2003-03-30
PRIOR PELING 
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US-10-783-128-1088
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US-10-783-128-642
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3577
SOFTWARE: Patentin version 3.1
SEQ ID NO 642
LENGTH: 19
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Pred. No. 2.5e+02;
2; Mismatches 3; Indels
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Pred. No. 2.5e+02;
4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1088, Application US/10783128 Publication No. US20050096284A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGAGCCTGCGGCCTTGTG 376
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Best Local Similarity 63.2%;
Matches 12; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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Best Local Similarity 73.7%;
Matches 14; Conservative 2
                                                                                                                                                                                                                                            TYPE: RNA.
ORGANISM: Artificial Sequence
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APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McGwiggen, James
APPLICANT: McGwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Treatment of Polyglutamine (PolyQ) Repe
TITLE OF INVENTION: Expansion Diseases Using Short Interfering Nucleic Acid (siNA)
FILE REFERENCE: 04-105 (400.146)
CURRENT PAPLICATION NUMBER: U5/10/783,128
CURRENT APPLICATION NUMBER: U5 10/757,803
PRIOR FILING DATE: 2004-01-14
PRIOR PILING DATE: 2003-11-24
PRIOR PILING DATE: 2003-11-24
PRIOR PILING DATE: 2003-10-23
PRIOR PILING DATE: 2003-10-23
PRIOR PILING DATE: 2003-05-23
PRIOR PILING DATE: 2003-05-23
PRIOR PILING DATE: 2003-04-24
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2003-04-16
PRIOR FILING DATE: 2003-04-16
PRIOR PILING DATE: 2003-04-16
PRIOR PILING DATE: 2003-04-16
PRIOR FILING DATE: 2003-04-16
PRIOR PILING DATE: 2003-02-20
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US-10-783-128-527
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                     CURRENT FILING DATE: 2004-02-20

PRIOR PLICATION NUMBER: US 10/757,803

PRIOR FILING DATE: 2004-01-14

PRIOR PLICATION NUMBER: US 10/720,448

PRIOR FILING DATE: 2003-11-24

PRIOR FILING DATE: 2003-11-23

PRIOR FILING DATE: 2003-10-23

PRIOR FILING DATE: 2003-05-23

PRIOR FILING DATE: 2003-04-24

PRIOR PILING DATE: 2003-04-24

PRIOR PILING DATE: 2003-04-16

PRIOR PILING DATE: 2003-02-10

PRIOR PILING DATE: 2003-02-10

PRIOR PILING DATE: 2003-02-10

PRIOR FILING DATE: 2003-02-10

PRIOR PILING DATE: 2003-03-10

PRIOR PILING DATE: 2003-03-10
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1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.5e+02;
Matches 14; Conservative 2; Mismatches 3; Indels
             CURRENT APPLICATION NUMBER: US/10/783,128
CURRENT FILING DATE: 2004-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-783-128-642
; Sequence 642. Application US/10783128
; Publication No. US2005096284A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                            PRDICANT: Sirna Therapeutics, Inc.

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: McSA4gean, James

ITILE OF INVENTION: RNA Interference Mediated Treatment of Polyglutamine (PolyQ) Repertant OF INVENTION: Expansion Diseases Using Short Interfering Nucleic Acid (sinNa)

FILE REFERENCE: 04-105 (400.146)

CURRENT ILLING DATE: 2004-01-14

FRICK FILING DATE: 2004-01-14

FRICK FILING DATE: 2004-01-14

FRICK FILING DATE: 2004-01-23

FRICK FILING DATE: 2003-10-23

FRICK FILING DATE: 2003-10-23

FRICK FILING DATE: 2003-05-23

FRICK FILING DATE: 2003-05-23

FRICK FILING DATE: 2003-05-24

FRICK FILING DATE: 2003-05-24

FRICK FILING DATE: 2003-05-26

FRICK FILING DATE: 2003-04-16

FRICK FILING DATE: 2003-04-16

FRICK FILING DATE: 2003-04-16

FRICK FILING DATE: 2003-04-16

FRICK FILING DATE: 2003-02-20

FRICK FILING DATE: 2003-03-20

FRICK FILING DATE: 2003-03-20
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APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RXpansion Diseases Using Short Interfering Nucleic Acid (sinA)
FILLE REPERENCE: 04-105 (400.146)
FRIOR PLLING DATE: 2004-01-14
FRIOR PLLING DATE: 2003-11-24
FRIOR PLLING DATE: 2003-11-24
FRIOR PLLING DATE: 2003-10-23
FRIOR PLLING DATE: 2003-10-23
FRIOR PLLING DATE: 2003-05-23
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Sequence 2279, Application US/10783128
Publication No. US20050096284A1
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Publication No. US20050096284A1
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ORGANISM: Artificial Sequence
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Best Local S
Matches 16
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Sequence 2840, Application US/10783128

Sequence 2840, Application NO. US200509628431

SEQUENCE 2840, Application NO. US200509628431

SEQUENCE 2840, Application NO. US200509628431

SETTIME OF INVENTION: NA INTERFERENCE INC.

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: McSwiggen, James

TITLE OF INVENTION: RNA Interference Mediated Treatment of Polyglutamine (PolyQ) Reper TITLE OF INVENTION: RNA INTERFERENCE: 04-105 (400.146)

FILE REFERENCE: 04-105 (400.146)

CURRENT FILING DATE: 2004-01-14-24

PRIOR PILING DATE: 2003-11-24

PRIOR APPLICATION NUMBER: US 10/493,059

PRIOR PILING DATE: 2003-10-23

PRIOR PILING DATE: 2003-10-24

PRIOR PILING DATE: 2003-04-24

PRIOR PILING DATE: 2003-04-24

PRIOR PILING DATE: 2003-04-24

PRIOR PILING DATE: 2003-04-24

PRIOR APPLICATION NUMBER: US 10/417,012

PRIOR PILING DATE: 2003-04-24

PRIOR PILING DATE: 2003-02-20

PRIOR PILING DATE: 2003-02-20
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                               Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 3577 SOFTWARE: PatentIn version 3.1
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Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3;
APPLICATION NUMBER: US 10/422,704
FILING DATE: 2003-04-24
APPLICATION NUMBER: US 10/417,012
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                                                                                                                                                                                                                          Sequence 79, Application US/09771357
; Sequence 79, Application US/09771357
; Publication No. USZ0030017454A1
; GENERAL INFORMATION:
    APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
    APPLICANT: EVRON, Ella
    APPLICANT: DOCLEY, William
    APPLICANT: DOCLEY, William
    APPLICANT: DAVIDSON, Nancy
    ITILE OF INVENTION: ABERBANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
    ITILE REFERENCE: JHU1630
    CURRENT APPLICATION NUMBER: US/09/771,357
    CURRENT PILLING DATE: 2001-01-26
    NUMBER OF SEQ ID NOS: 110
    SEQ ID NO 79
    ILENGTH: 20
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Publication No. US20030083282A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROSABINE M. Crooke
APPLICANT: ROSABINE M. Crooke
APPLICANT: Mark J. Graham
TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
CURRENT APPLICATION NUMBER: US/09/918,187

CURRENT FILING DATE: 2001-07-30
SEQ ID NO 73

LENGTH: 20
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1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
Query Match
1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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, OTHEN TOTHEN OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: PCR sense primer US-09-771-357-79
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                                                                                               358 GGGAGCCTGCGGCCTTGTG 376
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RESULT 337

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NAME/KEY: primer bind
LOCATION: (1).(20)
CTHER INFORMATION: reverse PCR primer sequence about 30 bp downstream of VncS SNP
US-10-054-225-12
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(SS-10-024-450-12/c

(SGUENCE 12, Application US/10024450

(SGUENCE 12, Application No. 102030032606A1

(SGUENCAL INPORMATION:

APPLICANT: Chadwick, Robert B.

TITLE OF INVENTION: Microsatellite-Instability Positive Tumors Using RIZ

TITLE OF INVENTION: Microsatellite-Instability Positive Tumors Using RIZ

TITLE OF INVENTION: Microsatellite-Instability Positive Tumors Using RIZ

CURRENT APPLICATION NUMBER: US/10/024,450

CURRENT APPLICATION NUMBER: US 60/256,582

PRIOR FILING DATE: 2000-12-19

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12

LENGTH: 20

TENGTH: 20
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1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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Sequence 73, Application US/10006883A

Publication No. US20030119767A1

GENERAL INFORMATION:

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF NOD1 EXPRESSION

FILE REFERENCE: RTS-0337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.3%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3;
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; OTHER INFORMATION: synthetic primer
US-10-024-450-12
                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Streptococcus pneumoniae
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ORGANISM: Artificial Sequence
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APPLICATION NUMBER: US 08/478,178
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                                                                                                                                                                                                                                                     TYPE: DNA
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APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: SUKUMAR. Saraswati
APPLICANT: BUKUMAR. Saraswati
APPLICANT: BUKUMAR.
APPLICANT: DOOLBY, William C.
APPLICANT: DOOLBY, William C.
APPLICANT: DAVIDBON, Nancy
APPLICANT: PACKLER, Mary Jo.
TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
PILE REPRESENCE: JHU1630-1
CURRENT APPLICATION NUMBER: US/10/059,579
PRIOR FILING DATE: 2003-02-03
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 136
SOFTWARE: Patentin version 3.1
SEQ ID NO 79
LENGTH: 20
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APPLICANT: Dean, Nicholas M.
APPLICANT: Holmlund, Jon T.
APPLICANT: Dorr, P. Andrew
TITLE OP INVENTION: Oligonucleotide Modulation Of Protein Kinase C
PILE REPERENCE: ISIS4954
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                                                                                                                                                                                                                                                                       Query Match
1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                      ; PEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-883A-73
CURRENT APPLICATION NUMBER: US/10/006,883A CURRENT FILING DATE: 2001-12-05 NUMBER OF SEQ ID NOS: 96
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CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US/10/025,139
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 08/829,637
PRIOR FILING DATE: 1997-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: PCR sense primer
US-10-059-579-79
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Publication No. US20030148989A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 79, Application US/10059579
Publication No. US20030138783A1
                                                                                                                                                                                                                                                                                                                                                                           1096 TTACCTGCTCATTTGTTTA 1114
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                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 84.2
Matches 16; Conservative
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                                                                       SEQ ID NO 73
LENGTH: 20
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NAME/KEY: primer bind LOCATION: (1)..(\overline{2}0) OTHER INFORMATION: reverse PCR primer sequence about 30 bp downstream of VncS SNP
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| Publication No. US20030190639A1
| GENERAL INFORMATION:
| APPLICANT: HUGOV, JEAN-PIERRE
| APPLICANT: THOMAS, GILLES
| APPLICANT: LESAGE, SUZANE
| APPLICANT: LESAGE, SUZANE
| APPLICANT: LESAGE, SUZANE
| APPLICANT: LESAGE, SUZANE
| APPLICANT: THAMAILLAND, MATHIAS
| TITLE OF INVENTION: THEREOF
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Sequence 12, Application US/10428617

Publication No. US20030175796A1

GENERAL INFORMATION:

APPLICANT: Saint Unde Children's Research Hospital

APPLICANT: Tuomanen, Elaine

APPLICANT: Atkinson, Robyn M

TITLE OF INVENTION: Diagnostic Assay for Antibiotic Tolerance

FILE REFERENCE: SJ-01-0022

CURRENT APPLICATION NUMBER: US/10/428,617

CURRENT APPLICATION NUMBER: US/10/054,225

PRIOR APPLICANTON NUMBER: US/110/054,225

PRIOR FILING DATE: 2001-11-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin version 3.1

SEQ ID NO 12

LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.3%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Antisense Oligonucleotide US-10-348-485-86
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/089,996
PRIOR FILING DATE: 1993-07-09
PRIOR FILING DATE: 1992-07-09
PRIOR PILING DATE: 1992-03-16
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 86
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434 AGAGGAGATGATTTTAGCT 452
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220 CATTGCCAAAAGAGTCACC 238
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US-10-154-708-86/c
US-10-154-708-86/c
; Sequence 86, Application US/10154708
; Publication No. US20030219895A1
; GENERAL INFORMATION:
APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: TYS-0213
; CURRENT PILING DATE: 2002-05-22
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 143
; SEQ ID NO 86
; LENGTH: 20
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1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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            CURRENT APPLICATION NUMBER: US/10/240,046A
CURRENT FILING DATE: 2003-04-02
PRIOR APPLICATION NUMBER: PCT/FR 01/00935
PRIOR FILING DATE: 2001-03-27
PRIOR PLILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: 20
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                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-10-240-046A-56
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APPLICANT: van Ommen, Garrit-Jan Boudewijn
APPLICANT: van Ommen, Garrit-Jan Boudewijn
APPLICANT: van Deutekom, Judith Christina Theodora
APPLICANT: den Dunmen, Johannes Theodorus
TITLE OF INVENTION: INDUCTION OF EXON SKIPPING IN EUKARYOTIC CELLS
FILE REFERENCE: 2183-5910US (REN/P54258US10)
CURRENT APPLICATION NUMBER: US/10/395,031
CURRENT APPLICATION NUMBER: PCT/NL01/00697
PRIOR APPLICATION NUMBER: PCT/NL01/00697
PRIOR APPLICATION NUMBER: PCT/NL01/00697
PRIOR APPLICATION NUMBER: DCT/NL01/00697
PRIOR PILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.2
SEQ ID NO 5
LENGTH: 20
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                                                                                                             Sequence 333, Application US/10300683

Sequence 333, Application US/10300683

Publication No. US20030235834A1

GENERAL INFORMATION:
APPLICANT: Weisel, James M.,
APPLICANT: Weisel, James M.,
TILLS OF INVENTION: APPROACHES TO IDENTIFY CYSTIC FIBROSIS
FILE REFERENCE: CHARDUN.010A

CURRENT APPLICATION NUMBER: US/10/300,683

CURRENT FILING DATE: 2002-11-19
PRIOR FILING DATE: 2001-11-19

PRIOR FILING DATE: 2001-11-19

NUMBER OF SEQ ID NOS: 554

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 333

LENGTH: 20
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1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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84.2%; Pred. No. 2.7e+02;
tive 0; Mismatches 3;
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US-10-349-143-9409/c
; Sequence 9409, Application US/10349143
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2 certrecagaddadreace 20
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ORGANISM: Artificial Sequence
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US-10-289-762-2125

Sequence 2125, Application US/10289762

Sequence 2125, Application US/10289762

Publication No. US20040006218A1

GENERAL INFORMATION:

APPLICAT: Griffais, R.

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/10/289,762

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 2125

LENGTH: 20
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APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION
FILE REFERENCE: PTS-0023
CURRENT APPLICATION NUMBER: US/10/190,366
CURRENT FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 409
SEQ ID NO 111
LENGTH: 20
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Publication No. US20040006031A1
GENERAL INFORMATION:
APPLICANT: Susan M. Dean
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION
FILE REPERBNCE: PTS-0023
CURRENT APPLICATION NUMBER: US/10/190,366
CURRENT FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 409
SEQ ID NO 308
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Pred. No. 2.7e+02;
0; Mismatches 3;
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84.2%; Pred. No. 2.7e+02;
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CRGANISM: Chlamydia pneumoniae
US-10-289-762-2125
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Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
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JOURDAY INVOLVED Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Chunakov, Ilya
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Chunakov, Ilya
JULIANT: Chunakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REPERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: EARLIER PILING DATE: 1999-04-21
PRIOR FILING DATE: EARLIER PILING DATE: 1999-04-21
PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-23
PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-23
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NOS: 11796
TANGER OF SEQ ID NOS: 11796
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| Sequence 69, Application US/10188470
| Publication No. US20040005707A1
| Sequence 69, Application US/10188470
| Publication No. US20040005707A1
| GENERAL INFORMATION:
| APPLICANT: Scott Cooper
| APPLICANT: Kenneth W. Dobie
| TILLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN BETA S EXPRESSION
| FILE REPERRENCE: PTG-0024
| CURRENT APPLICATION NUMBER: US/10/188,470
| CURRENT FILING DATE: 2002-07-02
| NUMBER OF SEQ ID NOS: 130
| SEQ ID NO 69
| SEQ ID NO 69
| LENGTH: 20
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1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-188-470-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1029 GAGAAGTAAACATCACACC 1047
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            US20040005584A1
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: primer_bind
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Best Local Similarity
Matches 16; Conserva
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US-10-190-366-111/c
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US-10-289-762-6581

Sequence 6581, Application US/10289762

Sequence 6581, Application US/10289762

Sequence 6581, Application No. US20040006218A1

GENERAL INFORMATION:
APPLICANT: Griffals, R.
TITLE OF INVENTION: Thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: US/10/289, 762

CURRENT APPLICATION NUMBER: US/10/289, 762

CURRENT PILING DATE: 2003-03-27

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 6581

LENGTH: 20
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Publication No. US20040115637A1
GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Remeth W. Dobie
TITLE OF INVENTION: MODULATION OF PPAR-ALPHA EXPRESSION
FILE REFERENCE: FIRS-038
                                                                                                                                                                                                Query Match 1.3%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3;
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CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 5166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 TGTCGGGAACTGGCATATT 284
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                                                                                                                                                                                                                                                                                            291 CTACTGGAATTGTTTC 309
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                                                                                                                                                                                                                                                                                                                     2 CTTCTGGAGTCGTTGTTTC 20
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                                                                                                                       TYPE: DNA ORGANISM: Chlamydia pneumoniae
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Matches 16; Conserv
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US-10-317-500-76/c
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                                                                                                  LENGTH: 20
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Sequence 5166, Application No. US20040006218A1

Publication No. US20040006218A1

GENERAL INFORMATION:

APPLICANT: Griffals, R.

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preversing of INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5159, Application US/10289762

Publication No. US20040006218A1

Publication No. US20040006218A1

Publication No. US20040006218A1

APPLICANT: Griffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preveritte OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT PAPLICATION WUMBER: US/10/289,762

CURRENT FILING DATE: 2003-03-27

NUMBER OF SEQ ID NOS: 6849

FERMING NOS: 6849
                                                                                                                                                                                           Sequence 4121, Application US/10289762

Publication No. US20040005218A1

GENERAL INFORMATION:
APPLICANT: Griffals, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/10/289,762

CURRENT APPLICATION NUMBER: 2003-03-27

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 4121

LENGTH: 20
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Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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84.2%; Pred. No. 2.7e+02;
tive 0; Mismatches 3;
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                         0; Mismatches
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; ORGANISM: Chlamydia pneumoniae
US-10-289-762-5159
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Best Local Similarity 84.2
Matches 16; Conservative
                            16; Conservative
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US-10-289-762-5166
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US-10-289-762-5159
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                                   Matches
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US-10-424-041-179
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84.2%; Pred. No. 2.7e+02;
ive 0; Mismatches 3; Indels
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84.2%; Pred. No. 2.7e+02;
tive 0; Mismatches 3; Indels
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| Sequence 105, Application US/204021806A1
| GENERAL INFORMATION:
| APPLICANT: C. Frank Bennett
| APPLICANT: Thomas Condon | APPLICANT: Susan M. Fraist
| APPLICANT: Susan M. Fraist
| TILL OF INVENTION: MODULATION OF TYROSINASE EXPRESSION | FILE REFERENCE: BIOLOGOSUS | CURRENT FILING DATE: 2003-04-25 | SUMBER OF SEQ ID NOS: 184 | SEQ ID NO 105 | LENGTH: 20 | LENGTH: 20
                           Sequence 310, Application US/10731739
Publication No. US20040176582A1
GENERAL INFORMATION:
APPLICANT: Carulli, John P.
APPLICANT: Little, Randall D.
APPLICANT: Recker, Robert R.
APPLICANT: APPLICANT: Johnson, Mark L.
TITLE OF INVENTION: High bone mass gene of 11q13.3
FILE REFERENCE: 032796-013
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-424-041-105
                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT PAPPLICATION NUMBER: US/10/731,739
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: US/09/544,398B
PRIOR FILING DATE: 2002-06-10
PRIOR FILING DATE: 1999-01-03
PRIOR PILING DATE: 1999-01-13
PRIOR PILING DATE: 1999-01-13
PRIOR PILING DATE: 1998-01-13
SPRIOR PILING DATE: 1998-01-13
PRIOR PILING DATE: 1998-01-13
SPRIOR PILING DATE: 1998-01-13
SOFTWARE: PSEC ID NOS: 641
SOFTWARE: PSEC ID NOS: 641
SOFTWARE: PSEC ID NOS: 641
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Best Local Similarity 84.2<sup>3</sup>
Matches 16; Conservative
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Matches 16; Conservative
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US-10-731-739-310
US-10-731-739-310/c
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RESULT 360 US-10-424-041-179

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Publication No. US20040221326A1

GENERAL INFORMATION:

APPLICANT: Bax, Frederick J. III

APPLICANT: Bax, Frederick J. III

APPLICANT: Bex, Frederick J. III

APPLICANT: Bex, Frederick J. III

APPLICANT: Bex, Frederick J. III

APPLICANT: Box, Frederick J. III

FILE REFERENCE: 032796-212

CURRENT APPLICATION NUMBER: US 60/290,071

FRIOR APPLICATION NUMBER: US 60/291,311

FRIOR FILING DATE: 2001-05-11

FRIOR APPLICATION NUMBER: US 60/353,058

FRIOR FILING DATE: 2002-05-01

FRIOR APPLICATION NUMBER: US 60/351,293

FRIOR FILING DATE: 2002-03-04

NUMBER OF SEQ ID NOS: 812

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 20

LENGTH: 20
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Pred. No. 2.7e+02;
5; Mismatches 3; Indels
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                                                                          APPLICANT: C. Frank Bennett
APPLICANT: Thomas Condon
APPLICANT: Thomas Condon
APPLICANT: Thomas Condon
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODILATION OF TYROSINASE EXPRESSION
TITLE OF INVENTION: MODILATION OF TYROSINASE EXPRESSION
CURRENT APPLICATION NUMBER: US/10/424,041
CURRENT FILING DATE: 2003-04-25
SEQ ID NOS: 184
SEQ ID NO 179
LENGTH: 20
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Publication No. US20040244069A1
GENERAL INFORMATION:
APPLICANT: Babij, Philip
APPLICANT: Yaworsky, Paul
Sequence 179, Application US/10424041
Publication No. US20040215006A1
GENERAL INFORMATION:
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Best Local Similarity 57.9 Matches 11; Conservative
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US-10-477-238A-310
                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: M. musculus
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TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION FILE REFERENCE: ISPH?0695 CURRENT APPLICATION NUMBER: US/10/484,442 CURRENT FILING DATE: 2004-01-29 PRIOR APPLICATION NUMBER: 09/918,187 PRIOR PAPLICATION NUMBER: 09/918,187 PRIOR FILING DATE: 2001-07-30 NUMBER OF SEQ ID NOS: 80 SEQ ID NO 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ROSADNA Crooke
APPLICANT: ROSADNA Crooke
TITLE OF INVENTION: MODULATION OF C-REACTIVE PROTEIN EXPRESSION
FILE REFERENCE: BIOLO014US
CURRENT APPLICATION NUMBER: US/10/858,500
CURRENT APPLICATION NUMBER: US 09/912,724
PRIOR PILING DATE: 2004-06-01
PRIOR PLILING DATE: 2001-07-25
PRIOR PLILING DATE: 2003-06-02
PRIOR PLILING DATE: 2003-06-02
PRIOR PLILING DATE: 2003-06-02
PRIOR PLILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 627
SEQ ID NOS: 627
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| Sequence 381, Application US/10858500
| Publication No. US20050014257A1
| GENERAL INFORMATION:
| APPLICANT: Rosanne M. Crooke
| APPLICANT: Rosanne M. Crooke
| APPLICANT: Mark J. Graham
| TITLE OF INVENTION: MODULATION OF C-REACTIVE PROTEIN EXPRESSION
| FILE REPERENCE: BIOLO014US
| CURRENT APPLICATION NUMBER: US/10/858,500
| CURRENT PILING DATE: 2004-06-01
| PRIOR PILING DATE: 2001-07-25
| PRIOR PILING DATE: US/09/912,724
| PRIOR PILING DATE: US/00-05
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pred. No. 2.7e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                        1.3%; Score 14.2; DB 1;
84.2%; Pred. No. 2.7e+02;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Antisense Oligonucleotide US-10-858-500-205
                                                                                                                                                                                                                                                                           FEATURE:
CTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 205, Application US/10858500; Publication No. US20050014257A1; GENERAL INFORMATION:
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Best Local Similarity 84.2%;
Matches 16; Conservative (
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 84.2
Matches 16; Conservative
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US-10-858-500-381/c
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US-10-858-500-205
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Sequence 4, Application US/10476960

Publication No. US20040248828A1

GENERAL INFORMATION:

APPLICANT: Brenda F. Baker

APPLICANT: Susan M. Frace

APPLICANT: Isla Pharmaceuticals, Inc.

APPLICANT: Isla Pharmaceuticals, Inc.

TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION

FILE REPRENEUE: F1SP-032-03-05-07

FULCANT: PLING DATE: 2003-11-05

PRIOR FILING DATE: 2001-05-07

NUMBER OF SEQ ID NOS: 88

SEQ ID NOS: 08
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                                        APPLICANT: Bex, Frederick J. III
PEPLICANT: Bodine, Peter Van Nest
TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation
FILE REPERENCE: 032796-179
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Pred. No. 2.7e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                      CURRENT APPLICATION NUMBER: US/10/680,287A
CURRENT APPLICATION NUMBER: US/10/680,287A
CURRENT FILING DATE: 2003-10-08
PRIOR APPLICATION NUMBER: PCT/US02/14876
PRIOR APPLICATION NUMBER: US 60/290,071
PRIOR APPLICATION NUMBER: US 60/291,311
PRIOR APPLICATION NUMBER: US 60/291,311
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2002-02-01
PRIOR FILING DATE: 2002-03-04
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 812
SOFTWARE: PRESEQ FOR WINDOWS VERSION 4.0
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Publication No. US20040254359A1
GENERAL INFORMATION:
APPLICANT: Isis Pharmaceuticals, Inc.
APPLICANT: Rosanne M. Crooke
APPLICANT: Mark J. Graham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   822 GCCTCTCATGACCCAGGAA 840
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Best Local Similarity 84.2%;
Matches 16; Conservative
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-476-960-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
US-10-680-287A-310
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LENGTH: 20
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US-10-619-253-73
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Sequence 73, Application US/10619253

Sequence 73, Application US/10619253

Sequence 73, Application US/10619253

Sequence 73, Application US/006043256A1

Sequence 73, Application No. US20050043256A1

GENERAL INFORMATION:

APPLICANT: ROBANNE M. Crooke

APPLICANT: MARTION:

AND TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION

TITLE OP INVENTION:

CURRENT PELING DATE: 2003-07-15

FRIOR APPLICATION NUMBER: US/10/619,253

CURRENT PILING DATE: 2001-07-30

FRIOR FILING DATE: 2001-07-30

SEQ ID NO 73

LENGTH: 20
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GENERAL INCOMMINION:
GENERAL INCOMMINION:
APPLICANT: Slettan, Audun
APPLICANT: Lingaas, Frode
TITLE OF INVENTION: Verification of Food Origin Based on
TITLE OF INVENTION: Verification of Food Origin Based on
TITLE OF INVENTION: Nucleic Acid Pattern Recognition
FILE REFRENCE: 66849-019
CURRENT APPLICATION NUMBER: US/10/643,775
CURRENT FILING DATE: 2003-08-18
PRIOR PILING DATE: 2003-08-18
NUMBER OF SEQ ID NOS: 1377
SOFTWARE: PESESCE for Windows Version 4.0
SEQ ID NO 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
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                          60/540,042
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CRGANISM: Oreochromis niloticus
US-10-643-775-1061
PRIOR FILING DATE: 2003-06-02
PRIOR APPLICATION NUMBER: US 60,
NUMBER OF SEQ ID NOS: 627
LENGTH: 20
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Best Local Similarity 84.2<sup>3</sup>
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-643-775-1061
                                                                                                                                                                                                       US-10-858-500-381
                                                                                                                                               TYPE: DNA
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Publication No. US20050070699A1
GENERAL INFORMATION:
APPLICANT: Genome Therapeutics Corporation and
APPLICANT: Allen, Kristina M.
APPLICANT: Avacrafy, Paul J.
APPLICANT: Anisowicz, Antun J.
APPLICANT: Anisowicz, Anthony
APPLICANT: Anisowicz, Anthony
APPLICANT: Liu, Wei
TITLE OF INVENTION: HBM Variants that Modulate Bone Mass and Lipid Levels
FILE REFREENCE: 023796-135
CURRENT APPLICANT: 2003-11-10
CURRENT FILING DATE: 2003-11-10
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APPLICANT: Massire, Christian
APPLICANT: Massire, Christian
APPLICANT: Hofstadler, Steven A.
APPLICANT: Swarze, Eric
APPLICANT: Swarze, Eric
APPLICANT: Benett, C. Frank
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
FILE REFERENCE: ISISO0031-100 (BIOL0008US)
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Query Match
1.3%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3;
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Pred. No. 2.7e+02;
0; Mismatches 3;
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PRIOR PILING DATE: 2001-05-11
PRIOR PILING DATE: 2001-05-11
PRIOR PILING DATE: 2001-05-17
PRIOR PILING DATE: 2001-05-17
PRIOR PILING DATE: 2002-02-01
PRIOR PILING DATE: 2002-02-01
PRIOR PILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 1086
SOFTWARE: PESESEQ for Windows Version 4.0
SSOFTWARE: PESESEQ for Windows Version 4.0
SERIOTH: 20
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Sequence 10393, Application US/10831901A
Publication No. US20050100885A1
GENERAL INPORMATION:
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                                                                                                      814 TGAAGCAGGCCTCTCATGA 832
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APPLICANT: Bcker, David J.
APPLICANT: Sampath, Rangarajan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.3%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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; ORGANISM: Homo sapiens
US-10-477-173-310
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Best Local Similarity 84.2%; Pred. No. 2.7e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11295
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Publication No. US20050100885A1
GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
APPLICANT: Ecker, David J.
APPLICANT: Sampath, Rangarajan
APPLICANT: Freier, Susan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Antisense compound US-10-831-901A-11295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1014 AGAAGCATCATAGAGA 1032
                                                                                             407 ATTCAAGGGTTTTTCCTTA 425
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Best Local Similarity 84.2%;
Matches 16; Conservative (
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ORGANISM: Artificial Sequence
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-10-831-901A-10394/C
Sequence 10394, Application US/10831901A
PUBLICANT NO. US20505100885A1
GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
APPLICANT: Ecker, David J.
APPLICANT: Ecker, David J.
APPLICANT: Ecker, Susan M.
APPLICANT: Hoderadler, Steven A.
APPLICANT: Massire, Christian M.
APPLICANT: Banet, Ristin Sannes
APPLICANT: Baker, Brenda F.
APPLICANT: Baker, Brenda F.
APPLICANT: Baker, Sissons J.
APPLICANT: Baker, Or The Treatment Of Severe
TITLE OF INVENTION: Compositions And Methods For The Treatment
TITLE OF INVENTION: Compositions And Methods For The Treatment
TITLE OF INVENTION: Compositions And Methods For The Treatment
TITLE OF INVENTION: Compositions And Methods For The Treatment
TITLE OF INVENTION: Compositions And Methods For The Treatment
TITLE OF INVENTION NUMBER: 06/466,426
PRIOR FILING DATE: 2003-04-28
PRIOR FILING DATE: 2003-04-30
PRIOR FILING DATE: 2003-04-30
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-04-30
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-10
PRIOR PRILICATION NUMBER: 60/469,579
PRIOR APPLICATION NUMBER: 60/467,770
PRIOR PRILING DATE: 2003-06-10
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                    PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: 60/468,562
PRIOR FILING DATE: 2003-06-06
PRIOR PILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: 60/468,627
PRIOR PILING DATE: 2003-04-30
PRIOR PILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/477,637
PRIOR FILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-10
PRIOR PILING DATE: 2003-06-10
PRIOR PILING DATE: 2003-06-27
NUMBER OF SEQ ID NOS: 30063
SOFTWARE: FRREESEQ FOR WINDOWS VERSION 4.0
SEG ID NO 10393
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SOTTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10394
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Antisense compound US-10-831-901A-10393
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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ò 셤 1.3%; Score 14.2; DB 1;

Query Match

US-10-831-901A-11295

Sequence 11295, Application US/10831901A

Publication No. US20050100885A1

GENERAL INFORMATION:

APPLICANT: Ecker, David J.

APPLICANT: Ecker, David J.

APPLICANT: Messive, Christian

APPLICANT: Mestadier, Steven A.

APPLICANT: Mestadier, Steven A.

APPLICANT: Lowery, Kristin Sannes

APPLICANT: Lowery, Kristin Sannes

APPLICANT: Bennet, C. Frank

TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe

TITLE OF INVENTION: Compositions And Methods For The Treatment C. Frank

TITLE OF INVENTION: Compositions And Methods (SARS)

TITLE OF INVENTION: Compositions And Methods (SARS)

TITLE OF INVENTION: Compositions And Methods (SARS)

FILLE REPERENCE: ISISSO83-100 (BIOLO008US)

CURRENT FILING DATE: 2004-04-28

PRIOR FILING DATE: 2003-04-28

PRIOR APPLICATION NUMBER: 60/466,527

PRIOR PLING DATE: 2003-06-06

PRIOR PLING DATE: 2003-06-06

PRIOR PLING DATE: 2003-06-10

PRIOR FILING DATE: 2003-06-10

PRIOR PRIUM DATE: 2003-06-10

PRIOR FILING DATE: 2003-06-10

PRIOR PRIUM DATE: 2003-06-10 ö ö Gaps Gaps . 0 ; Score 14.2; DB 1; Length 20; Pred. No. 2.7e+02; 0; Mismatches 3; Indels Massire, Christian Hofstadler, Steven A. Lowery, Kristin Sannes Swayze, Bric Baker, Brenda F.

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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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APPLICANT: Ecker, David J.
APPLICANT: Ecker, David J.
APPLICANT: Ecker, David J.
APPLICANT: Ecker, David J.
APPLICANT: Sampath, Rangarajan
APPLICANT: Hofstadler, Steven M.
APPLICANT: Wassire, Christian
APPLICANT: Swayze, Eric
APPLICANT: Swayze, Bric
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## APPLICANT: Bennett, C. Frank

ITILE OF INVENTION: Compositions And Methods For The Treatment Of Severe

TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)

FILE REFERENCE: ISISO083-100 (BIOL0008US)

CURRENT APPLICATION NUMBER: US/10/831,901A

CURRENT FILING DATE: 2004-04-26

FRIOR FILING DATE: 2003-04-28

FRIOR FILING DATE: 2003-04-28

FRIOR APPLICATION NUMBER: 60/468,562

FRIOR APPLICATION NUMBER: 60/468,562

FRIOR APPLICATION NUMBER: 60/467,770

FRIOR APPLICATION NUMBER: 60/467,770

FRIOR FILING DATE: 2003-04-30

FRIOR FILING DATE: 2003-05-60

FRIOR FILING DATE: 2003-05-60

FRIOR FILING DATE: 2003-06-10

FRIOR FILING DATE: 2003-06-27

FRIOR FILING DATE: 2003-06-27

NUMBER OF SEQ ID NOS: 30063

SOFTWARE: FastSEQ for Windows Version 4.0

FRIOR TILING DATE: 2013-06-27

NUMBER OF SEQ ID NOS: 30063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Antisense compound US-10-831-901A-11296
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 84.2%;
hes 16; Conservative
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Matches
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GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
APPLICANT: Ecker, David J.
APPLICANT: Ecker, David J.
APPLICANT: Ecker, David J.
APPLICANT: Ampatin, Rangarajan
APPLICANT: Freier, Sueven A.
APPLICANT: Massire, Christian
APPLICANT: Baker, Brenda F.
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Baker, Brenda F.
APPLICANT: Baker, Brenda F.
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Baker, Brenda F.
APPLICANT: Suyze, Bric
APPLICANT: Baker, Brenda F.
APPLICANTON NUMBER: 60/464,26
PRIOR FILING DATE: 2003-04-26
PRIOR PLING DATE: 2003-06-10
PRIOR APPLICATION NUMBER: 60/468,627
PRIOR APPLICATION NUMBER: 60/443,579
PRIOR PLILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-10
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                                                                                                              Score 14.2; DB 1; Length 20;
Pred. No. 2.7e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12115, Application US/10831901A Publication No. US20050100885A1 GENERAL INFORMATION:
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; Sequence 14584, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; OTHER INFORMATION: Antisense compound US-10-831-901A-12114
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                                                                                                                       1.3%;
84.2%;
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                                                                                                                                                             Best Local Similarity 84.2
Matches 16; Conservative
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Sequence 14587, Application US/10831901A

Publication No. US20050100885A1

GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
APPLICANT: Ecker, David J.
APPLICANT: Ecker, David J.
APPLICANT: Bampath, Rangarajan
APPLICANT: Massire, Christian
APPLICANT: Massire, Christian Applicant: Hofstadler, Steven A.
APPLICANT: Barer, Brenda F.
APPLICANT: Swayze, Exic
APPLICANT: Graych, Kristin Sannes
APPLICANT: Graych, Ristin Sannes
APPLICANT: Graych, Ristin Sannes
APPLICANT: Bahnett, C. Frant
APPLICANT: Bahnett, C. Frant
APPLICANT: Bahnet, C. Frant
APPLICANT: Bannet, C. Frant
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APPLICANT: Bannet, C. Frant
APPLICANT: Bannet, C. Frant
APPLICANT: Bannet
APPLICANT: Banne
                                                                                                                            APPLICANT: Hofstadler, Steven A.
APPLICANT: Hofstadler, Steven A.
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Savaze, Eric
APPLICANT: Baker, Brenda F.
APPLICANTON WUBBER: US/100008US)
FILE REFERENCE: ISISO083-100 (BIOL0008US)
FILE REFERENCE: 1SISO083-100 (BIOL0008US)
FILE REPERENCE: 1051003-100 (BIOL0008US)
FILE REPERENCE: 2003-04-28
FRIOR APPLICATION WUMBER: 60/468,562
FRIOR FILING DATE: 2003-05-06
FRIOR APPLICATION WUMBER: 60/468,627
FRIOR FILING DATE: 2003-06-10
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1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Antisense compound
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Sampath, Rangarajan
Freier, Susan M.
Massire, Christian
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LENGTH: 20
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Pred. No. 2.7e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                         Score 14.2; DB 1; Length 20;
Pred. No. 2.7e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-831-901A-15628

Sequence 15628, Application US/10831901A

Publication No. US20050100885A1

GENERAL INFORMATION:

APPLICANT: Ercker, David J.

APPLICANT: Ercker, David J.

APPLICANT: Freier, Susan M.

APPLICANT: Freier, Susan M.

APPLICANT: Freier, Susan M.

APPLICANT: Massire, Christian

APPLICANT: Howery, Kristin Sannes

APPLICANT: Gowery, Kristin Sannes

APPLICANT: Barer, Brid

TITLE OP INVENTION: Compositions And Methods For The Treatr

TITLE OP INVENTION: Acute Respiratory Syndrome (SARS)

TITLE OP INVENTION: Acute Respiratory

TITLE OF INVENTION: Acute Respiratory

CURRENT FILING DATE: 2003-04-28

FRIOR PELICATION NUMBER: 60/466,562

PRIOR PELICATION NUMBER: 60/466,562

PRIOR PELICATION NUMBER: 60/467,770

PRIOR FILING DATE: 2003-05-06

PRIOR FILING DATE: 2003-06-10

PRIOR FILING DATE: 2003-06-27

WUMBER OF SRO I'N MOMBER: 60/483,579
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15628
LENGTH: 20
PRIOR FILING DATE: 2003-06-10
PRIOR APPLICATION NUMBER: 60/483,579
PRIOR FILING DATE: 2003-06-27
NUMBER OF SEQ ID NOS: 30063
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14587
LENGTH: 20
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                                                                                                                                                                                                         TYPE: DNA

ORGANISM: Artificial Sequence

PRATURE:

PRATURE:

OTHER INFERMATION: Antisense compound

US-10-831-901A-14587
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Best Local Similarity 84.2%;
Matches 16; Conservative
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Best Local Similarity 84.2%;
Matches 16; Conservative
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Query Match
Best Local Similarity
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APPLICANT: Sampath, Rangarajan
APPLICANT: Sampath, Rangarajan
APPLICANT: Preier, Susan M.
APPLICANT: Hofstadler, Steven A.
APPLICANT: Hofstadler, Steven A.
APPLICANT: Howery, Kristin Sannes
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Swayze, Eric
APPLICANT: Baker, Brenda F.
APPLICANT: Brenda F.
APPLICANT:
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APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
FILE REFERENCE: ISISO003-100 (BIOL0008US)
CURRENT APPLICATION NUMBER: US/10/831,901A
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Sequence 26188, Application US/10831901A
Publication No. US2050100885A1
GENERAL INFORMATION:
APPLICANT: ERCEY. David J.
APPLICANT: Sempath, Rangarajan
APPLICANT: Freier, Susan M.
APPLICANT: Hofstadier, Steven A.
APPLICANT: Hofstadier, Steven A.
APPLICANT: Wassire, Christian
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Swayze, Eric
RESULT 379
US-10-831-901A-26183/C
Sequence 26183, Application US/10831901A
Publication No. US20050100885A1
GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
APPLICANT: Ecker, David J.
Pangarajan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Antisense compound US-10-831-901A-26183
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Matches 16; Conservative
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APPLICANT:
APPLICANT:
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APPLICANT: Freier, Suean M.
APPLICANT: Massire, Christian
APPLICANT: Hofstadler, Steven A.
APPLICANT: Hofstadler, Steven A.
APPLICANT: Swayze, Eric
APPLICANT: Baker, Brenda F.
APPLICANTON: Compositions And Methods For The Treatment Of Severe TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
CURRENT APPLICATION NUMBER: US/10/831,901A
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84.2%; Pred. No. 2.7e+02;
tive 0; Mismatches 3; Indels
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84.2%; Pred. No. 2.7e+02;
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PRIOR APPLICATION NUMBER: 60/466,426
PRIOR FILING DATE: 2003-04-28
PRIOR FILING DATE: 2003-04-28
PRIOR PILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/467,770
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-11
PRIOR FILING DATE: 2003-06-17
PRIOR PLING DATE: 2003-06-10
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PRIOR FILING DATE: 2003-05-06
PRIOR PILING DATE: 2003-05-06
PRIOR PILING DATE: 2003-04-30
PRIOR PILING DATE: 2003-04-30
PRIOR PILING DATE: 2003-06-06
PRIOR PILING DATE: 2003-06-06
PRIOR PILING DATE: 2003-06-10
PRIOR PILING DATE: 2003-06-10
PRIOR PILING DATE: 2003-06-17
NUMBER OF SEQ ID NOS: 30063
SOFTWARE: FESELSEQ for Windows Version 4.0
SEQ ID NO 26188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Antisense compound US-10-831-901A-26188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Matches 16; Conservative
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US-10-476-264-189/c
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APPLICANT: Hofstadler, Steven A.
APPLICANT: Hofstadler, Steven A.
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Swayze, Eric
APPLICANT: Baker, Brenda F.
APPLICANT: Baker, Brenda F.
APPLICANT: Baker, C. Frank
APPLICANT: Baker, C. Frank
APPLICANT: Baker, C. Frank
APPLICANT: Baker, C. Frank
TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
FILE REFREENCE: S103083-100 (BIOLO008US)
CURRENT APLICATION NUMBER: US/10/831,901A
CURRENT FILING DATE: 2003-04-28
PRIOR FILING DATE: 2003-04-28
PRIOR FILING DATE: 2003-04-30
PRIOR PELING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: 60/468,627
PRIOR PELING DATE: 2003-05-06
PRIOR FILING DATE: 2003-06-27
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Pred. No. 2.7e+02;
0; Mismatches 3; Indels
3; Indels
   0; Mismatches
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Sequence 26897, Application US/10831901A
PUBLICATION NO. US20050100885A1
GENERAL INFORMATION:
APPLICANT: CROOKE, Stanley T.
APPLICANT: Ecker, David J.
APPLICANT: Freder, Sampath, Rangarajan
APPLICANT: Freder, Susan M.
APPLICANT: Hofetadler, Steven A.
APPLICANT: Hofetadler, Steven A.
APPLICANT: LOWETY, Kristin Sannes
APPLICANT: Swayze, Eric
APPLICANT: Baker, Brenda F.
                                                                                                                                                                                                                                                                                                          Sequence 26696, Application US/10831901A
Publication No. US20050100885A1
GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
APPLICANT: Sampath, Rangarajan
APPLICANT: Freier, Susan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: Antisense compound US-10-831-901A-26896
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Best Local Similarity 84.2%;
Matches 16; Conservative (
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ORGANISM: Artificial Sequence
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       16; Conservative
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US-10-831-901A-26896
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APPLICANT:
              Matches
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TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe TITLE OF INVENTION: Acute Respiratory Syndrome (SARS) FILE REFERENCE: ISISO083-100 (BIOL0008US) CURRENT APPLICATION WUMBER: US/10/831,901A CURRENT FILING DATE: 2004-04-26 PRIOR APPLICATION NUMBER: 66/466,426 PRIOR APPLICATION NUMBER: 66/468,562 PRIOR FILING DATE: 2003-04-86 PRIOR FILING DATE: 2003-05-06 PRIOR FILING DATE: 2003-06-10 PRIOR FILING DATE: 2003-06-27 PRIOR PRIOR FILING DATE: 2003-06-27 PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR 
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; Sequence 189, Application US/10476264
; Publication No. US20050123910A1
; GENERAL INFORMATION:
; APPLICANT: Cockson, william Osmond Charles Michael
APPLICANT: Allen, Maxine
; APPLICANT: Allen, Maxine
; APPLICANT: Lench, Mick
; TITLE OF INVENTION: Enzyme and SNP marker for disease
; TILE REFERENCE: 16721-002U31
; CURRENT APPLICATION NUMBER: US/10/476,264
; CURRENT APPLICATION NUMBER: PCT/GB02/01887
; PRIOR FILING DATE: 2003-10-24
; PRIOR PLILING DATE: 2001-04-24
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 421
; SEOFWARE: PatentIn Version 3.1
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Pred. No. 2.7e+02;
0; Mismatches 3;
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Pred. No. 2.7e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTHER INFORMATION: Antisense compound US-10-831-901A-26897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               699 ATGTAGTCACGGTGCTCTC 717
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Best Local Similarity 84.2%;
Matches 16; Conservative C
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.2
Matches 16; Conservative
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RESULT 387
JS-11-039-629-125/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.3%; Score 14.2; DB 1; Length 20;
84.2%; Pred. No. 2.7e+02;
tive 0; Mismatches 3; Indels
                                                                                          ; OTHER INFORMATION: Forward Primer for GOS2 gene US-10-980-850-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10980850

Publication No. US20050152908A1

GENERAL INFORMATION:

APPLICANT: Liew, Choong-Chin

TITLE OF INVENTION: LIVER CANCER BIOMARKERS
FILE REPERENCE: 4231/2072

CURRENT APPLICATION NUMBER: US/10/980,850

CURRENT APPLICATION NUMBER: US/10/980,850

PRIOR APPLICATION NUMBER: US 60/516,853

PRIOR APPLICATION NUMBER: US 60/516,853

NUMBER OF SEQ ID NOS: 46

SOFTWARE: PatentIn version 3.1

LENGTH:: 20
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472 TATTCTGATTACAGTGCAT 490
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                  19 IGTTCTGGTTACAATGCAT 1
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Best Local Similarity 84.2
Matches 16; Conservative
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ORGANISM: Homo sapiens
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                                                                               US-10-834-377-310/c
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US-10-774-721-43

US-10-774-721-43

Sequence 43, Application US/10774721

Sequence 43, Application US/10774721

Sequence 43, Application US/20050009042A1

SPUBLICANT: USE OF UNCERTION:

APPLICANT: UNIVERTION: Olignoclectides Which inhibit Expression of the OB-RGRP Protein

TITLE OF INVENTION: AD Method For Detecting Compounds Which Modify The Interaction

TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor;

FILE REFERENCE: FRAV2003/0005 US NP

CURRENT APPLICATION NUMBER: US/10/774,721

CURRENT APPLICATION NUMBER: 0/461,005

FRIOR FILING DATE: 2003-04-07

FRIOR APPLICATION NUMBER: 0301543

FRIOR APPLICATION NUMBER: 0301543

FRIOR FILING DATE: 2003-02-10

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 43

LENGTH: 14
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Sequence 125, Application US/11039629

Publication No. US20050164271A1
GENERAL INFORMATION:
APPLICANT: Bhanot, Sanjay
APPLICANT: Dobie, Kenneth W.
APPLICANT: Preter, Susan M.
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: MODULATION OF GLUCOCORTICOID RECEPTOR
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-053US
CURRENT APPLICATION NUMBER: US/11/039,629
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: 60/538,173
PRIOR PILING DATE: 2004-03-03
PRIOR FILING DATE: 2004-03-03
PRIOR FILING DATE: 2004-03-03
PRIOR FILING DATE: 2004-03-03
SOFTWARE: PSEC FOR Windows Version 4.0
SSQ ID NO 125
LENGTH: 20
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1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 CCGTGGCAGGAAGC 39
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US-10-349-143-5553

is Sequence 5553, Application US/10349143

j. Sequence 5553, Application US/10349143

j. Sequence 5553, Application No. US20040005584A1

j. Publication No. US20040005584A1

j. Publication No. US20040005584A1

j. Publication No. US20040005584A1

j. Publication No. US2004000584A1

j. TITLE OF INVENTION: Biallelia markers for use in constructing a high density...

j. TITLE OF INVENTION: Biallelia markers for use in constructing a high density...

j. FILE REFERENCE: GENSET. 02007

CURRENT APPLICATION NUMBER: US/09/422,978

PRIOR PILING DATE: 1999-10-20

PRIOR PILING DATE: EARLIER PELING DATE: 1999-04-21

PRIOR PILING DATE: EARLIER PILING DATE: 1999-04-21

PRIOR PILING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR PILING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR PILING DATE: EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

j. FROM NOW SEQ ID NOS: 11796

j. FROM NO 5553
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US-10-719-933-55163

US-10-719-933-55163

Sequence 55163, Application US/10719993

Sequence 55163, Application No. US20040265849A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION UNMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342

SOFTWARE PRESEQ FOR WINGOWS VERSION 4.0

SEQ ID NO 55163
LENGTH: 19
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; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-706
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; OTHER INFORMATION: upstream amplification primer 99-5186 for SEQ 1619,
US-10-349-143-5553
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                                                                                                       Length 15;
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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0;
                                                                                                       Score 14; DB 1; 1
Pred. No. 1.7e+02;
4; Mismatches 0.
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                                                                                                             Query Match 1.3%;
Best Local Similarity 71.4%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                              TYPE: DNA
CORGANISM: Homo sapiens
US-10-719-993-55163
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ORGANISM: Homo Sapiens
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Best Local Similarity
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Sequence 706, Application US/09274553D

Sequence 706, Application US/09274553D

Sequence 706, Application US/09274553D

Sequence 706, Application US/09274553D

Sequence 706, Application US/092225A1

Sequence 706, Application US/092225A1

Sequence 706, Application US/09225A1

Septicant: Mcswiggen, James

APPLICANT: Mcswiggen, James

APPLICANT: Pavco, Pamela

APPLICANT: Macejak, Dennis

TITLE OF INVENTION: ENZYMATIC UUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE

TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

FILE REFERENCE: 1994-03-23

CURRENT APPLICATION NUMBER: 09/257,608

PRIOR APPLICATION NUMBER: 60/100,842

PRIOR APPLICATION NUMBER: 60/003,217

PRIOR APPLICATION NUMBER: 60/003,217

PRIOR APPLICATION NUMBER: 60/003,217

PRIOR PILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 3148

SOFFWARE: Patentin version 3.0
                                                                                                                                                 US-09-504-231A-706

1 Sequence 706, Application US/09504231A

1 Sequence 706, Application US/09504231A

1 Patent No. US20020013458A1

2 GENERAL INFORMATION:

3 APPLICANT: BLAtt, Lawrence

APPLICANT: McSwiggen, James

APPLICANT: Roberts, Beth

3 APPLICANT: Macjak, Dennis

TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE

TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

TITLE OF INVENTION NUMBER: 09/254,231A

CURRENT FILING DATE: 1999-03-15

PRIOR FILING DATE: 1999-02-24

PRIOR FILING DATE: 1999-02-24

PRIOR FILING DATE: 1998-09-18

PRIOR APPLICATION NUMBER: 60/083,217

PRIOR APPLICATION NUMBER: 60/083,217

PRIOR APPLICATION NUMBER: 60/083,217

PRIOR PRILING DATE: 1998-04-27

PRIOR PRILING DATE: 1998-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-706
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ORGANISM: Artificial Seguence
FEATURE:
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SOFWARE: PatentIn version 3.0
SEQ ID NO 706
LENGTH: 15
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LENGTH: 15
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Matches

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US-10-349-141-5624

is Sequence 5624, Application US/10349143

sequence 5624, Application Wo. US2004005584A1

sequence 5624, Application No. US20040051

sequence 5624, Application No. US20040051

sequence 762040061

se
                                                                                                                                        APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT APPLICATION NUMBER: US/10/422,978
FRIOR FILING DATE: 1999-10-20
FRIOR FILING DATE: 1999-10-20
FRIOR FILING DATE: BARLIER FILING DATE: 1999-04-21
FRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
FRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
FRIOR FILING DATE: BARLIER FILING DATE: 1998-04-21
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
FRIOR APPLICATION DATE: BARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
FRIOR APPLICATION DATE: BARLIER FILING DATE: 1998-04-21
FRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-04-21
FRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
FRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-04-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: upstream amplification primer 99-13853 for SEQ 251
US-10-349-143-4185
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100.0%; Pred. No. 2.9e+02;
tive 0; Mismatches 0; Indels
                                Sequence 4185, Application US/10349143
Publication No. US20040005584A1
GENERAL INFORMATION:
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo Sapiens
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LOCATION: 1..20
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Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
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                                                                                                                                                                                                                                                     RESULT 393
US-09-802-669-156/c
; Sequence 156, Application US/09802669
; Patent No. US20020004490Al
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Myatt, Jacqueline
; APPLICANT: Application Antisense Compound Modulation of Fas Mediated Signaling
; TITLE OF INVENTY Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/09/802,669
; PRIOR FILING DATE: 2001-03-18
; PRIOR PLING DATE: 1999-04-12
; PRIOR PLING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
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APPLICANT: Lex M. Cowmert
APPLICANT: Lex M. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF PTFN12 EXPRESSION
FILE REFERENCE: PTS-0016
CURRENT APPLICATION NUMBER: US/10/172,911
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.3%; Score 14; DB 1; Length 20; 100.0%; Pred. No. 2.9e+02; tive 0; Mismatches 0; Indels
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        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Antisense Oligonucleotide
    Mismatches
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                            1060 CTTTCCAGTGGCTA 1073
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                                                                                                                    1 CTTTCCAGTGGCTA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 14; Conservative
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Matches 14; Conservative
14; Conservative
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US-10-172-911-55
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LENGTH: 20
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NUMBER OF SEQ ID NOS: 30063
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18965
LENGTH: 20
PRIOR FILING DATE: 2003-06-10
PRIOR APPLICATION NUMBER: 60/483,579
PRIOR FILING DATE: 2003-06-27
NUMBER OF SEQ ID NOS: 30063
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 20
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                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Antisense compound US-10-831-901A-18964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                       FEATURE:
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| Sequence 186, Application No. US20040033979A1
| Publication No. US20040033979A1
| GENERAL INPORMATION:
| APPLICANT: Dean, Nicholas M.
| APPLICANT: DATE, Nacqueline
| APPLICANT: Myatt, Jacqueline
| APPLICANT: Myatt, Jacqueline
| APPLICANT: Myatt, Jacqueline
| APPLICANT: Myatt, Uscqueline
| PRIOR APPLICATION NUMBER: US/10/619,220
| PRIOR APPLICATION NUMBER: US/9/665,615
| PRIOR FILING DATE: 2000-09-18
| PRIOR FILING DATE: 1999-04-12
| NUMBER OF SEQ ID NOS: 180
| SEQ ID NO 156
| LENGTH: 20
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APPLICANT: Massire, Christian
APPLICANT: Hofstadler, Steven A.
APPLICANT: Hofstadler, Kristin Sannes
APPLICANT: Lowery, Kristin Sannes
APPLICANT: Swayze, Elic
APPLICANT: Baker, Brenda F.
APPLICANT: Baker, Brenda F.
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
FILE REFERENCE: ISISO083-100 (BIOL0008US)
CURRENT APPLICATION NUMBER: 60/466,426
PRIOR FILING DATE: 2004-04-26
PRIOR FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: 60/468,627
PRIOR FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: 60/468,627
PRIOR PILING DATE: 2003-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: Antisense Oligonucleotide US-10-619-220-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18964, Application US/10831901A
Publication No. US20050100885A1
GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
APPLICANT: Sampath, Rangarajan
APPLICANT: Freier, Susan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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                                                               324 CTGTTATTCTTGCT 337
                                                                                                        CTGTTATTCTTGCT 17
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APPLICANT:
APPLICANT:
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US-10-831-901A-18965
| Sequence 18965, Application US/10831901A
| Sequence 18965, Application US/10831901A
| Publication No. US20050100885A1
| GENERAL INFORMATION:
| APPLICANT: Crooke, Stanley T. APPLICANT: Sampath, Rangarajan APPLICANT: Baker, David J. APPLICANT: Recker, David J. APPLICANT: Baker, Steven M. APPLICANT: Hofstadler, Steven M. APPLICANT: Hofstadler, Steven M. APPLICANT: Lowery, Kristin Sannes APPLICANT: Baker, Brenda F. APPLICANT: Benert, C. Kristin Sannes APPLICANT: Benert, C. Krank
| TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe TITLE OF INVENTION: Compositions And Methods For The Treatment Of Stoken APPLICANT: APPLICATION NUMBER: US/10/831,901A
| TITLE OF INVENTION: Compositions And Methods For The Treatment Of Stoken FILING DATE: 2004-04-26
| PRIOR FILING DATE: 2003-06-06
| PRIOR FILING DATE: 2003-05-06
| PRIOR FILING DATE: 2003-05-06
| PRIOR FILING DATE: 2003-05-06
| PRIOR FILING DATE: 2003-06-10
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Query Match 1.3%; Score 14; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 14; Conservative 0; Mismatches 0; Indels
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FEATURE:
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APPLICANT: ECKET, Bayld J.
APPLICANT: Sampath, Rangarajan
APPLICANT: Massire, Christian
APPLICANT: Massire, Christian
APPLICANT: Massire, Christian
APPLICANT: Massire, Eric
APPLICANT: Baker, Sanda Methods For The Treatment Of Severe
TITLE OF INVENTION: Compositions And Methods For The Treatment
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
TITLE OF INVENTION NUMBER: 00/466,426
PRIOR PLILING DATE: 2003-04-28
PRIOR PILING DATE: 2003-05-06
PRIOR PILING DATE: 2003-05-06
PRIOR PILING DATE: 2003-05-06
PRIOR PLILING DATE: 2003-06-10
PRIOR PLILING DATE: 2003-06-10
PRIOR PLILING DATE: 2003-06-10
PRIOR PLILING DATE: 2003-06-10
PRIOR PLILING DATE: 2003-06-27
PRIOR PLILING DATE: 2003-06-10
PRIOR PLILING DATE: 2003-06-27
PRIOR PLING DATE: 2003-06-27
PRIOR PLILING DATE: 2003-06-27
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APPLICANT: Sampath, Rangarajan
APPLICANT: Rejer, Susan M.
APPLICANT: Massire, Christian
APPLICANT: Massire, Christian
APPLICANT: Howery, Kristin Sannes
APPLICANT: Swayze, Eric
APPLICANT: Baret, Branch
APPLICANT: Baret, Branch
APPLICANT: Baret, C. Frank
TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
FILE REFERENCE: ISISO003-100 (BIOL00008US)
CURRENT APPLICATION NUMBER: US/10/831,901A
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Sequence 18966, Application US/10831901A
Publication No. US20050100885A1
GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
APPLICANT: Ecker, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Antisense compound US-10-831-901A-18966
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PRIOR FILING DATE: 2003-04-28
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ORGANISM: Artificial Sequence
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Matches 14; Conservative
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US-10-831-901A-18967
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Publication No. US20050100885A1

Sequence 18966, Application US/10831901A

Publication No. US20050100885A1

GENERAL INFORMATION:

APPLICANT: Exercy, David J.

APPLICANT: Sampath, Rangarajan

APPLICANT: Sampath, Susan M.

APPLICANT: Hofstadler, Steven A.

APPLICANT: Basir's, Christian

APPLICANT: Baker, Benda F.

APPLICANT: Baker, Baker,
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100.0%; Pred. No. 2.9e+02;
7ative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
                             PRIOR APPLICATION NUMBER: 60/467,770
PRIOR FILING DATE: 2003-04-30
PRIOR FILING DATE: 2003-06-30
PRIOR FILING DATE: 2003-05-06
PRIOR PRILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-13
PRIOR FILING DATE: 2003-06-27
PRIOR SEQ ID NOS: 30663
SOFTWARE: PASLSEQ for Windows Version 4.0
SEQ ID NO 18967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION: Antisense compound US-10-831-901A-18967
LING DATE: 2003-05-06
PLICATION NUMBER: 60/467,770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 14; Conservative
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TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
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Best Local Similarity 100.
Matches 14; Conservative
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US-09-866-108-2563/c
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APPLICANT:
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APPLICANT: Sampath, Rangarajan
APPLICANT: Sampath, Rangarajan
APPLICANT: Freier, Susan M.
APPLICANT: Freier, Christian
APPLICANT: Massire, Christian
APPLICANT: Massire, Christian
APPLICANT: Massire, Execa A.
APPLICANT: Swayze, Eric
FILE REFERENCE: ISISON3-100 (BIOL000805)
CURRENT FILING DATE: 2003-04-26
PRIOR PILING DATE: 2003-05-06
PRIOR PLING DATE: 2003-05-06
PRIOR PLING DATE: 2003-06-10
PRIOR PLING DATE: 2003-06-10
PRIOR APPLICATION NUMBER: 60/468,627
PRIOR APPLICATION NUMBER: 60/468,627
PRIOR APPLICATION NUMBER: 60/483,579
PRIOR PLING DATE: 2003-06-10
PRIOR FILING DATE: 2003-06-10
PRIOR PLING DATE: 2003-06-10
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100.0%; Pred. No. 2.9e+02;
tive 0; Mismatches 0; Indels
   0; Indels
      0; Mismatches
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US-10-831-901A-18970
; Sequence 18970, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   Sequence 18966, Application US/10811901A
Publication No. US20050100885A1
GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
APPLICANT: Ecker, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Antisense compound US-10-831-901A-18969
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APPLICANT: Scher, David J.
APPLICANT: Sampath, Rangarajan
APPLICANT: Freder, Susan M.
APPLICANT: Massire, Christian
APPLICANT: Hofstadler, Steven A.
APPLICANT: Lowery, Kristin Sames
APPLICANT: Swayze, Eric
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ORGANISM: Artificial Sequence
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                                                                  311 GCCTTTGGATTTCC 324
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                                                                                                                              5 GCCTTTGGATTTCC 18
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Best Local Similarity 100.
Matches 14; Conservative
   14; Conservative
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         Matches
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APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe IIILE OF INVENTION: Acute Respiratory Syndrome (SARS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                               Acute Respiratory Syndrome (SARS)
0083-100 (BIOL0008US)
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100.0%; Pred. No. 2.9e+02;
tive 0; Mismatches 0;
                                                                             TITLE DEFENDENTION: ACUTE RESPITATORY SYNTON PILLE REFENDENCE: 10150003-100 (BIOLO008US); CURRENT APPLICATION NUMBER: US/10/831,901A CURRENT FILING DATE: 2004-04-26 PRIOR FLING DATE: 2003-04-28 PRIOR FILING DATE: 2003-04-28 PRIOR FILING DATE: 2003-05-06 PRIOR FILING DATE: 2003-04-30 PRIOR FILING DATE: 2003-05-06 PRIOR FILING DATE: 2003-05-06 PRIOR FILING DATE: 2003-04-30 PRIOR FILING DATE: 2003-04-30 PRIOR FILING DATE: 2003-04-30 PRIOR FILING DATE: 2003-06-10 PRIOR FILING DATE: 2003-06-10 PRIOR FILING DATE: 2003-06-10 PRIOR FILING DATE: 2003-06-10 PRIOR FILING DATE: 2003-06-27 NUMBER OF SEQ ID NOS: 30063 SOFTWARE FALING DATE: 2003-06-27 NUMBER PRIOR FILING DATE: 2003-06-27 NUMBER: PRESEQ FOR WINDOWS Version 4.0 ENGLISHENCE FREEEG FOR WINDOWS VERSION 4.0
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CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR PELLOTATION NUMBER: US/02/456
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-06-37
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PELLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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; Patent No. US20020048800A1
; GENERAL INFORMATION:
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US-09-866-108-6749
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APPLICANT: GU, Yizhong
APPLICANT: DI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David R.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
PILE REPERENCE: AEOMICAT:
CURRENT APPLICATION NUMBER: US/09/866,108
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   PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PRIOR DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PTLING DATE: 2000-09-21
PRIOR PTLING DATE: 2000-09-21
PRIOR PLING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine SEQ ID NO 2563
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PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-10-04

PRIOR PELING DATE: 2000-10-04

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30
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APPLICATION NUMBER: US 60/266,860
FILING DATE: 2001-02-05
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Patent No. US20020048800A1
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FILING DATE: 2001-01-30
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Best Local Similarity 88.2
Matches 15; Conservative
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US-09-866-108-2563
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APPLICANT: SHAMNOW MARK
TITLE OF INVENTION: WAYGSTN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERBRICE. ASONICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT APPLICATION NUMBER: US 60/20,456
PRIOR RELING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-00-37
PRIOR FILING DATE: 2000-00-37
PRIOR FILING DATE: 2000-00-37
PRIOR FILING DATE: 2000-00-37
PRIOR FILING DATE: 2001-00-37
PRIOR FILING DATE: 2001-01-30
PRIOR PAPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
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88.2%; Pred. No. 2.3e+02;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                         Length 17;
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                  Query Match
1.2%; Score 13.8; DB 1;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2;
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 2564
LENGTH: 17
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6749, Application US/09866108 Patent No. US20020048800A1
                                                                                                                                                                                                                                                                                                                                                                                                      760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                         744 GGCAGCTGCCACCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.2
Matches 15; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-866-108-2564
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Diagnosis, Therapy and Cellular and
Animal Models for Diseases Associated With Mitochondrial
                                                                          TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
Animal Models for Diseases Associated With Mitochondrial
Defects
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                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

REDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/978,600
FILING DATE: 15-OCt-2001
CLASSIFTCATION: CURNOW>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/413,740
FILING DATE: 30-MAR-1995
ATONNEY/AGENT INFORMATION:
NAME: BOHNAM: DAVIG B:
REGISTRATION NUMBER: 31297
REFERENCE/DOCKET NUMBER: 2105/7
TELEPHONE: (202) 429-1776
TELEPHONE: (202) 429-1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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88.2%; Pred. No. 2.3e+02;
ative 0; Mismatches 2;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                               ADDRESSEE: Kenyon & Kenyon STREET: 1025 Connecticut Avenue, N.W. CITY: Washington STATE: DC COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO
ANTI-SENSE: YES
SEQUENCE DESCRIPTION: SEQ ID NO: 140:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-9/Paction US/09978600
; Sequence 151, Application US/09978600
; Publication No. US20030087858A1
; GENERAL INFORMATION:
    APPLICANT: HERRNSTADT, CORINNA PARKER, WILLIAM D.
    DAVIS, ROBERT
; MILLER, SCOTT W.
    TITLE OF INVENTION: Diagnosis, The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
PARKER, WILLIAM D.
                                                               SCOTT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 regriririciaaracci 1
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                                                                                                                                                                                                      NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 88.2
Matches 15; Conservative
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US-09-978-600-151/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-978-600-140
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Sequence 3616, Application US/09848754A

Publication No. US20030073207A1

APPLICANT: Ribozyme Pharmaceuticals, Inc.

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate

TITLE OF INVENTION: Levels Of Epidemal Growth Factor Receptors

TITLE OF INVENTION: Levels OF Epidemal Growth Factor Receptors

FILE REPERENCE: MBHB00-958-1 (400/018)

CURRENT APPLICATION NUMBER: 2001-05-03

NUMBER OF SEQ ID NOS: 9645

SOFTWARE: PatentIn version 3.0
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APPLICANT: ALEATY
APPLICANT: ACSWIGGEN, Jim
APPLICANT: Chownize, Bharat
APPLICANT: Chownize, Bharat
APPLICANT: Chownize, Bharat
APPLICANT: Haeberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
TITLE OF INVENTION: MEBBO: 0870 and 0870 an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.2%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 2.3e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                      US-09-780-533A-2567/c
; Sequence 2567, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 410
US-09-978-600-140/c
Sequence 140, Application US/08978600
Publication No. US20030087858A1
CENERAL INFORMATION;
GENERAL INFORMATION
CORINNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                515
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                                                            836 AGGAAGGCCGGGGTGGA 852
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                                                                                                   1 AGGAAGGCCGTGGAGGA 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-780-533A-2567
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LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: RNA
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Therapy and Cellular and sls for Diseases Associated With Mitochondrial
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CONTY: USA

IP: 20036-5405

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/978,600

FILING DATE: 15-Oct-2001
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.2%; Score 13.8; DB 1;
88.2%; Pred. No. 2.3e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1025 Connecticut Avenue, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/413,740
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/413,740
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REPRENCE/DOCKET NUMBER: 2105/7
TELECOMMINICATION INFORMATION:
TELEPRANCE (202) 429-176
TELEPRANCE: (202) 429-0796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HERRNSTADT, CORINNA
PARKER, WILLIAM D.
DAVIS, ROBERT
MILLER, SCOTT W.
TITLE OF INVENTION: Diagnosis, Therapy
Animal Models for
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 185:
US-09-978-600-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2105/7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 186, Application US/09978600; Publication No. US20030087858A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               562 TGGGTTTTTAATACCT 578
                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 regrirircraaraccr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.2
Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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88.2%; Pred. No. 2.3e+02;
ive 0; Mismatches 2; Indels
                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR ENDING: JOHN CONTROL OF THING DATE: 15-Oct-2001
CLASSIFICATION: JOHN CONTROL OF THING DATE: 30-MAR-1995
APPLICATION NUMBER: 08/413,740
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAMM: BONDAM: DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAMM: BONDAM: DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 34297
TELEPRATION NUMBER: 34297
TELEPRATION NUMBER: 34297
TELEPRATION LAPPRAMATION:
TELEPRAMINICATION INFORMATION:
TELEPRAM: (202) 429-1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 206
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/978,600 FILING DATE: 15-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: YES
SEQUENCE DESCRIPTION: SEQ ID NO: 151:
US-09-978-600-151
COUNTRY: USA
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 185, Application US/09978600
Publication No. US20030087858A1
GENERAL INFORMATION:
APPLICANT: HERRNSTADT, CORINNA
PARKER, WILLLAM D.
DAVIS, ROBERT
MILLER, SCOTT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        562 TGGGTTTTTTAATACCT 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 151:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.2
Best Local Similarity 88.2
Matches 15; Conservative
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KESULT 415
US-09-827-395A-217/C

Sequence 217, Application US/09827395A

Publication No. US20030113891A1

Publicant Normation No. US20030113891A1

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: James McSwiggen

APPLICANT: James McSwiggen

APPLICANT: Bharat Chowitza

TITLE OF INVENTION: McHood and Reagent for the Inhibition of NOGO Receptor C

TITLE REPERENCE: MBHB00-878-C (400/017)

CURRENT APPLICATION NUMBER: US/09/827,395A

CURRENT FILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILICATION NUMBER: 60/181,797

PRIOR PILING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 2617

SOFTWARE: PatentIn version 3.0

LENGTH::77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lawrence Blatt
APPLICANT: Lawrence Blatt
APPLICANT: James McSwiggen
APPLICANT: James McSwiggen
APPLICANT: Barat Chowring
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Receptor (
PILE REFERENCE: MBHB00-878-C (400/017)
PILE REFERENCE: MBHB00-878-C (400/017)
PLICATION NUMBER: US/09/827,395A
CURRENT FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 2617
SOFTWARE: PATCHING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 2617
SEQ ID NO 888
LERGTH: 17
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                                                                                                  Length 17;
                                                                                                                                             Indels
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Pred. No. 2.3e+02;
                                                                                               Score 13.8; DB 1;
Pred. No. 2.3e+02;
0; Mismatches 2;
                                                                                                                                               0; Mismatches
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US-09-978-600-188
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; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                               563 GGGTTTTTAATACCTT 579
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                                                                                                  Query Match 1.2%;
Best Local Similarity 88.2%;
Matches 15; Conservative
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CORGANISM: Homo sapiens
US-09-827-395A-888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
CRGANISM: Homo mapiens
US-09-827-395A-217
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 416
US-09-827-395A-888/c
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PRKERS, WILLIAM D.
DAVIS, ROBERT
MILLER, SCOTT W.
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
Animal Models for Diseases Associated With Mitochondrial
Defects
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ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC Compatible
COMPUTER: 1BM PC COMPA: 10.0 Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/978,600
FILING DATE: 15-Oct-2001
CLASSIFICATION NUMBER: 08/413,740
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: PCT/US95/04063
APPLICATION NUMBER: PCT/US95/04063
ATTORNEY/AGENT INFORMATION:
NAME: BOTHAM: DATA:
NAME: BOTHAM: DATA:
REFERENCE/DOCKET NUMBER: 2105/7
TELEFRATION INFORMATION:
TELEFRAX: (202) 429-1776
TELEFRAX: (202) 429-0796
                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.2%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 2.3e+02; Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 206
CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                        ;
SEQUENCE DESCRIPTION: SEQ ID NO: 186:
US-09-978-600-186
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECILE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE PRESS: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 188, Application US/09978600
; Publication No. US20030087858A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  563 GGGTTTTTAATACCTT 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 GGTTTTTTTAATACCTT 1
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US-09-978-600-188/c
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Sequence 270, Application US/10339782
Sequence 270, Application US/10339782
Publication No. US20030166026A1
GENERAL INFORMATION:
APPLICANT: Lynx Therapeutics, Inc.
APPLICANT: Goodman, Laurie J
APPLICANT: Bowen, Benjamin A
TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells
FILE REFERENCE: 37.0001100S
CURRENT APPLICATION NUMBER: US/10/339,782
CURRENT FILING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 495
SOFTWARE: PatentIn version 3.1
LENGTH: 17
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APPLICANT: THOMAS, GILLES
APPLICANT: ZOUALI, MOHAMED
APPLICANT: ZOUALI, MOHAMED
APPLICANT: CESAGE, SUZANNE
APPLICANT: CHAMAILLARD, MATHIAS
TITLE OF INVENTION: THEREOF
FILE OF INVENTION: THEREOF
FILE REFERENCE: 37991-0009
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                        Length 17;
                                                                                       2; Indels
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                        Score 13.8; DB 1;
Pred. No. 2.3e+02;
0; Mismatches 2;
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Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2;
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CURRENT FILING DATE: 2003-04-02
PRIOR APPLICATION NUMBER: PCT/FR 01/00935
PRIOR FILING DATE: 2001-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-240-046A-64
; Sequence 64, Application US/10240046A
; Publication No. US20030190639A1
                                                                                                                                               673 AAATTATGTTACTTGTT 689
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                            Query Match 1.2%;
Best Local Similarity 88.2%;
Matches 15; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-782-270
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Best Local Similarity
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Varis, Thale
APPLICANT: Von Carlowitz, Ira
APPLICANT: WcSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Blis, Jonathan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inser
TITLE OF INVENTION: Method and Reagent for the STILL OF INVENTION: MEHBOO-901-A (400/013)
CURRENT APPLICATION NUMBER: US/09/792,818
CURRENT APPLICATION NUMBER: US/09/792,818
NUMBER OF SEQ ID NOS: 2304
SOFTWARE: Patentin version 3.0
SEQ ID NO 631
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      Gaps
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GENEMAL INVOCATION:

TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN

FILE REPERENCE: PB0177

CURRENT APPLICATION NUMBER: US/10/66,756A

CURRENT FILING DATE: 2002-01-30

PRIOR PLILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR PILING DATE: 2001-01-30

PRIOR PLING DATE: 2001-05-23

PRIOR PLING DATE: 2001-05-33

PRIOR PLING DATE: 2001-05-33
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   2; Indels
Mismatches
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; Publication No. US20030046717A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   Sequence 603, Application US/09792818
Publication No. US20030134806A1
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                                                           14 AGGCTGCCCGGGCCGTG 30
                                                                                                17 AGGCGCCCAGGCCGTG 1
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Matches 11; Conservative
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-060-756A-4243
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Matches
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US-1U-723-361-2563/ Application US/10723361

Sequence 2563, Application US/10723361

Sequence 2563, Application US/10723361

Sublication No. US20040137589A1

GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: FENN, Barron G.
APPLICANT: HANZEL, David K.
APPLICANT: HANK, David K.
APPLICANT: SHANNON, Mark
ITILE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN ITILE REFERENCE: PB0105
CURRENT APPLICATION NUMBER: US 10/723,361
CURRENT FILING DATE: 2001-05-25
FRIOR PRILING DATE: 2000-05-26
FRIOR PILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-10-04
FRIOR PILING DATE: 2000-09-27
FRIOR APPLICATION NUMBER: US 60/236,359
FRIOR PILING DATE: 2000-09-27
FRIOR FILING DATE: 2000-09-27
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                                                                                  Gaps
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APPLICANT: RAGINA, Tatsuo
APPLICANT: RAGINA, Tatsuo
APPLICANT: Matsumura, Yoshiyuki
APPLICANT: MATSUMURA, Tatsuo
APPLICANT: MATSUMURA, Tatsuo
APPLICANT: MATSIDA, Michio
APPLICANT: MISHIDA, Michio
TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
CURRENT APPLICATION NUMBER: US/10/297,068
CURRENT APPLICATION NUMBER: US/200-164798
PRIOR PILING DATE: 2002-11-27
PRIOR FILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 1298
SEQ ID NOS: 1298
SEQ ID NO 894
LENGTH: 17
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88.2%; Pred. No. 2.3e+02;
tive 0; Mismatches 2; Indels
                                       Length 17;
                                                                                     Indels
                                  Query Match
1.2%; Score 13.8; DB 1;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                            US-10-297-068-894
; Sequence 894, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACAATTACAGGGTTTTT 17
                                                                                                                                      14 AGGCTGCCCGGGCCGTG 30
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                                                                                                                                                                               17 Addecedeceadecera 1
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Best Local Similarity 88.29
Matches 15; Conservative
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US-10-723-361-2563/c
US-10-430-882-888
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APPLICANT: James McSwiggen
APPLICANT: James McSwiggen
APPLICANT: James McSwiggen
APPLICANT: James McSwiggen
APPLICANT: Bharat Chowiira
APPLICANT: Beatat Chowiira
APPLICANT: Peter Haeberii
TILLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor GILLE REFERENCE: BMBH800-879-H (400/112)
FILLE REFERENCE: BMBH800-879-H (400/112)
CURRENT APPLICATION NUMBER: 09/780,533
PRIOR FILLING DATE: 2001-04-05
PRIOR FILLING DATE: 2001-02-09
PRIOR FLILING DATE: 2001-02-09
PRIOR FILLING DATE: 2000-02-01
PRIOR FILLING DATE: 2000-02-01
PRIOR FILLING DATE: 2000-02-11
PRIOR FILLING DATE: 2000-02-11
PRIOR FILLING DATE: 2000-02-11
PRIOR FILLING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 2617
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1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                            Sequence 217, Application US/10430882
Publication No. US20030203870A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 888, Application US/10430882 Publication No. US20030203870A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
US-10-430-882-217
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                                                                                US-10-430-882-217/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 217
LENGTH: 17
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APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTYON: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
FILE REFERENCE: PB0105
CURRENT PILING DATE: 2003-11-26
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,66
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR PLING DATE: 2001-01-30
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NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 6749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Sequence 4243, Application US/10890776A
Sequence 4243, Application US/10890776A
Sequence 4243, Application US/10890776A
SENERAL INFORMATION:
APPLICANT: Zhang, Jian
TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
FILE REFERENCE: P80177
CURRENT APPLICATION NUMBER: US/10/890,776A
CURRENT FILING DATE: 2004-07-14
                                                            Score 13.8; DB 1; Length 17;
Pred. No. 2.3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13.8; DB 1; Length 17;
Pred. No. 2.3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6749, Application US/10723361
Publication No. US20040137589A1
GENERAL INFORMATION:
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ilarity 88.2%;
Conservative (
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: CHEN, Wensheng
                                                                                                                                                                                                                                               17 GGCAGCTGCCGCCTTCT
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                               Best Local Similarity
Matches 15; Conserv
                                                                      Query Match
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APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: GHEN, Wensheng
APPLICANT: GHEN, Wark
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
FILE REPERENCE: P80105
CURRENT PELING DATE: 2001-11-26
PRIOR PRING DATE: 2001-05-25
PRIOR PAPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PAPLICATION NUMBER: GC 0/236,359
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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Gaps
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NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.2%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 2.3e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2564, Application US/10723361
Publication No. US20040137589A1
GENERAL INPORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              745 GCAGCTGCCACCTTATG 761
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Best Local Similarity 88.2
Matches 15; Conservative
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; ORGANISM: Homo sapiens
US-10-723-361-2563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-361-2564
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Sequencing List
APPLICANT: Kwangmyung Sungae Medical Foundation
APPLICANT: Kwangmyung Sungae Medical Foundation
TITLE OF INVENTION: GAP VECTOR FOR B. COLI STOP CODON ASSAY AND METHOD FOR DETECTING
TITLE OF INVENTION: HETEROZYGOUS MUTATION USING THE SAME
FILE REPRENCE: Sungae-1
CURRENT APPLICATION NUMBER: US/09/888,625
CURRENT FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Kopatentin 1.71
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 37, Application US/10265689; Publication No. US20030119775A1; GENERAL INFORMATION:
                                                                     Sequence 17, Application US/0988625 Publication No. US20030064365A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1000 CACATGAAAGTTTGAGA 1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CRGANISM: Artificial Sequence
FATURE:
CTHER INFORMATION: Primer BV-b5
US-09-888-625-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 430
US-10-265-689-37/c
                                                         US-09-888-625-17
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GENERAL INFORMATION:
APPLICANT: Schlauder, George G.
APPLICANT: Erker, James C.
APPLICANT: Dawson, George G.
APPLICANT: Dawson, George J.
APPLICANT: Dawson, George J.
APPLICANT: Dawson, George J.
APPLICANT: MUSHARWAR, I. K.
TITLE OF INVENTION: HERATITIS E VIRUS
TITLE OF INVENTION NUMBER: US 09/173,141
EARLIER PILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: US 60/061,199
EARLIER APPLICATION NUMBER: US 60/061,199
EARLIER PILING DATE: 1997-10-15
NUMBER OF SEQ ID NOS: 258
SOUTHWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13.8; DB 1; Length 17;
Pred. No. 2.38+02;
0; Mismatches 2; Indels
PRIOR APPLICATION NUMBER: US 10/060,756
PRIOR FILING DATE: 2002-01-30
PRIOR PILING DATE: 2002-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-00-09
NUMBER OF SEQ ID NOS: 4809
NUMBER OF SEQ ID NOS: 4809
SECO TWARE: ABENICATION NUMBER: US 60/327,898
PRIOR PILING DATE: 2001-00-9
NUMBER OF SEQ ID NOS: 4809
SEQ ID NO 4243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-468-147-6
Sequence 6, Application US/09468147A
Publication No. US20030049601A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1035 TAMACATCACACCCAAC 1051
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COTHER INFORMATION: Primer C375
US-09-468-147-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 88.2%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
US-10-890-776A-4243
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Description of Artificial Sequence:

) OTHER INFORMATION: Oligonucleotide

US-10-265-689-37
APPLICANT: SURMIT, ALLERAND S.
APPLICANT: COLLINS, SHEILA A.
APPLICANT: COLLINS, SHEILA A.
APPLICANT: SELDIN, MICHAEL F.
APPLICANT: SELDIN, MICHAEL F.
APPLICANT: SELDIN, MICHAEL F.
APPLICANT: BUULLAUD, FREDERIC
TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
FILE REPERENCE: 1579-376
CURRENT APPLICATION NUMBER: US/09/353,645
PRIOR FILING DATE: 1999-07-15
PRIOR FILING DATE: 1999-07-15
PRIOR PILING DATE: 1997-04-22
PRIOR APPLICATION NUMBER: 60/034,960
PRIOR FILING DATE: 1997-01-15
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 3T
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.2%; Score 13.8; DB 1;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2;
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US-10-349-143-6041

Sequence 6041, Application US/10349143

Sequence 6041, Application US/10349143

Publication No. US20040005584A1

Sequence 6041, Application US/10349143

Sequence 6041, Application US/0040005584A1

Sequence 6041, Application US0040005584A1

Sequence 6041, Application Daniel

APPLICANT: Cohen, Daniel

APPLICANT: Chumakov, Ilya

TITLE OF INTENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE GENERT: 02073-01-21

PRIOR PILING DATE: 1999-10-20

PRIOR APPLICATION NUMBER: US/09/422,978

PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US 09/298,850

PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21

PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-23

PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR FILING DATE: EARLIER FILING DATE: 1998-14-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 6041

LENGTH: 18
                                                  APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
ITTLE OF INVENTION: Biallelic markers for use in constructing a high density...
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT APPLICATION NUMBER: US/09/422,978
FRIOR FILING DATE: 1999-10-20
FRIOR PELING DATE: 1999-10-20
FRIOR PELICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
FRIOR PELICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
FRIOR APPLICATION NUMBER: EARLIER PELICATION NUMBER: US 60/082,614
FRIOR APPLICATION NUMBER: EARLIER PELICATION NUMBER: US 60/082,614
FRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
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; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-8576 for SEQ 2107,
US-10-349-143-6041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..18 OTHER INFORMATION: upstream amplification primer 99-1739 for SEQ 798.
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88.2%; Pred. No. 2.5e+02;
tive 0; Mismatches 2;
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Publication No. US20040005584A1
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Best Local Similarity 88.2
Matches 15; Conservative
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Matches 15; Conserv
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US-10-108-260A-5064
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                                                                                                                                            APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Schlauder, George G.
APPLICANT: Schlauder, George G.
APPLICANT: Bawson, George J.
APPLICANT: Dawson, George J.
APPLICANT: Dawson, George J.
APPLICANT: Dawson, George J.
APPLICANT: Dawson, George J.
APPLICANT: MARBARARI I. K.
ITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION: HEPATITIS E VIRUS
FILE REFERENCE: 6232 U.8.Pl
CURRENT APPLICATION NUMBER: US/10/319,745
CURRENT PILING DATE: 2002-12-13
FRIOR FILING DATE: BARLIER FILING DATE: 1999-12-21
FRIOR PELING DATE: EARLIER FILING DATE: 1999-12-15
FRIOR PELING DATE: EARLIER FILING DATE: 1999-10-15
FRIOR PELING DATE: EARLIER FILING DATE: 1997-10-15
FRIOR FILING DATE: EARLIER FILING DATE: 1997-10-15
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; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT PEPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SEQ ID NO 5664
; LENGTH: 18
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                                                     Sequence 6, Application US/10319745 Publication No. US20030211467Al GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 15, Conservative
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US-10-349-143-4732/c
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% Sequence 63, Application US/10352179

% Sequence 63, Application US/10352179

% Publication No. US200400067881

% Publication No. US200400067881

% Publication No. US200400067881

% Publication No. US200400067881

% APPLICANT: Liu, Guifu

APPLICANT: Liu, Guifu

APPLICANT: Liu, Guifu

GURRENT APPLICANT: US/10/352,179

CURRENT APPLICATION NUMBER: US/10/352,106

PRIOR PILING DATE: 2002-01-25

% NUMBER OF SEQ ID NOS: 97

% SOFFWARE: Patentin version 3.1

% SEQ ID NO 63
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US-10-486-319A-277/c

US-10-486-319A-277/c

Sequence 277, Application US/10486319A

Publication No. US2005064410A1

GENERAL INFORMATION:

APPLICANT: Bygenomics AG

TILLE OF INVENTION: Method and nucleic acids for the analysis of colon cancer;

FILE REPERENCE:

CURRENT APPLICATION NUMBER: US/10/486,319A

CURRENT PILING DATE: 2004-02-09

NUMBER OF SEQ ID NOS: 527

SEQ ID NO 277
                                       Sequence 275, Application US/10486319A
Sequence 275, Application US/10486319A
Bublication No. US20050064410A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Method and nucleic acids for the analysis of colon cancer
CURRENT APPLICATION NUMBER: US/10/486,319A
CURRENT FILING DATE: 2004-02-09
NUMBER OF SEQ ID NOS: 527
SEQ ID NO 275
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Pred. No. 2.5e+02;
0; Mismatches 2;
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Best Local Similarity 88.2%
Matches 15; Conservative
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Matches 15; Conservative
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               RESULT 437
US-10-486-319A-275
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US-10-395-143-11352/C
Sequence 11352, Application US/10349143
Sequence 11352, Application No. US20040005584A1
GENERAL INFORMATION:
Sequence 11352, Application No. US20040005584A1
GENERAL INFORMATION:
Sequence 11352, Application No. US20040005584A1
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TTILLO PINVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENGET. 02001
CURRENT APPLICATION NUMBER: US/10/349, 143
CURRENT APPLICATION NUMBER: US/09/422, 978
FRIOR PILING DATE: 1999-10-20
FRIOR FILING DATE: 1999-10-20
FRIOR FILING DATE: BARLIER PILING DATE: 1998-11-23
FRIOR FILING DATE: BARLIER FILING DATE: 1998-11-23
FRIOR FILING DATE: BARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
LENGTH: 18
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LENGTH: 18
TURNEL OF SEQ ID NOS: 11796
LENGTH: 18
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Sublication No. US2004003826A1

Sublication No. US2004003826A1

GENERAL INFORMATION:
APPLICANT: Neo Gen Screening, Inc.
APPLICANT: Neo Gen Screening the Detection of Hearing Loss in Newborns through
TITLE OF INVENTION: Parallel Genetic Analysis
FILE REFERENCE: 2175
CURRENT APPLICATION NUMBER: US/10/443,545
CURRENT PRILING DATE: 2003-05-22
PRIOR PILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.2
SEQ ID NO. 10
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1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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1.2%; Score 13.8; DB 1;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2;
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AATCTCAACCCCCACTC 18
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ORGANISM: Homo sapiens
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ORGANISM: Homo Sapiens
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                                                                                                      1.2%; Score 13.8; DB 1; Length 19; 88.2%; Pred. No. 2.8e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-444-795B-600

Sequence 600, Application US/1044795B

Publication No. US2040077574A1

GENERAL INFORMATION:

APPLICANT: Klinghoffer, Richard

APPLICANT: Lewis, Stephen Partrick

TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL

TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL

TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE

FILE REPERRNCE: 200125-449

CURRENT FILING DATE: 2003-05-23

NUMBER OF SEQ ID NOS: 842

SOFTWARE PASSEQ for Windows Version 4.0

SEQ ID NO 600
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lewis, Stephen Patrick
TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
FILE REFERENCE: 200125.494
CURRENT APPLICATION NUMBER: US/10/444,795B
CURRENT FILING DATE: 2003-05-23
NUMBER OF SEQ ID NOS: 842
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Small interfering RNA - hTCPTP1.5
US-10-444-795B-599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Small interfering RNA - hTCPTP1.5 US-10-444-795B-600
                                                                                                                                                                                                                                                                                                    RESULT 440
15-10-444-795B-599/c
18-20-ence 599, Application US/1044795B
Publication No. US20040077574A1
                                                                                                                                                                                            414 GGTTTTTCCTTATATTT 430
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                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Klinghoffer, Richard
                                                                                                                                                                                                                     19 GGTTTTCTTTGTATTT 3
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 64.74
Matches 11; Conservative
                                                                                                      Query Match
Best Local Similarity 88.2
Matches 15; Conservative
                  ; TYPE: DNA
; ORGANISM: Oryza minuta
US-10-352-179-63
  LENGIH: 19
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343 GGCTGTGATCAAATGGG 359 | |:|:||:||

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US-10-735-461-89

US-10-735-461-89

Sequence 89, Application US/10735461

Publication No. US20050014264A1

GENERAL INFORMATION:

APPLICANT: CZECH, Michael P.

APPLICANT: JIANG, Zhen

TITLE OF INVENTION: METHOD OF INTRODUCING SIRNA INTO

TITLE OF INVENTION: METHOD OF INTRODUCING SIRNA INTO

TITLE OF INVENTION: METHOD OF INTRODUCING SIRNA INTO

TITLE OF INVENTION: MADIPOCYTES

FURRENT FILING DATE: 2003-12-11

PRIOR APPLICATION NUMBER: 60/432427

PRIOR RELING DATE: 2002-12-11

PRIOR PLING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 141

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | FUDILGALION NO. USZUDSUUJ4264A1
| GENERAL INFORMATION:
| APPLICANT: CZECH, Michael P.
| APPLICANT: ZHOU, Qionglin
| APPLICANT: JIANG, Zhon
| TITLE OF INVENTION: METHOD OF INTRODUCING SIRNA INTO
| TITLE OF INVENTION: ADIPOCYTES
| FILE REFERENCE: UNY-055,461
| CURRENT APPLICATION NUMBER: US/10/735,461
| PRIOR APPLICATION NUMBER: 60/432427
| PRIOR APPLICATION NUMBER: 60/432427
| PRIOR PRINTON DATE: 2002-12-11
| NUMBER OF SEQ ID NOS: 141
| SOFTWARE: FASESEQ FOR WINDOWS VERSION 4.0
| SEQ ID NO 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.2%; Score 13.8; DB 1;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2;
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; Sequence 222, Application US/10918896
; Publication No. US20050164966A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-735-461-90
; Sequence 90, Application US/10735461
; Publication No. US20050014264A1
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CORGANISM: Mus musculus
US-10-735-461-90
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; ORGANISM: Mus musculus
US-10-735-461-89
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Best Local Similarity
Matches 15; Conserv
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US-10-203-329-124/C
Sequence 124, Application US/10923329
Publication No. US20050164968A1
Sequence 124, Application US/10923329
Publication No. US20050164968A1
Sequence 124, Application No. US20050164968A1
SepticANT: String Therapeutics, Inc.
APPLICANT: Richards, Ivan
APPLICANT: Richards, Ivan
APPLICANT: Richards, Ivan
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/225 (WEHB04-672)
FILE REFERENCE: 400/225 (WEHB04-672)
CURRENT FILING NATE: 2004-08-20
PRIOR PILLOR DATE: 2004-08-20
PRIOR PILLOR DATE: 2004-08-24
PRIOR PILLOR DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 10/826,966
PRIOR APPLICATION NUMBER: US 60/292,217
PRIOR FILING DATE: 2004-02-13
PRIOR FILING DATE: 2004-03-16
PRIOR FILING DATE: 2001-07-20
PRIOR PRIOR PRIOR PRIOR PARENT PA
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OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense 1
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PRIOR FILING DATE: 2003-11-24

PRIOR APPLICATION NUMBER: US 10/693,059

PRIOR PLING DATE: 2003-11-23

PRIOR PLING DATE: 2003-11-23

PRIOR PLING DATE: 2003-05-23

PRIOR PLING DATE: 2003-05-23

PRIOR PLING DATE: 2003-02-20

PRIOR PLING DATE: 2003-02-20

PRIOR PLING DATE: 2003-02-20

PRIOR PLING DATE: 2003-02-20

PRIOR PLING DATE: 2002-02-20

PRIOR PLING DATE: 2002-02-20

PRIOR PLING DATE: 2002-02-20

PRIOR PLING DATE: 2008-02-30

PRIOR PLING DATE: 2008-03-30

PRIOR PLING DATE: 2008-03-30

PRIOR PLING DATE: 2008-02-30

PRIOR PLING DATE: 2008-02-30

PRIOR PLING DATE: 2008-02-30

PRIOR PLING DATE: 2008-02-30

PRIOR PLING DATE: 2008-03-30

PRIOR PLING DATE: 2008-0
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1.2%; Score 13.8; DB 1;
Best Local Similarity 82.4%; Pred. No. 2.8e+02;
Matches 14; Conservative 1; Mismatches 2;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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VS-10-1918-896-499

VS-10-1918-896-499

VS-10-1918-896-499

VS-20050164966A1

Sequence 499, Application US/10918896

Publication No. US20050164966A1

GENERAL INFORMATION:

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Beigelman, James

APPLICANT: Chowrirs, Bharat

TITLE OF INVENTION: Interference Mediated Inhibition of Type 1 Insulin-like

TITLE OF INVENTION: Interfering Nucleic Acid (siNA)

TITLE OF INVENTION: Interfering Nucleic Acid (siNA)

TITLE OF INVENTION: Interfering Nucleic Acid (siNA)

TITLE OF INVENTION: UNMER: US/10/918,896

CURRENT APPLICATION NUMBER: US/10/918,896

CURRENT APPLICATION NUMBER: US/10/918,896

PRIOR APPLICATION NUMBER: US/10/826,966

PRIOR FILING DATE: 2004-05-24

PRIOR FILING DATE: 2004-01-14

PRIOR FILING DATE: 2004-01-14

PRIOR APPLICATION NUMBER: US 10/757,803

PRIOR FILING DATE: 2004-01-14

PRIOR PRILING DATE: 2004-01-14
                                                                                                                                                                                                       APPLICANT: ChowTita, Haharat
APPLICANT: ChowTita, Haharat
TITLE OF INVENTION: Growth Factor Receptor (IGF-IR) Gene Expression Using Short
TITLE OF INVENTION: Interfering Nucleic Acid (siNA)
TITLE OF INVENTION: Interfering Nucleic Acid (siNA)
TITLE OF INVENTION: Interfering Nucleic Acid (siNA)
CURRENT FILLING DATE: 2004-08-16
PRIOR PELICATION NUMBER: US/0918, 996
CURRENT FILLING DATE: 2004-08-16
PRIOR PELICATION NUMBER: PCT/US04/16390
PRIOR FILLING DATE: 2004-06-16
PRIOR APPLICATION NUMBER: US 10/826, 966
PRIOR PELICATION NUMBER: US 10/720, 448
PRIOR PELICATION NUMBER: US 10/720, 448
PRIOR PELICATION NUMBER: US 10/444, 853
PRIOR PELICATION NUMBER: US 10/444, 853
PRIOR PELICATION NUMBER: US 10/444, 853
PRIOR PELICATION NUMBER: US 0003-11-24
PRIOR PELICATION NUMBER: US 003-01-24
PRIOR PELICATION NUMBER: US 003-02-20
PRIOR PELICATION NUMBER: PCT/US03/05346
PRIOR PELICATION NUMBER: US 60/358,580
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US-10-918-896-222
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Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 CGGGCGTGGCAGGAAG 38
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ORGANISM: Artificial Sequence
                                                                                              McSwiggen, James
Beigelman, Leo
Chowrira, Bharat
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Movelet Jim
TITLE OF INVENTION: Beidermal Growth Factor Receptors
TITLE OF INVENTION: Beidermal Growth Factor Receptors
TITLE OF INVENTION: UNABLE: US/10/64)
CURRENT APPLICATION NUMBER: US/10/277,494
CURRENT FILING DATE: 2002-10-21
NUMBER OF SEQ ID NOS: 446
SOFTWARE: Patentin version 3.0
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .; LOCATION: (1357006)...(1357020)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1542
US-10-339-674-1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors FILE REFERENCE: MBHB00-958-J (400/032)
CURRENT APPLICATION NUMBER: US/09/916,466
CURRENT FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 446
SCOFTWARE: Patentin version 3.0
SEQ ID NO 24
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; Sequence 24, Application US/10277494
; Publication No. US20030186909A1
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Best Local Similarity 93.3
Matches 14; Conservative
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CORGANISM: Homo sapiens
US-09-916-466-24
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US-10-277-494-24
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Sirna Thexapeuties, Inc.
APPLICANT: Sirna Thexapeuties, Inc.
APPLICANT: Richards, Ivan
ITILE OF INVENTION: Unding Short Interfering Nucleic Acid (sinA)
ITILE OF INVENTION: Unding Short Interfering Nucleic Acid (sinA)
FILE REPERBNICS: 400/225 (MRHB04-672)
CURRENT APPLICATION NUMBER: US 10/929, 329
CURRENT FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: US 10/826,966
PRIOR APPLICATION NUMBER: US 10/780,447
PRIOR APPLICATION NUMBER: US 10/780,447
PRIOR APPLICATION NUMBER: US 60/292,217
PRIOR APPLICATION NUMBER: US 60/322,016
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-19
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 60/343,480
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/543,480
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/543,480
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/543,480
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2
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US-09-316-466-24/C
US-09-316-46-24/C
Sequence 24, Application US/09916466
Sequence 24, Application World 100-10-316-466
Publication No. US20030064945A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Applicant, Saghir
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or conditions Relate
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                                                                                           1.2%; Score 13.8; DB 1; Length 19;
88.2%; Pred. No. 2.8e+02;
tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 320, Application US/10923329
Publication No. US20050164968A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          452 TGGGAGCAGTGGTAGCA 468
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                                                                                  Query Match
Best Local Similarity 88.2°
Matches 15; Conservative
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US-10-923-329-320
         US-10-923-329-124
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DOCATION: (1618564)...(1618579)

CHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 1350
US-10-255-120-890
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LOCATION: (821578)...(821593)
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber =
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GU, Yathong
APPLICANT: FENN, Sharron G.
APPLICANT: FENN, Sharron G.
APPLICANT: GHEN, Wensheng
APPLICANT: GHEN WOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
CURRENT APPLICATION NUMBER: US/09/866,108
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Sequence 466, Application US/10255120
Publication No. US20040091865A1
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Helicobacter pylori, strain J99 complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/255,120
CURRENT FILING DATE: 2002-11-19
NUMBER OF SEQ ID NOS: 903
SOFTWARE: PROPITIE 2002-11-19
SEQ ID NO 466
LENGTH: 16
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US-10-255-120-890
Sequence 890. Application US/10255120
Publicant Comparison of US2004091865A1
Sequence BOO. Application No. US2004091865A1
SEGUERAL INFORMATION: Achard J.; Global Determinants, Inc.
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVERTION: Helicobacter pylori, strain J99 complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/255,120
CURRENT FILING DATE: 2002-11-19
NUMBER OF SEQ ID NOS: 903
SOFTWARE: Proprietary
SEQ ID NO 890
LENGTH: 16
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1.2%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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ORGANISM: Helicobacter pylori, strain J99 complete genome.
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ORGANISM: Helicobacter pylori, strain J99 complete genome.
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Matches 14; Conserv
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| OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = US-10-339-674-3197
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Publication No. US20040091880A1
| Publication No. US20040091880A1
| CENERAL INFORMATION:
| APPLICANT: Weidner, Heiko
| APPLICANT: Schmitt-Ohn, Thomas
| APPLICANT: Weidner, Jurgen
| TITLE OF INVENTION: A Method For Direct Genetic Analysis of
| TITLE OF INVENTION: A Method For Direct Genetic Probes
| TITLE OF INVENTION: Target Cells by Using Fluorescence Probes
| TITLE OF INVENTION: Target Cells by Using Fluorescence FILE REFERENCE: 3515.1000-000
| CURRENT APPLICATION NUMBER: US/10/342,450
| CURRENT APPLICATION NUMBER: PCT/EP01/08202
| PRIOR FILING DATE: 2001-07-16
| PRIOR FILING DATE: 2001-07-14
| NUMBER OF SEQ ID NOS: 10
| SOFTWARET FREEE FREEEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                 Sequence 3197, Application US/10339674
Sequence 3197, Application US/10339674
Publication No. US20030204318A1
GENERAL INFORMATION:
APPLICANT: Feldaman, Richard J.; Global Determinants, Inc.
APPLICANT: Feldaman, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT PAPLICATION NUMBER: US/10/339,674
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 3537
SEQ ID NO 3197
LENGTH: 15
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1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
                                          Indels
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ORGANISM: Escherichia coli K-12 MG1655 complete genome.
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                                             Mismatches
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Best Local Similarity 93.3%;
Matches 14; Conservative (
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                                                Matches 14; Conservative
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ORGANISM: Homo Sapiens
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US-10-255-120-466
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LENGTH: 15
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PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
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Patent, No. US20020048800A1
GENERAL INFORMATION:
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-6287
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APPLICANT: GU, Yizhong
APPLICANT: HANZEL, David R.
APPLICANT: HANZEL, David R.
APPLICANT: HANZEL, David R.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: ALGONICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-4
PRIOR PILING DATE: 2000-10-4
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-10-04
PRIOR PLLING DATE: 2000-10-04
PRIOR PLLING DATE: 2000-09-27
PRIOR PLLING DATE: 2000-09-27
PRIOR PPLICATION NUMBER: US 60/236,359
PRIOR PLLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR PLLING DATE: 2001-01-30
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Patent No. US20020048800A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-866-108-2567
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APPLICANT: RANKEL, David R.

APPLICANT: RANKEL, David R.

APPLICANT: SHANNON, Mark

APPLICANT: SHANNON, MARK

ITILE OF INVENTION: WOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REPERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108

CURRENT FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30 Gaps ö Query Match 1.2%; Score 13.4; DB 1; Length 17; Best Local Similarity 93.3%; Pred. No. 2.5e+02; Matches 14; Conservative 0; Mismatches 1; Indels PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-02-31
PRIOR PRILING DATE: 2001-02-31
PRIOR PRILING DATE: 2001-02-31
PRIOR PILING DATE: 2001-02-31
PRIOR FILING DATE: 2001-02-31
PRIOR PILING DATE: 2001-02-31
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PRIOR FILING DATE: 2001-02-31
PRIOR FILING DATE: 2001-02-31
PRIOR FILING DATE: 2001-02-31
PRIOR FILING DATE: 2001-02-31
PRIOR PILING DATE: 2001-02-31 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00668

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TYPE: RNA
ORGANISM: Homo sapiens
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US-09-780-533A-818
                                                                                                                                                             TYPE: DNA
COCANISM: Homo sapiens
US-09-866-108-6289
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Sequence 6289, Application US/09866108

Sequence 6289, Application US/09866108

Sequence 6289, Application US/09866108

APPLICANT: 01, Youngang

APPLICANT: 1, Youngang

APPLICANT: HANZEL, David K.

APPLICANT: SHAWN WEARS: US/09/866,108

UUREANT APPLICANTON WURBER: US/05/20,456

PRIOR APPLICANTON WURBER: US/05/20,456

PRIOR APPLICANTON WURBER: US/02/20,456

PRIOR APPLICANTON WURBER: US/02/20,456

PRIOR PAPLICANTON WURBER: US/02/20,456

PRIOR PAPLICANTON WURBER: US/02/20,456

PRIOR PLING DATE: 2000-10-04

PRIOR PLING DATE: 2000-10-04

PRIOR PLING DATE: 2000-10-30

PRIOR PLING DATE: 2001-01-30

PRIOR PRIING DATE: 2001-01-30

PRIOR PRIING DATE: 2001-01-30

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Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1;
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2001-05
PRIOR PILING DATE: 2001-05
PRIOR PILING DATE: 2001-05
PRIOR PILING DATE: 2001-05
PRIOR PRIOR PRIOR PRIOR SEQ ID NOS: 15752
SOGTWARE: Acomica Sequence Listing Engine
SEG ID NO 6288
LENGTH: 17
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CAGANISM: Homo sapiens
US-09-866-108-6288
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US-09-780-533A-818

Sequence 818, Application US/09780533A

Publication No. US20030060611A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, Jim
APPLICANT: McMara
PITLE OF INVENTION: McHod and Reagent for the Inhibition of NOGO Gene
TITLE OF INVENTION: McHod 878-4 (400/011)
CURRENT FILING DATE: 2000-20-19

PRIOR APPLICATION NUMBER: US 60/181,797

PRIOR APPLICATION NUMBER: US 60/181,797

NUMBER OF SEQ ID NOS: 6679

SOFTWARE: Patentin version 3.0

SEQ ID NO 818

LENGTH: 17
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APPLICANT: Blatt, Larry
APPLICANT: Chowitze, Dim
APPLICANT: Chowitze, Dim
APPLICANT: Chowitze, Dim
APPLICANT: Chowitze, Dim
APPLICANT: Haeberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
TITLE OF INVENTION: METHOD, 878-A (400/011)
CURRENT APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SEQ ID NO 819
LENGTH: 17
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1.2%; Score 13.4; DB 1;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 1; Mismatches 1;
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Pred. No. 2.5e+02;
0; Mismatches 1;
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Sequence 819, Application US/09780533A
Publication No. US20030060611A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 6289
LENGTH: 17
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Best Local Similarity 93.3%;
Matches 14; Conservative
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APPLICANT: NIDOSYME PRAIMMCEULICALB, AUC.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwigen, June
APPLICANT: McSwigen, June
APPLICANT: McSwigen, June
TITLE OF INVENTION: Mcthod and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: MBHB00-845-H (400/029)
CURRENT FILING DATE: 2001-12-31
FRIOR APPLICATION NUMBER: US 09/531,025
FRIOR APPLICATION NUMBER: US 09/531,025
FRIOR APPLICATION NUMBER: US 09/533,035
FRIOR PLING DATE: 2000-03-20
FRIOR FILING DATE: 2000-04-0-03
FRIOR FILING DATE: 1994-03-07
FRIOR FILING DATE: 1995-05-04
FRIOR PLING DATE: 1995-05-04
FRIOR FILING DATE: 1995-10-08
FRIOR FILING DATE: 1995-11-08
FRIOR FRIOR DATE: 1995-11-
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TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
FILE REFERENCE: PB0177
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Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 8; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4244, Application US/10060756A; Publication No. US20030046717A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-877-478-1483
; Sequence 1483, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
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PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6586
SOFTWARE: PatentIn version 3.0
SEQ ID NO 949
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                                                                                                                                                                   TYPE: RNA
CRGANISM: Hepatitis B virus
US-09-877-478-949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Hepatitis B virus US-09-877-478-1483
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Best Local Similarity
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US-09-877-478-949
; Sequence 949, Application US/09877478
; Publication Wo. US2030068301A1
; GENERAL INPORMATION:
    APPLICANT: Ribozyme Pharmaceuticals, Inc.
    APPLICANT: Draper, Kenneth
    APPLICANT: Blatt, Larry
    APPLICANT: Blatt, Larry
    APPLICANT: Morisleev, Dave
    TILE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
    TILE REPERENCE: MRH800-845-H (400/029)
    CURRENT APPLICATION NUMBER: US 07/982,712
    PRIOR APPLICATION NUMBER: US 07/882,712
    PRIOR APPLICATION NUMBER: US 09/531,025
    PRIOR FILING DATE: 2000-03-20
    PRIOR APPLICATION NUMBER: US 09/536,385
    PRIOR FILING DATE: 2000-03-20
    PRIOR PILING DATE: 2000-03-20
    PRIOR PILING DATE: 2000-03-20
    PRIOR FILING DATE: 2000-03-20
    PRIOR PILING DATE: 2000-03-20
    PRIOR FILING DATE: 1994-02-07
    PRIOR FILING DATE: 1994-02-07
    PRIOR FILING DATE: 1995-05-04
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Publication No. US20030060611A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Plantmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: Habbrit, Pete

TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene

TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene

TILE REFERENCE: MBHB00,878-40(90/011)

CURRENT APPLICATION NUMBER: US 60/181,797

PRIOR APPLICATION NUMBER: US 60/181,797

PRIOR APPLICATION NUMBER: US 60/181,797

NUMBER OF SEQ ID NOS: 6679

SOFTWARE: PatentIn version 3.0

LENGTH: 17
                                                                                                                                           Gaps
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                                                                  Query Match 1.2%; Score 13.4; DB 1; Length 17; Best Local Similarity 86.7%; Pred. No. 2.5e+02; Matches 13; Conservative 1; Mismatches 1; Indels
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APPLICATION NUMBER: US 08/434,504
FILING DATE: 1995-05-04
APPLICATION NUMBER: US 09/436,430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
ORGANISM: Homo sapiens
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Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                       RESULT 461
US-09-780-533A-2566/C
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   US-09-780-533A-819
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588 ATGITCACTITAAGA 602
675 ATTATGTTACTTGTT 689
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; ORGANISM: Hepatitis B virus
US-10-342-902-949
                                        1 ATTATGTTTCTTGTT 15
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CORGANISM: Homo sapiens
US-10-339-782-483
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US-10-060-756A-4245
IS-060-756A-4245
Sequence 4245, Application US/10060756A
Publication No. US20030046717A1
FULL GALONT: Zhang, Jian
TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PRING DATE: 2001-01-30

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1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
    CURRENT APPLICATION NUMBER: US/10/060,756A
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 4804
SOFTWARE: Acomica Sequence Listing Engine
SEGO ID NO 4444
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Best Local Similarity 93.3
Matches 14; Conservative
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CORGANISM: Homo sapiens
US-10-060-756A-4245
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US-10-060-756A-4244
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US-10-142-902-949

Sequence 949, Application US/10342902

Sequence 949, Application US/10342902

Sequence 949, Application US/2040054156A1

GENERAL INFORMATION:
APPLICANT: Sirnar Therapeutics, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: McMabER: US/10/342,902

TITLE REFERENCE: 400/075 (MeHB00-845-1)
CURRENT FILING DATE: 2001-06-08
FRIOR FILING DATE: 2001-06-08
FRIOR FILING DATE: 2000-03-20
FRIOR FILING DATE: 2000-03-20
FRIOR FILING DATE: 2000-04-09
FRIOR FILING DATE: 2000-04-09
FRIOR FILING DATE: 1994-02-07
FRIOR FILING DATE: 1999-11-08
FRIOR FILING DATE: 1990-11-08
FRIOR FILING DATE: 1994-02-07
FRIOR FILING DATE: 1994-02-07
FRIOR FILING DATE: 1990-11-08
US-10-339-782-483/c
US-10-339-782-483/c
US-10-339-782-483/c
US-10-339-782-483/c
Sequence 483, Application US/10339782
Publication No. US20030166026A1
GENERAL INFORMATION:
APPLICANT: Bowen, Benjamin A
APPLICANT: Bowen, Benjamin A
TITLE OF INVEXTION Identification of Specific Biomarkers for Breast Cancer Cells
TITLE REFERENCE: 37-000110US
CURRENT APPLICATION NUMBER: US/10/339,782
CURRENT FILING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 495
SOFTWARE: Patentin version 3.1
SEQ ID NO 483
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US-10-287-949A-4443/C
US-10-287-949A-4443/C

Sequence 4443, Application US/10287949A

Publication No. US20040102389A1

Fublication No. US20040102389A1

Fublicant: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Rescobed, Jaime

APPLICANT: Stinchcomb, Dan

APPLICANT: Stanchcomb, Dan

APPLICANT: Bescobed, Jaime

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: US-00-876-N (400/049)

CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 20822

SOFTWARE: Patentin version 3.0

SEQ ID NO 4443

LENGTH: 17
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
Length 17;
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Query Match 1.2%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1;
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                                                                                                                                                626 GITTIATICICAGCA 640
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
CORGANISM: Homo sapiens
US-10-138-674-9117
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US-10-287-949A-4443
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                                                                                                                                                                                                  Sequence 1483, Application US/10342902
| Sequence 1483, Application US/10342902
| Publication No. US20040054156A1
| GENERAL INFORMATION |
| APPLICANT SITUAT Herapeutics, Inc. |
| APPLICANT Blatt, Larry |
| APPLICANT BLACK Larry |
| APPLICANT BLACK Larry |
| APPLICANT BLACK LARRY |
| APPLICANT MORTISBS, DAVE |
| THIE OF INVERTION WHERE: US/10/342,902 |
| THIE REFERENCE: 400/075 (MBHB00-845-1) |
| CURRENT PILING DATE: 2001-06-08 |
| PRIOR PILING DATE: 2001-06-08 |
| PRIOR FILING DATE: 2001-06-08 |
| PRIOR FILING DATE: 2000-08-09 |
| PRIOR PILING DATE: 2000-08-09 |
| PRIOR PILING DATE: 2000-08-09 |
| PRIOR PILING DATE: 1994-02-07 |
| PRIOR PILING DATE: 1994-02-07 |
| PRIOR PILING DATE: 1994-02-07 |
| PRIOR FILING DATE: 1994-02-07 |
| PRIOR FILING DATE: 1994-02-07 |
| PRIOR FILING DATE: 1994-01-08 |
| PRIOR FILING DATE: 1994-01-08 |
| PRIOR FILING DATE: 1999-11-08 |
| NUMBER OF SEQ ID NOS: 6592 |
| SEQ ID NO 1483 |
| LARGH IN APPLICATION WHERE: US OBJAS6, 430 |
| PRIOR FILING DATE: 1999-11-08 |
| NUMBER OF SEQ ID NOS: 6592 |
| PRIOR PILING DATE: 1999-11-08 |
| NUMBER OF SEQ ID NOS: 6592 |
| PRIOR PILING DATE: 1999-11-08 |
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| NUMBER OF SEQ ID NOS: 6592 |
| PRIOR PILING DATE: 1999-11-08 |
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| Sequence 4443, Application US/10136674
| Sequence 4443, Application US/10136674
| Publication No. US-20040077565A1
| GENERAL INFORMATION | DESCRIPTION | PAUC.) PAUC. PAPLICANT: Bavco. Pam | APPLICANT: Brinchcomb, Dan | APPLICANT: Dan | APPLICANT:
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570 TTAATACCTTTATAT 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Hepatitis B virus US-10-342-902-1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                   RESULT 468
US-10-342-902-1483
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APPLICANT: James, McSaiggen
APPLICANT: James, McSaiggen
APPLICANT: James, McSaiggen
APPLICANT: James, McSaiggen
APPLICANT: Barala, Morrisesy
APPLICANT: Remeath, Draper
APPLICANT: Remeath, Draper
APPLICANT: Remeath, Draper
APPLICANT: Elisabeth, Roberts
APPLICANT: Blisabeth, Roberts
APPLICANT: Blisabeth, Roberts
APPLICANTION: VIRON ERPLICATION
TITLE OF INVENTION: VIRON ERPLICATION
TITLE OF INVENTION: VIRON ERPLICATION
FILE REPERBACE: 400/04205 (WRHB02-240-E)
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: US 60/296, 876
PRIOR APPLICATION NUMBER: US 60/335,059
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 60/335,059
PRIOR FILING DATE: 2001-12-05
PRIOR PLILING DATE: 2001-12-05
PRIOR FILING DATE: 2001-22-0
PRIOR FILING DATE: 2001-22-0
PRIOR FILING DATE: 2002-02-10
PRIOR FILING DATE: 2000-12-18
PRIOR PRILICATION NUMBER: US 60/354,321
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 60/354,321
PRIOR PRILING DATE: 2000-03-16
PRIOR PRILING DATE: 2000-03-07
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40.0%; Pred. No. 2.5e+02;
tive 8; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                     Length 17;
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1.2%; Score 13.4; DB 1;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 8; Mismatches 1;
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; Publication No. US20040127446A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Lawrence, Blatt
APPLICANT: Dennis, Macejak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             569 TITAATACCITTATA 583
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NUMBER OF SEQ ID NOS: 16207
SOFTWARE: Patentin version 3.0
SEQ ID NO 949
LENGTH: 17
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1 UUAAUGCCUUUAUAU 15
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Best Local Similarity 40.vv
                                                                                                                                                                                                    ; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-949
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US-10-669-841-1483
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APPLICANT: Grant Therapeutics, Inc.
APPLICANT: Grant Therapeutics, Inc.
APPLICANT: Grant Therapeutics, Inc.
APPLICANT: Grant Gran
                                                                                                                                    Sequence 9117, Application US/10287949A

Sequence 9117, Application No. US20040102389A1

Publication No. US20040102389A1

Publication No. US20040102389A1

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stoneda, Jaime

APPLICANT: Stinchcomb, Dan

APPLICANT: Stoneda, Jaime

APPLICANT: Stinchcomb, Dan

APPLICA
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; Sequence 949, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-10-287-949A-9117
                                                                                             RESULT 472
US-10-287-949A-9117/c
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Sequence 6288, Application US/10723361

Sequence 6288, Application US/20040137589A1

GENERAL INPORMATION:
APPLICANT: GU, Yizhong
APPLICANT: PENN, Sharron G.
APPLICANT: PENN, Sharron G.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: SHANNON, Wark
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART APPLICANT: CHEN, WOMBER: US/10/723,361

CURRENT APPLICATION NUMBER: US/10/723,361
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                                                           PRIOR FILING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-05
PRIOR PELING DATE: 2000-10-03
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 09/866,108
PRIOR PLING DATE: 2001-05-25
PRIOR PLING DATE: 2001-05-25
PRIOR PELING DATE: 2000-05-26
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PLING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/207,456
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Best Local Similarity 93.3.
The Conservative
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ORGANISM: Homo sapiens
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Sequence 2657, Application US/10723361
Sequence 2657, Application US/10723361
Sequence 2657, Application US/10723361
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APPLICANT OF VIZONG
APPLICANT SHANCON WASTON OF SEPTICANT SHANCON SEPTICANT SEPTIC
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: Bann, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MARK
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
FILE REFERENCE: PB0105
CURRENT APPLICATION NUMBER: US/10/723,361
CURRENT FILING DATE: 2003-11-26
PRIOR FILING DATE: 2001-05-25
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Publication No. US20040137589A1
GENERAL INFORMATION:
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Best Local Similarity 93.3
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-10-723-361-2567
                                                                   US-10-723-361-2567/c
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APPLICANT: Pavco, Pamela APPLICANT: Pavco, Pamela APPLICANT: Pavco, Pamela APPLICANT: Pavco, Pamela APPLICANT: Sandberg, Jennifer APPLICANT: Sandberg, Jennifer APPLICANT: Gandberg, Jennifer Gardon, Gilad Gardon, Gilad Stinchcomb, Dan Stinchcomb, Dan Stinchcomb, Dan Stinchcomb, Dan TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACT TITLE OF INVENTION: NECEPTOR FOR THE TREATMENT OF ANGIOGENESIS RELATED DISEASES AND TITLE OF INVENTION NUMBER: US/10/12,633
CURRENT PAPLICATION NUMBER: US 60/065,974
PRIOR PLILNG DATE: 1996-01-0
PRIOR PLILNG DATE: 1996-01-0
PRIOR PLILNG DATE: 1996-01-0
PRIOR PLILNG DATE: 2000-01-07
PRIOR PLILNG DATE: 2000-01-07
PRIOR PLILNG DATE: 2001-10-7
PRIOR PLILNG DATE: 2001-10-7
PRIOR PLILNG DATE: 2001-10-7
PRIOR PLILNG DATE: 2001-11-07
PRIOR PLILNG DATE: 2001-06-03
NUMBER OF SEQ ID NOS: 5889
SOUTH APPLICATION NUMBER: US 10/138,674
PRIOR PLILNG DATE: PARENTH OF PAR
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APPLICANT: BavCo, Pamela
APPLICANT: Sandberg, Jennifer
APPLICANT: Sandberg, Jennifer
APPLICANT: Gordon, Gilad
APPLICANT: Gordon, Gilad
APPLICANT: Gordon, Gilad
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: RECEPTOR FOR THE TREATMENT OF VASCULAR ENDOTHELIAL GROWTH FACI
TITLE OF INVENTION: RECEPTOR FOR THE TREATMENT OF ANGIGGENESIS RELATED DISEASES AND
TITLE OF INVENTION: BORDON-325PCT (400/447)
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR PELING DATE: 1995-10-26
PRIOR PELING DATE: 1995-00-108
PRIOR PELING DATE: 1995-00-10
PRIOR PELING DATE: 1995-00-10
PRIOR APPLICATION NUMBER: US 09/371,772
PRIOR PELING DATE: 1995-00-10
PRIOR APPLICATION NUMBER: US 09/371,772
PRIOR APPLICATION NUMBER: US 09/371,772
PRIOR PELING DATE: 2000-11-07
PRIOR PELING DATE: 2001-05-29
PRIOR PELING DATE: 2001-01-30
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Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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US-10-712-633-4385/c
Sequence 4385, Application US/10712633
PORTICATION NO. US20040220128A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                     APPLICANT: Ribozyme Pharmaceuticals, Inc. APPLICANT: Pavco, Pamela
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US-10-712-633-348
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SOFTWARE: Acomica Sequence Listing Engine
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                                                                                                                                                                                                                      Query Match 1.2%; Score 13.4; DB 1; Length 17; Best Local Similarity 93.3%; Pred. No. 2.5e+02; Matches 14; Conservative 0; Mismatches 1; Indels
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 6288
LENGTH: 17
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Best Local Similarity 93.3%;
Matches 14; Conservative (
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CORGANISM: Homo sapiens
US-10-723-361-6289
                                                                                                                      TYPE: DNA
COGANISM: Homo sapiens
US-10-723-361-6288
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US-10-712-633-348/c
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LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 812, Application US/10494343
; Sequence 812, Application US/10494343
; Publication No. US20040248138A1
; GENBEAL INFORMATION:
    APPLICANT: Shannon, Mark
; APPLICANT: Shannon, Mark
; APPLICANT: Shannon, HuMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; FRIOR APPLICATION NUMBER: US to be assigned
; PRIOR PRILING DATE: 2002-11-01
; PRIOR FILING DATE: 2002-11-01
; PRIOR FILING DATE: 2001-11-01
; RUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 812
; LENGTH: 17
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FULLICATION NO. US20040248138A1

GENERAL INFORMATION:
APPLICANT: Shannon, Mark
APPLICANT: Shannon, Mark
TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1

FILE REFERENCE: P80184
CURRENT FILING DATE: 2004-04-30

PRIOR APPLICATION NUMBER: US/10/494,343

CURRENT FILING DATE: 2002-11-01

PRIOR PILING DATE: 2002-11-01

PRIOR FILING DATE: 2002-11-01

PRIOR FILING DATE: 2001-11-01

NUMBER: OF SEQ ID NOS: 870

SOFTWARE: Asomica Sequence Listing Engine
PRIOR APPLICATION NUMBER: US 10/138,674
PRIOR FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 5989
SOFTWARE: Patentin version 3.0
SEQ ID NO 4385
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                                                                                                                                            ; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-712-633-4385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-812
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US-10-494-343-812/c
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                                                                                                                    LENGTH: 17
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FILE REPERENCE: PB0177
CURRENT APPLICATION HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
FILE REPERENCE: PB0177
CURRENT FILING DATE: 2004-07-14
PRIOR PILING DATE: 2004-07-130
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                            US-10-494-343-814/C

Sequence 814, Application US/10494343

Sequence 814, Application US/10494343

Publication No. US20040248138A1

GENERAL INFORMATION:
APPLICANT: Shannon, Mark
APPLICANT: Phan, Thuymy
TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
FILE REFERENCE: PB0184

CURRENT FILING DATE: 2004-04-30

PRIOR APPLICATION NUMBER: US/10/494,343

CURRENT FILING DATE: 2004-04-30

PRIOR APPLICATION NUMBER: US to be assigned

PRIOR APPLICATION NUMBER: US 60/334,773

PRIOR FILING DATE: 2002-11-01

PRIOR FILING DATE: 2001-11-01

PRIOR FILING DATE: 2001-11-01

SOFTWARE: Aeomica Sequence Listing Engine

SEQ ID NOS: 870

SEQ ID NOS: 870

SEQ ID NOS: 870
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                                                                                                                                                                                                                                       393 TCATTTTCCTTACAA 407
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                                                                                                               Query Match
Best Local Similarity 93.33
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Homo sapiens
US-10-494-343-814
TYPE: DNA
CORGANISM: Homo sapiens
US-10-494-343-813
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Query Match
Best Local Similarity 93.33
Matches 14; Conservative
BRAUN, ANDREAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
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TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
FILE REPERENKE: PB0177

CURRENT APPLICATION NUMBER: US/10/890,776A

CURRENT FILING DATE: 2004-07-14

PRIOR PAPLICATION NUMBER: US 10/060,756

PRIOR PLILING DATE: 2002-01-30

PRIOR PLILING DATE: 2001-01-30

PRIOR PLILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                Query Match
1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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SOFTWARE: Aeomica Sequence Listing Engine
            PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/327,898
PRIOR FILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 4809
SEQ ID NO 4244
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4245, Application US/10890776A Publication No. US20050129683A1 GENERAL INFORMATION:
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is Sequence 258, Application US/10704513
Publication No. US20050170500A1
GENERAL INFORMATION:
APPLICANT: ROTH, RICHARD B.
APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: KAMMERER, STEFAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              675 ATTATGTTACTTGTT 689
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
US-10-890-776A-4245
                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-890-776A-4244
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US-10-890-776A-4245
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AFFILIANI E BEADLY, ANUMENTOS FOR IDENTIFYING RISK OF MELANOMA AND TREATMENTS TITLE OF INVENTION: THEREOF FOR IDENTIFYING RISK OF MELANOMA AND TREATMENTS TITLE OF INVENTION: THEREOF FILE REFERENCE: SEQ-4062-UT CURRENT APPLICATION NUMBER: US/10/704,513
CURRENT FILING DATE: 2003-11-06
PRIOR PILING DATE: 2003-01-06
PRIOR PILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 774
SOFTWARE: PATENTIN VETSION 3.3
SEQ ID NO 258
LIBROTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer
US-10-704-513-258
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; Sequence 3260, Application US/09969373
; Patent No. US20020133852A1
; GARERAL INFORMATION:
    APPLICANT: Hauge, Brian M.
    TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
    FILE REFERENCE: 38-10(52679)A
; CURRENT FILING DATE: 2001-10-02
; PRIOR PELICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-13
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR APPLICATION NUMBER: US 09/855,768
; RIOR APPLICATION NUMBER: US 09/855,768
; ROLID NOS: 4593
; SEQ ID NOS: 4593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.2%; Score 13.4; DB 1; Length 17; Best Local Similarity 93.3%; Pred. No. 2.5e+02; Matches 14; Conservative 0; Mismatches 1; Indels
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US-09-816-814-2

Sequence 2. Application US/09816814

Publication No. US20030027136A1

GENERAL INFORMATION:
APPLICANT: GOTOMINY, JOTG J.
APPLICANT: Weyand, Cornella M.
TITLE OF INVENTION: RHEUMATOID ARTHRITIS MARKERS
FILE REPRESENCE: 707039-251001

FILE REPRESENCE: 2001-03-23

CURRENT APPLICATION NUMBER: US/09/816,814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   994 TGTATGCACATGAAA 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  702 TAGTCACGGTGCTCT 716
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
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TYPE: DNA
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Sequence 43, Application US/10138316

Bublication No. US20030054380A1

GENERAL INPORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Splawski, Igor
TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
TITLE OF INVENTION: KCNEI AS AN LQT GENE
FILE REFERENCE: 2323-162-06-06
FILE REFERENCE: 2323-162-06-06
FRIOR APPLICATION NUMBER: 09/444,295
FRIOR PELING DATE: 1998-08-17
FRIOR PILING DATE: 1998-08-17
FRIOR PILING DATE: 1996-10-29
FRIOR PELING DATE: 1996-10-29
FRIOR APPLICATION NUMBER: 60/094,477
FRIOR PILING DATE: 1998-07-29
FRIOR FILING DATE: 1998-07-29
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Publication No. US20030134272A1
GENERAL INFORMATION:
APPLICANT: Universiteit Gent
TITLE OF INVENTION: Improved mutation analysis of the NF1 Gene
FILE REFERENCE: UG-005-PCT
CURRENT APPLICATION NUMBER: US/10/128,560
CURRENT FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: EP 99870216.1
                                                                                                                                                                                                                                                                                                                                Query Match
1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO. 2
LENGTH: 18
                                                                                                                                                                                                                                ; OTHER INFORMATION: primer for PCR
US-09-816-814-2
                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277 GCCATATTTCTTCAC 291
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ORGANISM: Homo sapiens
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US-10-128-560-139/c
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US-10-138-316-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Improved mutation analysis of the NF1 Gene FILE REFERENCE: UG-005-PCT CURRENT PELLORION NUMBER: US/10/128,560 CURRENT FILING DATE: 2002-04-18 PRIOR PELICATION NUMBER: EP 99870216.1 PRIOR APPLICATION NUMBER: EP 00870122.9 PRIOR FILING DATE: 2000-06-05 PRIOR FILING DATE: 2000-06-05 PRIOR FILING DATE: 2000-06-05 PRIOR FILING DATE: 2000-06-16 NUMBER: OF SEQ ID NOS: 264 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                               1.2%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                Indels
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Fublication No. US20030170708A1
GENERAL INFORMATION
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Curran, Mark E.
APPLICANT: Landes, Gregory M.
APPLICANT: Landes, Timothy D.
APPLICANT: Burn, Timothy C.
APPLICANT: Splawski, Igor
ITILE OF INVENTION' SPLAWSKI, Igor
ITILE OF INVENTION' SVIQOR
ITILE OF INVENTION' SVIQOR
CURRENT APPLICATION NUMBER: US/10/368,643
CURRENT APPLICATION NUMBER: 2003-02-20
CURRENT FILING DATE: 2000-06-19
                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: BP 00870122.9
PRIOR FILING DATE: 2000-06-05
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 264
SOSTWARE: PATENTIN VET. 2.1
SEQ ID NO 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 491
US-10-128-560-195/c
; Sequence 195, Application US/10128560
; Publication No. US20030134272A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  416 TITITCCTIAIATIT 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416 TTTTTCCTTATATTT 430
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US-10-128-560-139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Homo sapiens
US-10-128-560-195
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-368-643-43
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APPLICANT: Chumakov, 11ya

1 TTLE OF INVENTION: Blallelic markers for use in constructing a high density...

FILE REFERENCE: GENSET.020CP1

CURRENT APPLICATION NUMBER: US/10/349,143

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US/09/422,978

PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US 09/298,850

PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1999-04-21

PRIOR PILING DATE: BARLIER FILING DATE: 1998-11-23

PRIOR FILING DATE: BARLIER FILING DATE: 1998-11-23

PRIOR FILING DATE: BARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 5744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; NAME/KEY: primer_bind
: LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-6557 for SEQ 1810,
US-10-349-143-5744
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1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.88+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 81, Application US/10764238
; Sequence 81, Application US/10764238
; Publication No. US20040219616A1
; GENERAL INFORMATION:
; APPLICANT: Birx Therapeutics Ltd.
; APPLICANT: Berxy Liam
; APPLICANT: Hayes, Iam
; APPLICANT: Murphy, Filabarr
; TITLE OF INFURNITON: Apoptosis-Related Kinase/GPCRs
; TITLE OF INVENTION: Apoptosis-Related Kinase/GPCRs
; FILE REFERENCE: 8912/2012
; CURRENT APPLICATION NUMBER: US/10/764,238
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: UK 301566.5
; PRIOR PELICATION NUMBER: UK 301566.5
; RIOR PILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 1.2%; Score 13.4; DB 1; 1 Similarity 93.3%; Pred. No. 2.8e+02; 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: QPCR REverse Primer (Bcl2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-861-520-43
; Sequence 43, Application US/10861520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carcrececarece 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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Sequence 5495, Application US/10349143

Publication No. US20040005584A1

GENERAL INFORMATION:
APPLICANT: Cohon, Daniel
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET: 02002-01-21
CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US/09/422.978
PRIOR APPLICATION NUMBER: US/09/422.978

PRIOR PILING DATE: 1999-10-20
PRIOR PLILING DATE: 1999-10-20
PRIOR PLILING DATE: EARLIER FILING DATE: 1999-04-21
PRIOR PLILING DATE: EARLIER PLILING DATE: 1999-04-21
PRIOR PLILING DATE: EARLIER PLILING DATE: 1999-11-23
PRIOR PLILING DATE: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR PLILING DATE: EARLIER PLILING DATE: 1998-11-23
PRIOR PLILING DATE: EARLIER PLILING DATE: 1998-04-21

NUMBER: OF SEQ ID NOS: 11796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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1.2%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1;
                     PRIOR APPLICATION NUMBER: US 09/135,010
PRIOR FILING DATE: 1998-08-17
PRIOR PELING DATE: 1998-08-17
PRIOR FILING DATE: 1998-07-29
PRIOR PILING DATE: 1997-08-29
PRIOR PILING DATE: 1997-08-29
PRIOR FILING DATE: 1996-10-29
PRIOR FILING DATE: 1996-10-29
PRIOR PILING DATE: 1996-10-29
PRIOR FILING DATE: 1996-10-29
PRIOR FILING DATE: 1996-11-22
NUMBER OF SEQ ID NOS: 116
SOFTHARE: PATENT VET: 2.0
SEQ ID NO 43
LENGTH: 18
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; Sequence 5744, Application US/10349143
; Sequence 5764, Octobro 105/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1060 CTTTCCAGTGGCTAA 1074
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: primer_bind
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Matches 14; Conserv
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LENGTH: 18
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Sequence 43, Application US/10911678

Publication No. US2005003433A1

Sequence 43, Application US/10911678

Publication No. US2005003433A1

APPLICANT: Sanguinteti, Michael C.

APPLICANT: Sanguinteti, Michael C.

APPLICANT: Sanguinteti, Michael C.

TITLE OF INVENTION: MUTATIONS IN THE KCNEI GENE ENCODING HUMAN minK WHICH

TITLE OF INVENTION: ACAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING

TITLE OF INVENTION: MUTATIONS IN LQT GENE

FILE REFERENCE: 2323-169

CURRENT PILLING DATE: 2002-06-06

PRIOR PILLING DATE: 1099-11-22

PRIOR APPLICATION NUMBER: 09/135,020

PRIOR PILLING DATE: 1999-10-22

PRIOR PILLING DATE: 1999-08-17

PRIOR FILLING DATE: 1997-08-29

PRIOR FILLING DATE: 1997-08-29

PRIOR PILLING DATE: 1998-07-29

PRIOR PILLING DATE: 1998-07-29

PRIOR PILLING DATE: 1998-07-29

NUMBER OF SEQ ID NOS: 114

SOFTWARE PATELCATION NUMBER: 60/019,014

PRIOR FILLING DATE: 1998-07-29

NUMBER OF SEQ ID NOS: 114
GENERAL INPORMATION:
APPLICANT: Sacting, Mark T.
APPLICANT: Sandinetti, Michael C.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Splawski, 1gor
TITLE OF INVENTION: MUTATION IN THE KCNEI GENE ENCODING HUMAN mink WHICH
TITLE OF INVENTION: ACNEI AS AN LQT GENE
TITLE OF INVENTION: KCNEI AS AN LQT GENE
TITLE OF INVENTION: KCNEI AS AN LQT GENE
TITLE OF INVENTION: MUMBER: US/10/861,520
CURRENT APPLICATION NUMBER: US/10/861,520
CURRENT APPLICATION NUMBER: US/13,316
PRIOR PILING DATE: 1999-10-25
PRIOR PELING DATE: 1999-10-25
PRIOR PELING DATE: 1999-08-17
PRIOR PILING DATE: 1995-00-29
PRIOR APPLICATION NUMBER: 08/739,383
PRIOR FILING DATE: 1995-10-29
PRIOR PELING DATE: 1995-10-29
PRIOR PELING DATE: 1995-10-29
PRIOR PELING DATE: 1995-10-29
PRIOR APPLICATION NUMBER: 60/019,014
PRIOR PILING DATE: 1998-07-29
PRIOR APPLICATION NUMBER: 60/019,014
PRIOR PILING DATE: 1998-07-29
PRIOR APPLICATION NUMBER: 60/019,014
PRIOR FILING DATE: 1998-07-29
NUMBER: OF SEQ ID NOS: 114
SOFTWARE: PATENTIN VUMBER: 60/019,014
SEQ ID NO 43
LENGTH: 18
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Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-861-520-43
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                                                                                              Score 13.4; DB 1; Length 18;
Pred. No. 2.8e+02;
0; Mismatches 1; Indels
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APPLICANT: Hayes, Ian
APPLICANT: Hayes, Ian
APPLICANT: Murphy, Finbarr
TITLE OF INVENTION: Apoptosis-Related Kinase/GPCRs
FILE REFERENCE: 8912/2015
CURRENT APPLICATION NUMBER: US/10/781,581
CURRENT FILING DATE: 2004-02-18
PRIOR PILING DATE: 2004-01-23
PRIOR PILING DATE: 2003-03-25
PRIOR PILING DATE: 2003-03-25
PRIOR PILING DATE: 2003-03-25
PRIOR PILING DATE: 2003-03-25
NUMBER OF SEC ID NOSS: 226
SOFTWARE: Patentin version 3.2
SEC ID NOSS: 226
SEC ID NOSS: 226
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1.2%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1;
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US-10-781-581-81
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Patent No. US20020119460A1

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Cohen, Daniel

APPLICANT: Chumakov, Ilya

APPLICANT: Buugueleret, Lydie

TITLE OF INVENTION: Prostate Cancer Gene

FILE REFERENCE: GEN-T11XC3D2

CURRENT APPLICATION NUMBER: US/09/901,484A

CURRENT FILING DATE: 2001-07-09

PRIOR APPLICATION NUMBER: US 08/996,306

PRIOR APPLICATION NUMBER: US 09/96,306

PRIOR APPLICATION NUMBER: US 09/96,588

PRIOR FILING DATE: 1998-09-09

PRIOR FILING DATE: 1998-12-22

PRIOR FILING DATE: 1999-16-23
                                                                                                                                                                                                                                                                                                                                                       US-10-781-581-81
; Sequence 81, Application US/10781581
; Publication No. US20050019746A1
; Publication No. US20050019746A1
; APPLICANT: Birx Therapeutics Ltd.
                                                                                                      1.2%;
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                                                                                                 Query Match 1.29
Best Local Similarity 93.39
Matches 14; Conservative
TYPE: DNA
CORGANISM: Homo sapiens
US-10-911-678-43
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IITLE OF INVENTION: Biallelic markers for use in constructing a high density...
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Matches
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                                                                                                                                                                                                                                                                                                                                FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(19)

COTHER INFORMATION: upstream amplification primer for SEQ 251, SEQ 328
US-09-901-484A-372
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1.2%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Ilya, Chumakov
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: PROSTATE CANCER GENE
FILE REFERENCE: GENSET.18CPLCP
CURRENT APPLICATION NUMBER: US/09/853,526
CURRENT FILING DATE: 1999-06-23
PRIOR PILING DATE: 1999-06-23
PRIOR FILING DATE: 1997-12-22
PRIOR PILING DATE: 1997-12-22
PRIOR PILING DATE: 1997-12-22
PRIOR FILING DATE: 1997-12-22
PRIOR FILING DATE: 1998-10-09
PRIOR FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 578
SOFTWARE: PARENT PRIOR PLING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 578
SOFTWARE: PARENT PRIOR PLING DATE: PARENT PRIOR PLING DATE: PARENT PARENT PRIOR PLING DATE: PARENT PARE
                   PRIOR APPLICATION NUMBER: US 09/853,526
PRIOR FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 578
SEQ ID NO 372
LENGTH: 19
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US-10-349-143-4387/C
US-10-349-143-4387/C
PUDICACTION NO. US20040005584A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, 11ya
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Patent No. US20020165345A1
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Best Local Similarity 93.33
Matches 14; Conservative
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                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION:'1..19 -
OTHER INFORMATION: downstream amplification primer 99-4233 for SEQ 3461, in compleme
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US-10-349-143-11326

US-10-349-143-11326

Sequence 11326, Application US/10349143

Sequence 11326, Application No. USC0040005584A1

Sequence 11326, Application No. USC0040005584A1

SEQUENCAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Cohen, Daniel

APPLICANT: Cohen, Ilya

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE: GENSET.020CP1

CURRENT PILING DATE: 2003-01-21

CURRENT PILING DATE: 1999-10-20

PRIOR PILING DATE: EARLIER FILING DATE: 1999-04-21

PRIOR PILING DATE: EARLIER FILING DATE: 1999-04-21

PRIOR PILING DATE: EARLIER PILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732

PRIOR PILING DATE: EARLIER FILING DATE: 1998-04-21

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796
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FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
LENGTH: 19
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1.2%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1;
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ORGANISM: Homo Sapiens
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Publication No. US20040185530A1
Publication No. US2004185530A1
GENERAL INFORMATION:
APPLICANT: McHenry, Charles
TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III HOLOENZYME
FILE REFERENCE: 1794.003004
CURRENT FPLING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: US/09/818,780
PRIOR FILING DATE: 2001-03-28
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1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 10; Conservative 4; Mismatches 1; Indels
US-10-444-795B-774/C
; Sequence 774, Application US/10444795B
; Publication No. US20440077574A1
; GENERAL INFORMATION:
APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patriok
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REPERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SEQ ID NO 774
; SEQ ID NO 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Kinghoffer, Richard
APPLICANT: Lewis, Stephen Patrick
TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
FILE REFERENCE: 200125.449
CURRENT FILING DATE: 2003-05-23
NUMBER OF SEQ ID NOS: 842
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 775
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Small interefering RNA - TCPTP2
US-10-444-795B-775
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US-10-444-795B-774
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US-10-746-167-80/c
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA
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APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Richards, Ivan
APPLICANT: MCSWiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Interleukin and
TITLE OF INVENTION: Interleukin Receptor Gene Expression Using Short Interfering
TITLE OF INVENTION: NUCLEA: 400/163 (MSH03)-094-D)
CURRENT APPLICATION NUMBER: US/10/863,973
CURRENT PILING DATE: 2004-06-09
PRIOR FILING DATE: 2004-05-24-D
PRIOR PILING DATE: 2004-05-24-0
PRIOR FILING DATE: 2004-05-24-0
PRIOR PILING DATE: 2004-05-14-04-16
PRIOR PILING DATE: 2004-01-14
PRIOR PILING DATE: 2004-01-14
PRIOR PILING DATE: 2003-01-24
PRIOR PILING DATE: 2003-01-24
PRIOR PILING DATE: 2003-01-24
PRIOR PILING DATE: 2003-01-24
PRIOR PILING DATE: 2003-05-23
PRIOR PILING DATE: 2003-05-23
PRIOR PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US/10/803/05028
PRIOR PILING DATE: 2003-02-20
PRIOR PILING DATE: 2003-03-20
PRIOR PILING DATE: 2003-03-30
PRIOR PILING DATE: 2003-
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US-10-863-973-728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 19;
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US-10-746-167-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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1.2%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1;
PRIOR APPLICATION NUMBER: US 60/192,736
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 80
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-863-973-728
; Sequence 728, Application US/10863973
; Publication No. US20050143333A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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SEQ ID NO 728
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US-10-923-522-1547/C

US-10-923-522-1547/C

Sequence 1547, Application US/10923522

Publication No. US20050159381A1

GENERAL INFORMATION:
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RN Interference Mediated Inhibition of Chromosome Translocation
TITLE OF INVENTION: RN Interference Mediated Inhibition of Chromosome Translocation
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (sink)
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (sink)
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (sink)
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (sink)
TITLE OF INVENTION UNMERS: US/10/2234
PRIOR PILING DATE: 2003-01-14
PRIOR PILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: US 10/44,039
PRIOR PILING DATE: 2004-04-16
PRIOR PILING DATE: 2004-01-14
PRIOR PILING DATE: 2004-01-14
PRIOR PILING DATE: 2004-01-14
PRIOR PILING DATE: 2004-01-12
PRIOR PILING DATE: 2004-01-23
PRIOR PILING DATE: 2003-010-23
PRIOR PILING DATE: 2003-010-23
PRIOR PILING DATE: 2003-02-20
PRIOR PILING DATE: 2003-02-20
PRIOR PILING DATE: 2003-02-20
PRIOR PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 10/693,059
PRIOR PILING DATE: 2003-02-20
PRIOR PILING DATE: 2003-02-20
PRIOR PILING DATE: 2003-02-20
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US-10-923-522-1371
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                                            PRIOR FILING DATE: 2003-01-14
PRIOR FILING DATE: 2003-01-14
PRIOR FILING DATE: 2003-01-14
PRIOR PELICATION NUMBER: US 60/404,039
PRIOR PELICATION NUMBER: PCT/US 04/16390
PRIOR PELICATION NUMBER: US 10/826,966
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-01-14
PRIOR FILING DATE: 2003-11-24
PRIOR FILING DATE: 2003-11-24
PRIOR FILING DATE: 2003-11-24
PRIOR FILING DATE: 2003-10-23
PRIOR FILING DATE: 2003-10-23
PRIOR FILING DATE: 2003-05-23
PRIOR FILING DATE: 2003-05-23
PRIOR PRIOR PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR PRIOR APPLICATION NUMBER: PCT/US03/05346
PRIOR FILING DATE: 2003-05-23
PRIOR PRIOR APPLICATION NUMBER: PCT/US03/05346
PRIOR PRIOR DATE: 2003-05-23
PRIOR PRIOR APPLICATION NUMBER: PCT/US03/05346
PRIOR APPLICATION NUMBER: PCT/US03/05346
PRIOR PRIOR APPLICATION NUMBER: PCT/US03/05346
PRIOR PRIOR APPLICATION NUMBER: PCT/US03/05346
PRIOR APPLICATION NUMBER: PCT/US03/05346
PRIOR PRIOR APPLICATION NUMBER: PCT/US03/05346
PRIOR APPLICATION NUMBER: PCT/US03/05346
PRIOR PCT/US03/05346
PCT/US03/053
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         US 60/439,922
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ORGANISM: Artificial Sequence
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US-10-863-973-799/

Publication No. US20050143333A1

GENERAL INPOGRANTON:

APPLICANT: Richards, Ivan
APPLICANT: Mcargen, Jana
APPLICANT: Mcargen, Mcarge
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Sequence 1371, Application US/10923522

Sequence 1371, Application US/10923522

Sequence 1371, Application OS USCO050159381A1

Sequence 1371, Application OS USCO050159381A1

Sequence 1371, Application OS USCO050159381A1

SEQUENCE INCOMPATION: Application James

APPLICANT: Sina Therapeutics, Inc.

APPLICANT: Chowrira, Bharat

APPLICANT: Conversion James

APPLICANT: Beigelman, Leonid

TITLE OF INVENTION: The Expression Using Short Interfering Nucleic Acid (sina)

FILE REFERENCE: 400/192 (MBHB03-026-B)

FILE REFERENCE: 2004-08-20

CURRENT FILING DATE: 2004-08-20

PRIOR APPLICATION NUMBER: PCT/US 03/05234
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1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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ORGANISM: Artificial Sequence
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5 GUUUUUCCUUGUAUU 19
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Search completed: August 19, 2005, 10:59:40 Job time : 13 secs
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   370 CCTTGTGTTGGCAGG 384
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                                                                                                                                                                                                  Gaps
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1779
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1547
LENGTH: 19
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                                                                                                                                                                Query Match 1.2%; Score 13.4; DB 1; Length 19; Best Local Similarity 93.3%; Pred. No. 3.1e+02; Matches 14; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                    ; Sequence 66, Application US/10864044; Publication No. US20050171040A1; GENERAL INFORMATION:
                                                                          TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                            958 CTGGACCCAGGACAT 972
||||||||||||||||||||||15 CTGGACTCAGGACAT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                         FEATURE:
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US-10-68-4044-66

US-10-68-4044-66

Sequence 166, Application US/10864044

Publication No. US20050171040A1

GREREAL INRORANITON:
APPLICANT: SITUAT Therapeutics, Inc.
APPLICANT: SITUAT Therapeutics, Inc.
APPLICANT: House, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Cholesteryl Ester Transfe
TITLE OF INVENTION: Procein (CEPT) Gene Expression Using Short Interfering Nucleic /
TITLE OF INVENTION: Procein (CEPT) Gene Expression Using Short Interfering Nucleic /
TITLE OF INVENTION: (siAN)
TITLE OF INVENTION NUMBER: US 10/826,966
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THOR FILING DATE: 2004-01-14
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THOR APPLICATION NUMBER: PCT/US03/0536
THOR TILING DATE: 2003-02-20
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THOR TILING DATE: 2 ö , OTHER INFORMATION: Description of Artificial Sequence: Target/siNA sense US-10-864-044-166 Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 326 . 0 Query Match 1.2%; Score 13.4; DB 1; Length 19; Best Local Similarity 60.0%; Pred. No. 3.1e+02; Matches 9; Conservative 5; Mismatches 1; Indels

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OM nucleic - nucleic search, using sw model

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August 19, 2005, 10:54:17; Search time 6 Seconds (without alignments) 2.738 Million cell updates/sec

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Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 0.5

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                                                 APPLICANT: HESS, JOHN W.
APPLICANT: HESS, JOHN W.
APPLICANT: HIU, QINGYUN
APPLICANT: LIU, QINGYUN
APPLICANT: PHILLIPS, MICHAEL SEAN
TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOANNE M. GIESSER - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: AFFWETIX, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
                                                                                                                                                                                                                                                                                                                     100.0%; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-09-396-196G-107033/c
; Sequence 107033, Application US/09396196G
; Parent No. 6821724
; GENERAL INFORWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GIESSER, JOANNE M
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19642Y
TELECHOMONICATION INFORMATION:
TELEFHONE: 732-594-3046
       Sequence 51, Application US/08803346; Patent No. 6281346; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 TCGTGGCATTATCCTTCAG 108
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 19 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                          ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                        CITY: RAHWZ
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-803-346-51
JS-08-803-346-51
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                                                                                                                                                                                                                                                                                        Query Match
1.7%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HESS, JOHN W.
APPLICANT: HESS, JOHN W.
APPLICANT: CASKEY, C. THOMAS
APPLICANT: LIU, QINGYUN
APPLICANT: PHILLIPS, MICHAEL SEAN
ITITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 77
CORRESPONDENCES: 77
ADDRESSEE: JOANNE M. GIESSER - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE --P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-09-396-125800
; Sequence 125800, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Mitcheal Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; WINGER OF SEQ ID NOS: 127806
; SEQ ID NO 125800
; LENGTH: 25
; LENGTH: 25
; LENGTH: 25
; LENGTH: 25
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSED for Windows Version 4.0
SEQ ID NO 17033
LENGTH: 25
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COMPUTER READABLE FORM:
                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-107033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CORGANISM: mus musculus
US-09-396-196G-125800
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STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-803-346-50
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         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESEQ for Windows Version 2.0
CURRNT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,346
FILING DATE: 20-FEB-1997
CLASSIFCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.6%; Score 18; DB 1;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-008-180-562-30/C

1 Sequence 30, Application US/08780562

Patent No. 6541604

GENERAL INFORMATION:

APPLICANT: Matthews, William

APPLICANT: Bennett, Brian

ITILE OF INVENTION:

WUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTY: COUNTY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P0986R1
                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GIESSER, JOANNE M
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 1964
TELECOMUNICATION INFORMATION:
TELEPHONE: 732-594-3046
TELEPHONE: 732-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08/585005
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585'
FILING DATE: 01/08/97
PRIOR APPLICATION NUMBER: 60/
FILING DATE: 01/08/97
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
LENGTHE: nucleic acid
STRANDEDNESS: single
Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: CDNA
US-08-803-346-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
  MEDIUM TYPE:
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1 GCTGGGATGTGCCTTAGA 18

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TYPE: DNA
CORGANISM: Mus musculus
US-09-396-196G-20048
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                                                                                                                                                                                                               1.6%; Score 18; DB 1; Length 18; 100.0%; Pred. No. 17; trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,562
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31, Application US/08780562

Patent No. 6541604

GENERAL INFORMATION:
APPLICANT: Matthews, William
APPLICANT: Bennett, Brian
TITLE OF INVENTION: WSX RECEPTOR
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DALL
ATTORNEY/AGENT INFORM.
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986R1
TELECOMMUNICATION INFORMATION:
TELEFAX: 415/225-1994
TELEFAX: 415/225-1994
TELEFAX: 415/922-9881
TELER: 910/31-7168
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: Nucleic Acid
TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P0986R1
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TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                 136 GCTGGGATGTGCCTTAGA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/5850
FILING DATE: 01/08/97
PRIOR APPLICATION NUMBER: 60/
FILING DATE: 01/08/97
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                        18 GCTGGGATGTGCCTTAGA 1
                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.C
Matches 18; Conservative
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US-08-780-562-31
                                                                                                                                                              Linear
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US-08-780-562-30
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US-08-780-562-31
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136 GCTGGGATGTGCCTTAGA 153

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RESULT 8

US-08-222-177A-296

US-08-222-177A-296

Sequence 295, Application US/08222177A

Patent No. 5582979

GENERAL INPORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CORRESPONDENCE: 460

CORRESPONDENCE ADDRESS:
ADDRESSER: Dewitt Ross & Stevens, S.C.
STREET: Wisconsin
COUNTRY: USA

ZIP: 53717-1914

COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: USA

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/222,177A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
US-09-196-196G-20048/C
US-09-196-196G-20048/C
Sequence 20048 Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT FILING DATE: 1999-09-15
CURRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FRSLSEQ for Windows Version 4.0
SEQ ID NO 20048
LEAGTH: 25
LEAGTH: 2
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REPERSINCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          957 TCTGGACCCAGGACATTTTGATGA 980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.6
Best Local Similarity 83.3
Matches 20; Conservative
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RESULT 10
US-08-836-261A-72
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LENGTH: 21
                                                                                                                                                                                                                                                                                                                               STATE:
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                                                                                                                                                                              1.5%; Score 16.2; DB 1; Length 21; 85.7%; Pred. No. 41; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 21;
                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 600, Application US/08117952
; Patent No. 5851760
; GENERAL INFORMATION:
    APPLICANT: Evans, Glen A.
    TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE; TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES; NUMBER OF SEQUENCES; 797
; CORRESPONDENCE ADDRESS:
    ADDRESSER: Pretty, Schroeder, Brueggemann & Clark STREET: Los Angeles
    CITY: Los Angeles
    CITY: Los Angeles
    CATATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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BEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,952
PLING DATE: 10.76PF-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/471
FILING DATE: 15-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Relear. Stephen E.
REGISTRATION NUMBER: 91,192
REFERENCE/DOCKET NUMBER: P41,9423
TELEPHONE: 619-546-437
TELEPHONE: 619-546-437
INFORMATION FOR SEQ ID NO: 600:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: NORLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
1.5%; Score 16.2; DB 1;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 41;
0; Mismatches
                                                                                                                                                                                                                                                              513 ATCTGTATACATGTGCACATG 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513 ATCTGTATACATGTGCACATG 533
                                                                                                                                                                                                                                                                                         1 ATCTGTATATATGTGTACCTG 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: Oligonucleotide
HYPOTHETICAL: NO
                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: mfd90p2
US-08-222-177A-296
                                                                                                                                                                            Query Match
Best Local Similarity 85.7<sup>1</sup>
Matches 18; Conservative
21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SENSE:
US-08-117-952-600
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Sequence 72. Application US/08836261A
Fatent No. 6221582
GENERAL INFORMATION:
APPLICANT: QUINT, WILHELMUS
APPLICANT: QUINT, WILHELMUS
TITLE OF INVENTION: NEW POLYNUCLEIC ACID SEQUENCES FOR USE IN THE TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF PROKARYOTIC ORGANISMS
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSER: ARNOLD, WHITE & DURKEE
STREET: PO. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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COMPUTER: 16AAS

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: 1BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MICROSIC WOLD 6.0 / ASCII text output

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836,261A

FILING DATE: 25 Apr 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/04264

FILING DATE: 30 Oct 1995

FILING DATE: 28 Oct 1995

PILING DATE: 28 Oct 1994

ATTORNEY/AGENT INFORMATION:

NAME: KAMMERER, PATRICIA A.

REFERENCE/DOCKET NUMBER: 29,775

INFORMATION FOR SEQ ID NO: 72:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Meyand, COTHELIA M.
TITLE OF INVENTION: REMEMBATIOD ARTHRITIS MARKERS
FILE REFERENCE: 07039-251001
CURRENT APPLICATION NUMBER: US/09/816,814
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.4%; Score 15.8; D
Best Local Similarity 89.5%; Pred. No. 49;
Matches 17; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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                                                                                                                                                                                                                                                                                                          CITY: HOUSTON
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DB 1; Length 18;
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                                1; Indels
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Sequence 65, Application PC/TUS9406331A
GENREAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: METHOD AND RAGENT FOR TITLE OF INVENTION: PIBROUS TISSUE DISEASE
NUMBER OF SEQUENCES: 67
CORRESPONDENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Liyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Cyclin B1 xibozyme binding site US-09-696-791-3309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 90017
COMPUTER REALABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: IBM MS-DOS (Version 5.0) SOFTWARE: WOORDPEFECT (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/06331A FILING DATE: June 2, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 94.1%; Pred. No. 58;
Matches 16; Conservative 0; Mismatches
Query Match
1.4%; Score 15.4; 1
Best Local Similarity 94.1%; Pred. No. 57;
Matches 16; Conservative 0; Mismatches
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PRIOR APPLICATION DATA: incl
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            790 TGTGCTTGGAGAGGCAG 806
                                                                       104 TICAGIGGGCTATIGG 120
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                                                                                                      2 TTCAATGGGGCTATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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CLASSIFICATION:
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NAME/KEY: primer_bind

LOCATOR: 1..18

LOCATOR: 1..18

CONTEX INFORMATION: downstream amplification primer 99-21246 for SEQ 3795, in complem
US-09-422-978-11660
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Sequence 11660, Application US/09422978

Patent No. 6537751

GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET. 020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
CURRENT PILING DATE: 1999-10-20
CURRENT PLING DATE: 1999-11-23

EARLIER FILING DATE: 1999-11-23

EARLIER FILING DATE: 1998-11-23

EARLIER FILING DATE: 1998-04-21

EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 11660
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                                                                                                                                                                                           DB 1; Length 22;
                                               Query Match 1.4%; Score 15.8; DB 1; Length 21; Best Local Similarity .89.5%; Pred. No. 49; Matches 17; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.4%; Score 15.8; D
Best Local Similarity 89.5%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337 TCGTGTGCTGTGATCAAA 355
; OTHER INFORMATION: primer for PCR US-09-816-814-7
                                                                                                                          38 GCCGGAAGCAGCCGCGGCC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 rcgreregerierrerean 1
                                                                                                                                                       21 GCTGGAAGCAGCCGTGGCC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: DNA primer US-09-792-024-382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo Sapiens
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                                                                                                                   ; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium ; OTHER INFORMATION: diernhoferi US-09-980-052-219
                                                                                                                                                                                                                                                                                                                    Gaps
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; Sequence 15. Application US/09280799
; Patent No. 6136603
; GREMEAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marras, James G
; APPLICANT: Marras, James G
; TITLE OF INVENTION: TRANSDUCTION
; TITLE OF INVENTION: TRANSDUCTION
; FILE REFERENCE: ISPH-0340
; CURRENT APPLICATION NUMBER: US/09/280,799
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 690, Application US/09657472
; Sequence 690, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Daley, George Q.
; APPLICANT: Michele
; APPLICANT: Michele
; APPLICANT: Bolk, Stacey
; APPLICANT: Michele
; TILLE OF INVENTYON: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT FILING DATE: 2000-09-07
; FRIOR APPLICATION NUMBER: US 60/153,357
; FRIOR PILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; FRIOR APPLICATION NUMBER: US 60/225,724
; FRIOR PILING DATE: 2000-09-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE FREESE FREESEQ for Windows Version 4.0
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1.4%; Score 15.2; I
Best Local Similarity 85.0%; Pred. No. 65;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                1.4%; Score 15.2; I
85.0%; Pred. No. 64;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     998 TGCACATGAAAGTTTGAGAA 1017
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                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 21
US-09-657-472-690/c
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LENGTH: 20
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Sequence 219, Application US/09980052

Patent NO. 6670130

GENERAL INFORMATION:

APPLICANT: KIM, Cheol Min

APPLICANT: KIM, Cheol Min

APPLICANT: KIM, Cheol Min

APPLICANT: RIM, Cheol Min

APPLICANT: PARK, Hee Kyung

TITLE OF INVENTION: Oligonuclectide for detection and identification of Mycobacteria

FILE REFERENCE: PPO5020/PCT

CURRENT APPLICATION NUMBER: US/09/980,052

CURRENT APPLICATION NUMBER: KR 10-1999-0019631

PRIOR FILING DATE: 1999-05-29

PRIOR PILING DATE: 1999-05-29

PRIOR PILING DATE: 1999-05-29

PRIOR FILING DATE: 1999-05-29

PRIOR PILING DATE: 1999-05-39

PRIOR PILING DATE: 1999-05-39
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Sequence 6064, Application US/09198452A

Sequence 6064, Application US/09198452A

Sequence 6064, Application US/09198452A

GENERAL INPORMATION:

TILE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering Reference: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6819

SEQ ID NO 6064
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                                                                                                                                                                                                                                                                                         DB 1; Length 20;
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                      ; OTHER INFORMATION: Antisense Oligonucleotide US-09-428-584-11
                                                                                                                                                                                                                                                                                      Query Match 1.4%; Score 15.2; D
Best Local Similarity 85.0%; Pred. No. 64;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               459 AGTGGTAGCACTTTATTCTG 478
                                                                                                                                                                                                                                                                                                                                                                                                                          62 TCGGGAGACATGGCGGCGT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 AGCGGTAGCAGTTTCTTCTG 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Chlamydia pneumoniae US-09-198-452A-6064
                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS:
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Best Local Similarity
Matches 17; Conserv
                           SEQ ID NO 11
LENGTH: 20
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GENERAL INFORMATION:

APPLICANT: Brown, Steven Joel
APPLICANT: Brown, Steven Joel
APPLICANT: Dattagupta, Nanibhushan
APPLICANT: Naidu, Yathi M.
TITLE OF INVENTION: METHOD FOR INHIBITING CELLULAR
TITLE OF INVENTION: MRNA
TITLE OF INVENTION: mRNA
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSES: Gen-Probe Incorporated
ADDRESSES: Of Probe Incorporated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/09428584

Sequence 11, Application US/09428584

GENERAL INFORMATION:
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF METHIONINE AMINOPEPTIDASE 2 EXPRESSION
FILLE REFREENCE: RTS-0114
CURRENT APPLICATION NUMBER: US/09/428,584

CURRENT FILING DATE: 1999-10-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
SUBTRAIT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,570
FILING DATE:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/486,408
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: PISHAR CHARLES
                                                                                                                                                                                                                                                                                                                                                      STREET: 9880 Campus Point Drive CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CBI009
                                                                                                                                                        Sequence 14, Application US/08975570 Patent No. 5945336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fisher, Carlos A REGISTRATION NUMBER: 36,510 REFERENCE/DOCKET NUMBER: CB1 TELECOMMUNICATION INFORMATION: 619-535.2807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 CAGGAAGCCGGAAGCAG 48
             32 CAGGAAGCCGGAAGCAG 48
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Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 619-546-7929
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US-09-428-584-11/c
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                                                                                                                        RESULT 17
US-08-975-570-14/c
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US-08-975-570-14
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APPLICANT: Brown, Steven Joel
APPLICANT: Dattagupta, Nanibhushan
APPLICANT: Dattagupta, Nanibhushan
APPLICANT: Naidu, Yakhi M.
TITLE OF INVENTION: METHOD FOR INHIBITING CELLULAR
TITLE OF INVENTION: PROLIFERATION USING ANTISENSE OLIGONUCLEOTIDES TO INTERLEUKIN-
TITLE OF INVENTION: MRNA
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                              Score 15.4; DB 1; Length 19;
Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                               1; Indels
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Best Local Similarity 94.1%; Pred. No. 58;
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTENT READBAILE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COPENATING SYSTEM: DOS
SOFTWARE: FRATSEQ VERSION 1.5
SOFTWARE: FRATSEQ VERSION 1.5
CURRENT APPLICATION NUMBER: US/08/486,408
FILING DATE: 07-UN-1995
CLASSIFICATION NUMBER: BPLICATION NUMBER:
FILING DATE: TISHER: TISHER: FISHER: FISHER: FISHER: FISHER: FISHER: FISHER: FISHER: TRECASTRATION NUMBER: 36,510
REFERENCE/DOCKET NUMBER: GAIOO9
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 619-535-2807
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELERX: 67-3510
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Gen-Probe Incorporated STREET: 9880 Campus Point Drive CITY: San Diego STATE: CA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-486-408-14/c
; Sequence 14, Application US/08486408
; Patent No. 5716846
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LENGTH: 20 base pairs
TYPE: nucleic acid
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Best Local Similarity 94.1
Matches 16; Conservative
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                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-06331A-65
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US-09-277-020-16
US-09-277-020-16
Sequence 16, Application US/09277020
Patent No. 6210892
GENERAL INFORMATION:
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
TITLE OF INVENTION: Of mRNA Processing.
FILE REFERENCE: ISPH-0339
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 09/167,921
SARLIER PILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 65
SEQ ID NO 16
LENGTH: 20
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APPLICANT: The Government of the United
APPLICANT: States of America as represented by the
APPLICANT: Secretary, Department of Health and Huan
APPLICANT: Services; Callahan, Robert; Marchetti,
APPLICANT: Antonio; Buttitta, Finama; Smith, Gilbert H.
TITLE OF INVENTION: Nucleotide And Deduced
TITLE OF INVENTION: Amino Acid Sequences Of A New Tumor Gene,
TITLE OF INVENTION: Infe, And the Use of Reagness Derived From
TITLE OF INVENTION: These Sequences In Diagnostic Assays,
TITLE OF INVENTION: Vaccines, Immunotherapy And Gene Therapy
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                                              ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic US-09-280-799-152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-277-020-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 2; Indels
                                                                                                                       1.3%; Score 14.8; DB 1; Length 20; 88.9%; Pred. No. 77;
                                                                                                                                                                        Indels
                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 345 PARA.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
MEDIUM TYPE: PLOPPY DISK
OMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-875-847B-9/c
; Sequence 9, Application US/08875847B
; Patent No. 6255105
                                                                                                                                                                                                                         1050 ACTTCCTTATCTTTCCAG 1067
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ORGANISM: Artificial Sequence
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                                                                                                                    Query Match
Best Local Similarity 88.99
Matches 16; Conservative
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TITLE OF INVENTION: Inve
TITLE OF INVENTION: Thee
TITLE OF INVENTION: Vacc
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
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Gaps
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Sequence 9, Application US/09378842

BENERAL INFORMATION:
APPLICANT: The Government of the United
APPLICANT: States of America as represented by the
APPLICANT: Services; Callahan, Robert; Marchetti,
APPLICANT: Antonio; Buttltta, fiamm; Smith, Gilbert H.
TITLE OF INVENTION: Nucleotide And Deduced
TITLE OF INVENTION: Amino Acid Sequences Of A New Tumor Gene,
TITLE OF INVENTION: Inte, And the Use Of Reagents Derived From
TITLE OF INVENTION: These Sequences In Diagnostic Assays,
TITLE OF INVENTION: Vaccines, Immunotherapy And Gene Therapy
NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
ADDRESSES: MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 20;
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                                                                          FILING MALE: 07-EB-1390
CLASSIFICATION: 435
PRIOR APPLICATION 1435
APPLICATION NUMBER: 08/385,998
FILING DATE: 09-FEB-1995
CLASSIFICATION: 435
ATTORNEY/ABRIT INFORMATION:
NAME: William S. Feiler
REGISTRATION NUMBER: 26,728
REGISTRATION NUMBER: 26,728
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14.8; D
Pred. No. 77;
0; Mismatches
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                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,847B
FILING DATE: 09-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,847
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: 08/385,998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         926 CITATIAGAAAIGCAGAA 943
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                                                                                                                                                                                                                                                                                                         TELEFAX: (212.)
TELEFAX: (212.)
TELEFAX: 421792
; INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
""OR: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 09-FEB-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       William S. Feiler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 88.9°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
MS WORD 97
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US-08-875-847B-9
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PAPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: BINNES, Barron G.
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: GHANNON, MAIR E.
APPLICANTON NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-01-30
PRIOR PLING DATE: 2001-01-30
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SOFTWARE Acomics Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 2565
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CURRENT APPLICATION NUMBER: US/09/657,472
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/153,357
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2551
SOFTWARE: FateSEQ for Windows Version 4.0
SEQ ID NO 1333
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-866-108A-2565/C
; Sequence 2565, Application US/09866108A
; Patent No. 6686188
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Best Local Similarity 80.0%;
Matches 16; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRGANISM: Homo sapiens US-09-657-472-1733
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Best Local Similarity
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US-09-859-152B-9/C

US-09-86-152B-9/C

Sequence 9, Application US/09858152B

Patent No. 6/37251

GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
APPLICANT: HUMAN SERVICES
APPLICANT: Marchetti, Antonio
APPLICANT: Marchetti, Antonio
APPLICANT: Smith, Gilbert H.
APPLICANTON: NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF TUMOR GENE INTE
CURRENT FILING DATE: 2001-05-14

NUMBER OF SEQ ID NOS: 36

SOSTWARE PATENTING DATE: 2001-05-14

NUMBER OF SEQ ID NOS: 36

SOSTWARE PATENTING DATE: PATENTI
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Sequence 1733, Application US/09657472

Patent No. 6727063

GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Treland, James S.
APPLICANT: Treland, James S.
APPLICANT: Daley, George Q.
APPLICANT: MCCATCHY, Jeanette J.
APPLICANT: MCCATCHY, Jeanette J.
APPLICANT: MCATCHY, Jeanette J.
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88.9%; Pred. No. 77;
tive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.3%; Score 14.8; Best Local Similarity 88.9%; Pred. No. 77; Matches 16; Conservative 0; Mismatches
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O OTHER INFORMATION: Oligonucleotide primer
US-09-858-152B-9
                                  REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4179PCT
TELECOMMUTICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  926 CTTATTAGAAATGCAGAA 943
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                         TELEX: 421792
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLIGY: linear
US-09-378-842-9
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Best Local Similarity
Matches 16; Conserv
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US-09-696-791-3308/c
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LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                     APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
PILE REFERENCE: AEOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT FILING DATE: 2001-05-25

PRIOR PELICATION NUMBER: US 60/207,456

PRIOR PELICATION NUMBER: US 60/207,456

PRIOR PELING DATE: 2000-05-25

PRIOR PELING DATE: 2000-01-00-40

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR PILING DATE: 2000-09-27

PRIOR PELING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30
      Gaps
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   1; Indels
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Patent No. 6770461
GENERAL INFORMATION:
APPLICANT: Carulli, John P.
APPLICANT: Little, Randall D.
APPLICANT: Recker, Robert R.
APPLICANT: Heady Mark L.
TITLE OF INVERTION: High bone mass gene of 11q13.3
FILE REFERENCE: 032796-013
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 2566
                                                                                                                                                                                              RESULT 29
US-09-866-108A-2566/C
Sequence 2566, Application US/09866108A
Parent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
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                                                         743 AGGCAGCTGCCACCTT 758
                                                                                                            17 AGGCAGCTGCCCCTT 2
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15; Conservative
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ORGANISM: Homo sapiens
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Matches
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GENERAL INFORMATION:
APPLICANT: Robbins, Joan M.
APPLICANT: Robbins, Joan M.
APPLICANT: Tritz, Richard
TITLE OF INVENTION: RIBBATE THERAPY FOR THE TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: SKIN AND EXE DISEASES
FILE REFERENCE: 480124.407
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Little, Randall D.
APPLICANT: Lottle, Randall D.
APPLICANT: Recker, Robert R.
APPLICANT: Recker, Robert R.
TITLE OF INVENTION: High bone mass gene of 11q13.3
FILE REFERENCE: 032796-014
CURRENT APPLICATION NUMBER: US/09/543,771B
CURRENT APPLICATION NUMBER: US 09/229,319
PRIOR PILLING DATE: 1999-01-13
FRIOR PILLING DATE: 1999-01-13
FRIOR PILLING DATE: 1999-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: Cyclin B1 ribozyme binding site
US-09-696-791-3308
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.3%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 1;
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Pred. No. 91;
0; Mismatches
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US 09/229,319
PRIOR FILING DATE: 1999-01-13
PRIOR FILING DATE: 1999-01-13
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 641
SOFTWARE: PASCESEQ for Windows Version 4.0
SEQ ID NO 588
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3308, Application US/09696791
Patent No. 6770633
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-544-398B-588
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ORGANISM: Homo sapiens
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RESULT 35
US-09-953-318-37
is Gauence 37, Application US/09953318

Sequence 37, Application US/09953318

Sequence 37, Application US/09953318

SERVERAL INFORMATION:
APPLICANT: Andrew T. Watt

APPLICANT: C. Frank Bennett

APPLICANT: Andrew T. Watt

TITLE OF INVENTION: EXPRESSION

STILE REFERENCE: 2001-09-13

NUMBER OF SEQ ID NOS: 154

SEQ ID NO 37

LENGTH: 20

LENGTH: 20

LENGTH: 20
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US-09-917-963-91/C
US-09-917-963-91/C
Sequence 91, Application US/09917963
Sequence 91, Application US/09917963
GENERAL INFORMATION:
APPLICANT: Mark J. Graham
APPLICANT: Mark J. Graham
TITLE OF INVENTION: ARTHSENSE MODULATION OF MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN
TITLE OF INVENTION: ARTHSENSE: US/09/917,963
TITLE OF INVENTION NUMBER: US/09/917,963
CURRENT APPLICANTON NUMBER: US/09/917,963
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 137
SEQ ID NO 91
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.3%; Score 14.4; DB 1; Length 20;
93.8%; Pred. No. 92;
tive 0; Mismatches 1; Indels
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                                                                                                                 Indels
                                                           Query Match
Best Local Similarity 93.8%; Pred. No. 92;
Matches 15; Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.3%; Score 14.4; L
Best Local Similarity 93.8%; Pred. No. 92;
Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .; OTHER INFORMATION: Antisense Oligonucleotide US-09-953-318-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 TCTTATGCTGGGATGT 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 rcrrardcrddcardr 3
                                                                                                                                                                             287 TICACIACIGGAATIG 302
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                             19 TTCACTACGGGAATTG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 93.8<sup>1</sup>
Matches 15; Conservative
                           US-09-198-452A-1803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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US-09-198-452A-1803/c
Sequence 1803, Application US/09198452A
Sequence 1803, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: GTIffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: 1996-199
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1803
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6795, Application US/09422978

Sequence 6795, Application US/09422978

Patent No. 6537751

GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
TITLE OF INVENTION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-04-21
CURRENT FILING DATE: 1999-04-21
SARLIER FILING DATE: 1999-04-21
EARLIER PILING DATE: 1998-11-23
SARLIER FILING DATE: 1998-11-23
SARLIER FILING DATE: 1998-11-23
SARLIER FILING DATE: 1998-14-21
SARLIER FILING DATE: 1998-14-21
SARLIER FILING DATE: 1998-14-21
SARLIER FILING DATE: 1998-04-21
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; OTHER INFORMATION: upstream amplification primer 99-19464 for SEQ 2861,
US-09-422-978-6795
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1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 92;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                Query Match 1.3%; Score 14.4; DB 1; Length 19; Best Local Similarity 93.8%; Pred. No. 91; Matches 15; Conservative 0; Mismatches 1; Indels
        PRIOR APPLICATION NUMBER: US 60/105,511
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 641
SOFTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 588
LENGTH: 19
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 TTCATTGCCAAAAGAG 233
                                                                                                                                                                                                                                                                                                                                                                                  295 TGGAATTGTTGTTTCT 310
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                        ; ORGANISM: Homo sapiens US-09-543-771B-588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 33
US-09-422-978-6795
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APPLICANT: DE BLAS BEORLEGII, Carmen
APPLICANT: DE BLAS BEORLEGII, Carmen
APPLICANT: DONS ASCASO, Ferrando
APPLICANT: TORRES PASCUAL, Vicente
TITLE OF INVENTION: PROCEDURE FOR THE DETECTION AND
TITLE OF INVENTION: IDENTIFICATION OF VIRAL AND SUBVIRAL PATHOGENS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
STREET: 1180 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred, No. 1e+02;
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COMPUTER: TOUGH
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: TBM PC 
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1.3%; Score 14.2; D
Best Local Similarity 84.2%; Pred. No. 1e+0
Matches 16; Conservative 0; Mismatches
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; Sequence 9, Application US/08389067
; Patent No. 5714312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 carcrircarcas 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-105-483-336
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COMPUTER READABLE FORM:
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036
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Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Paoletti, Enzo
APPLICANT: Perkus, Marion E.
APPLICANT: Taylor, Jili
APPLICANT: Taylor, Jili
APPLICANT: Taylor, Jili
APPLICANT: Taylor, Jili
APPLICANT: Riviere, Michel
APPLICANT: de Taisne, Charles
APPLICANT: Johnson, Gerard P.
APPLICANT: Johnson, Gerard P.
APPLICANT: Pincus, Steven E.
APPLICANT: Audonnet, Jean-Christophe Francis
APPLICANT: Gettig, Russell Robert
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
GONDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FAPPLICATION NUMBER: US/08/458,101
FILING DATE: 01-JUN 1995
CLASSIFICATION: 424
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ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2740
TELEPHONE: (212) 840-3333
TELEPAX: (212) 840-3333
INFORMATION FOR SEQ ID NO: 336:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Curtis, Morris & Safford ADDRESSEE: c/o William S. Frommer STREET: 530 Fifth Avenue CITY: New York
                                                                                                                                                                                                                                                                                        394 CATITICCTIACAATICAA 412
                                                                                                                                                                                                                                                                                                                1 CATGTTCCTTTCAAGTCAA 19
                TELEPHONE: (312) 840-3333
TELEFAX: (212) 840-0712
INPORMATION FOR SEQ ID NO: 336:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-709-2356
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rypE: nucleic acid
STRANDEDNESS: single
; TOPOLOGY: linear
US-08-458-101-336
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COUNTRY: US
ZIP: 10036
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Similarity 84.2%; Pred. No. 1e+02;
16; Conservative 0; Mismatches 3; Indels
Score 14.2; DB 1; Length 20;
Pred. No. 1e+02;
0; Mismatches 3; Indels
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COMPUTER READABLE FORM:
COMPUTER: 19103
COMPUTER: IBM PS/2
CIASSIFICATION DATA:
APPLICATION NUMBER: 1514
PRIOR APPLICATION NUMBER: 15192
ATTORNEY/AGBNT INFORMATION:
NAME: Rebecca Ralph Gaumond
RESTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: 151S-1154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 86:
SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Account 48 - 177-86/C
; Sequence 86, Application US/08488177
; Sequence 86, Application US/08488177
; Fatent No. 5885970
; Fatent No. 5885970
; APPLICATION: Oligonuclectide Modulation of TITLE OF INVENTION: Protein Kinase C
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                              FESOUR 478-178A-86/C

Sequence 86, Application US/08478178A

Sequence 86, Application US/08478178A

Patent No. 5882927

GENERAL NIFORMATION:

APPLICANT: Nicholas Dean, C. Frank Bennett

TITLE OF INVENTION: Oligonuclectide Modulation of

TITLE OF INVENTION: Proctein

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5882927ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
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             1.3%;
                  Query Match
Best Local Similarity 84.23
Matches 16; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: Yes
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USA
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Best Local Simi]
Matches 16; (
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566 TTTTTAATACCTTTATAT 584
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Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 20
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY:
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-481-072A-86
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Sequence 24, Application US/08634350
Fatent No. 2911982
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FITLE OF INVENTION:
TITLE OF INVENTION:
TOWNERS OF SEQUENCES:
CORRESPONDENCE ADDRESS:

ADDRESSEE: CULTIS, MOTTIS & Safford, P.C.
                                                                                                                   COUNTRY: USA
ZIP: 19103
ZIP: 19103
COMPUTER READBLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDFREECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,177
FILING DATE: O7-UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 184,852
FILING DATE: March 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 138,534
REFERENCE/DOCKET NUMBER: 138,534
REFERENCE/DOCKET NUMBER: 13,534
REFERENCE/CONTENTION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHOME: (215) 568-3100
TELECHOME: (215) 568-3100
TELECHOME: (215) 568-3100
TELECHOME (215) 568-3100
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BY SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,350
FILING DATE: 18-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 530 Pifth Avenue CITY: New York
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: MacKiewicz & No. 5885970ris
STREET: One Liberty Place - 46th Floor
CITT: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: United States of America
ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ANTI-SENSE: yes
US-08-488-177-86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1e+02; tive 0; Mismatches 3; Indels
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ZIP: 19103
COMPUTER READBLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,072A
FILING DATE: herewith
CLASSIFICATION NUMBER: B52,852
FILING DATE: March 16, 1992
ATTORNEY APPLICATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: 35,153
RELEPHONE: (215) 568-3100
TELLEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-481-072A-86/c
; Sequence 86, Application US/08481072A
; Patent No. 5918607
; GRNERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett
; TITLE OF INVENTION: Oligonuclectide Modulation of
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Moodcock Washburn Kurtz
ADDRESSE: Moodcock Washburn Kurtz
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.3%; Score 14.2; D
Best Local Similarity 84.2%; Pred. No. 1e+0
Matches 16; Conservative 0; Mismatches
NAME: Lawrence, William F.
REGISTRATION NUMBER: 28,029
REFRENCE/DOCKET NUMBER: 516450-2008
FELECOMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
FELEFRA: (212) 840-0712
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0.3
Dest Local Similarity 84.2
Matches 16; Conservative
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STRANDENNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: Yes
US-08-481-066A-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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US-06-664-336-86/C
Sequence 86, Application US/08664336
Sequence 86, Application US/08664336
Sequence 86, Application US/08664336
Series No. 5922686
FRIERAL INFORMATION:
TITLE OF INVENTION: Oligonucleotide Modulation of Protein TITLE OF INVENTION: Oligonucleotide Modulation of Protein NUMBERS OF SEQUENCES:
ADDRESSEE: Moodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5922686ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STREET: One Liberty Place - Afth Floor
STREET: One Liberty Place - Afth Floor
STREET: DANS TREET: DONN
STREET: DANS TREET: DANS TREET:
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Pred. No. 1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READMALE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 720 kb STORAGE
COMPUTER: IEM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/664,336
FILING DATE: Herewith
CLASSIFICATION STA
FILING DATE: Herewith
CLASSIFICATION NUMBER: 052,852
FILING DATE: March 16, 1992
FILING DATE: March 16, 1992
FILING DATE: July 9, 1993
ATTORNEY/AGENT INFORMATION:
NAME: PAPLICATION NUMBER: 089,996
APPLICATION NUMBER: 151S-2345
FEFERENCE/DOCKET NUMBER: 181S-2345
REFERENCE/DOCKET NUMBER: 181S
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Sequence 86, Application US/08481066A
Sequence 86, Application US/08481066A
Sequence 86, Application US/08481066A
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonuclectide Modulation of
TITLE OF INVENTION: Protein Kinase C
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Moodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5959096ris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
1.3%; Score 14.2; D
Best Local Similarity 84.2%; Pred. No. 1e+0
Matches 16; Conservative 0; Mismatches
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434 AGAGGAGATGATTTTAGCT 452
                                                                                            19 AGAGAAGAGGATTTTGGCT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; STRANDEDNESS: Bir; TOPOLOGY: linear; ANTI-SENSE: yes US-08-664-336-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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US-08-518-615A-94/C

US-08-578-615A-94/C

Sequence 94, Application US/08578615A

Sequence 94, Application US/08578615A

Sequence 94, Application US/08578615A

Sequence 94, Application US/08578615A

GENERAL INFORMATION:
TITLE OF INVENTION: Oligonuclectide Modulation of Protein KinaseC

TITLE OF INVENTION: Oligonuclectide Modulation of Protein KinaseC

TITLE OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
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84.2%; Pred. No. 1e+02;
tive 0; Mismatches 3; Indels
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COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,615A
FILING DATE: 11-JAN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 052,852
FILING DATE: 16-MAR-1992
FILING DATE: 16-MAR-1993
APPLICATION NUMBER: 08/089,996
FILING DATE: 22-FEB-1994
FILING DATE: 22-FEB-1994
                                                                                                                                                                     ZIP: 19103
ZIP: 19103
ZEP: 19103
COMPUTER READABLE FORM:
MEDIUM TYBE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
SOPETARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION: 514
FILING DATE: herewith
FILING DATE: March 16, 1992
ATTORNEY/AGENI INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
REJECTATION NUMBER: 35,152
REJECTATION NUMBER: 35,152
REJECTATION NUMBER: 35,153
REJECTATION NUMBER: 35,154
REJECTATION NUMBER: 151S-1154
REJECTATION NUMBER: 35,153
REJECTATION NUMBER: 151S-1154
STREET: One Liberty Place - 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434 ACAGGAGATGATTTTAGCT 452
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Sequence 86, Application US/08829637A

Sequence 86, Application US/08829637A

Patent No. 6339066

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Phillip Dan Cook

APPLICANT: Claim Hoke

TITLE OF INVENTION: PHOSPHOROTHIOATE LINKAGES OF HIGH CHIRAL PURITY AND

TITLE OF INVENTION: PHOSPHOROTHIOATE AI, aII, k, n, AND ISOFORMS OF

TITLE OF INVENTION: PROTEIN KINASE C

NUMBER OF SEQUENCES: 136

CORRESPONDENCE ADDRESS:

ADDRESSEE: Washburn Kurtz Mackiewicz & No. 6339066ris

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

CITY: Philadelphia
                                                                                                    Gaps
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                                                      Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUMING.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MD STORAGE
COMPUTER: IBM PS/2
PS-DOS
                                              Score 14.2; DB 1;
Pred. No. 1e+02;
                                                 Query Match
1.3%; Score 14.2; Di
Best Local Similarity 84.2%; Pred. No. 1e+0:
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COPERATING SYSTEM: PC-DOS
SOCTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,637A
FILING DATE: herewith
CLASSIFFCATION: S14
PRIOR APPLICATION NUMBER: US 08/481,066
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/40,129
FILING DATE: 06-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,851
FILING DATE: 06-UN-1995
PRIOR APPLICATION NUMBER: US 08/469,569
FILING DATE: 06-UN-1995
PRIOR APPLICATION NUMBER: US 08/469,569
FILING DATE: 06-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/089,996
FILING DATE: 09-UL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/58,023
FILING DATE: 05-WAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/777,007
FILING DATE: 16-COT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/777,007
FILING DATE: 16-COT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/777,007
FILING DATE: 16-COT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/829,637A
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                                                                                                                                                      800 GAGGCAGATAACGCTGAAG 818
                                                                                                                                                                                            19 GAGGAAGATGACTCTGAAG 1
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                             RESULT 50
US-08-829-637A-86/c
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     US-09-433-699-36
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GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Elizabeth J. Ackermann

APPLICANT: Lex M. Cowsert

TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSIC

FILE REFERENCE: RTS-0072

CURRENT APPLICATION NUMBER: US/09/392,580

CURRENT FILING DATE: 1999-09

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 12

LENGTH: 20
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Patent No. 6165786
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. COWSETT
TITLE OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION
CURRENT APPLICATION NUMBER: US/09/433,699B
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 89
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1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Antisense Oligonucleotide US-09-392-580-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Antisense Oligonucleotide
               REGISTRATION NUMBER: 39,534
REGISTRATION NUMBER: 39,534
REPERENCE/DOCKET NUMBER: 1818-1568
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-34.99
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI SENSE: yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09392580 Patent No. 6087173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434 AGAGGAGATGATTTTAGCT 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 TATTTTCAAGAGAAGATGA 2
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ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 48
US-09-392-580-12/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-433-699-36/c
                                                                                                                                                                                                                                                                                                                                                   US-08-578-615A-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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US-09-668-313A-208/c
US-09-668-313A-208/c
US-09-668-313A-208/c
Sequence 208, Application US/09668313A
Sequence 208, Application US/09668313A
Sequence 208, Application US/09668313A
APPLICANT: Brate P. Monia
APPLICANT: Gusan M. Freder
APPLICANT: Jacqueline Wyatt
TITLE REPRENCE: RTS-0127
CURRENT APPLICATION NUMBER: US/09/668,313A
CURRENT FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 247
SEQ ID NO 208
LENTH: 20
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LOCATION: 1..20

OTHER INFORMATION: downstream amplification primer 99-449 for SEQ 1544, in complem

US-09-422-978-9409
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US-09-422-978-9409/c
; Sequence 9409, Application US/09422978
; Sequence 9409, Application US/09422978
; Patent No. 6537751
; Patent No. 6537751
; Patent No. 6537751
; PAPLICANT: Cohen, Daniel
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; CURRENT APPLICATION NUMBER: US/09/422, 978
; CURRENT PILING DATE: 1999-10-20
; CURRENT PILING DATE: 1999-10-20
; CARLIER PILING DATE: 1998-11-23
; EARLIER FILING DATE: 1998-11-23
; EARLIER FILING DATE: 1998-04-21
; RARLIER FILING DATE: 1998-04-21
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                                                                                                                            Query Match
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Antisense Oligonucleotide US-09-668-313A-208
                                                       ; OTHER INFORMATION: Antisense Oligonucleotide US-09-792-594-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              932 AGAAATGCAGAATCTGAAG 950
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ORGANISM: Artificial Sequence
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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US-09-851-520-4
Sequence 4, Application US/09851520
Patent No. 639379
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
CURRENT APPLICATION NUMBER: US/09/851,520
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 4
LENGTH: 20
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GENERAL INFORMATION:

APPLICANT: DAID T. Ward

APPLICANT: DAID T. Wath

TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL4 EXPRESSION

TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL4 EXPRESSION

TITLE OF INVENTION: NUMBER: US/09/792,594

CURRENT FILING DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 89

SEQ ID NO S7

LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.3%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 1e+02; Mismatches 16; Conservative 0; Mismatches 3; Indels
       APPLICATION NUMBER: US 07/566,977 FILING DATE: 13-AUG-1990 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/436,358 FILING DATE: 11-JAN-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 57, Application US/09792594; Patent No. 6436706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          822 GCCTCTCATGACCCAGGAA 840
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                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
REFERENCE/DOCKET NUMBER: ISIS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INPORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 AGAGAAGAGGATTTTGGCT 1
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: PCR Primer US-09-851-520-4
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
; TOPOLOGY: linear
JANTI-SENSE: yes
US-08-829-637A-86
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Sequence 4121, Application US/09198452A

Sequence 4121, Application US/09198452A

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Griffals, R.
APPLICANT: Griffals, R.
APPLICANT: Griffals, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevs
TITLE OF INVENTION: and treatment of infection
FILE REPERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
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Pred. No. 1e+02;
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940 AGAATCTGAAGCCCCACTC 958
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; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5159
                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3%;
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Best Local Similarity 84.2%;
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Best Local Similarity 84.2*
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US-09-198-452A-5166
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                                                                                                                US-09-198-452A-4121
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                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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Patent No. 6559294
GEMERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preverint BREERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT PILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 2125
LENGTH: 20
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                                                      Indels
                Score 14.2; DB 1;
Pred. No. 1e+02;
              Query Match
1.3%; Score 14.2; D
Best Local Similarity 84.2%; Pred. No. 1e+0
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                                           Sequence 86, Application US/10025139
Patent No. 6537973
                                                                                          427 ATTIGGAAGAGAGATGAT 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               434 AGAGGAGATGATTTTAGCT 452
                                                                                                                               19 AGTTGGAGGGGGAGATGAT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-2125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 16; Conservative
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US-09-198-452A-2125
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APPLICANT: THE OCHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: THE OCHNS, Saraswati
APPLICANT: SUKUMAR, Saraswati
APPLICANT: SUKUMAR, Salaswati
APPLICANT: BORON, Ella
APPLICANT: DOLEY, Milliam
APPLICANT: DAVIDSON, Nancy
TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
TITLE OF INVENTION: ABERRANTLY METHYLATED
CURRENT FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 110
SEQ ID NO 79
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 1.3%; Score 14.2; DB 1; Length 20; 1 Similarity 84.2%; Pred. No. 1e+02; 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 63
US-09-544-398B-310/c
; Sequence 310, Application US/09544398B
; Patent No. 6770461
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
APPLICANT: Little, Randall D.
APPLICANT: Little, Randall D.
APPLICANT: Necker, Robert R.
APPLICANT: Oblinson, Mark L.
TITLE OF INVENTION: High bone mass gene of 11q13.3
FILE REFERENCE: 032796-013
CURRENT APPLICATION NUMBER: US/09/544,398B
CURRENT FILING DATE: 1999-01-13
FRIOR FILING DATE: 1999-01-13
FRIOR PILING DATE: 1998-01-13
FRIOR RILING DATE: 1998-01-13
FRIOR RILING DATE: 1998-01-13
FRIOR RILING DATE: 1998-01-13
FRIOR RILING DATE: 1998-10-23
; RADIOR FILING DATE: 1998-10-23
; RADIOR FILING DATE: 1908-10-23
; RADIOR FILING DATE: 1908-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FASTERQ for Windows Version 4.0
; LENGTH. ON 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: PCR sense primer US-09-771-357-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              882 AAAAGTGTGGCCCACAGAC 900
                                                                                                                                                   ; Sequence 79, Application US/09771357; Patent No. 6756200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 TTAGAGGATTATGGCGTTT 167
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1 ATTGATTTTCTTCTAACTC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial sequence
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Best Local Similarity 84.2
Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserv
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US-09-544-398B-310
                                                                                                                                        US-09-771-357-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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Sequence 6581, Application US/09198452A

Patent No. 655292104

GREERAL INFORMATION:

APPLICANT: Griffals, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preverting OF INVENTION: and treatment of infection

TITLE OF INVENTION: and treatment of infection

TITLE OF INVENTION: and treatment of infection

GURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT PILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 6581

LENGTH: 20
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; LOCATION: (1)..(20)
; OTHER INFORMATION: reverse PCR primer sequence about 30 bp downstream of VncS SNP
; US-10-054-225-12
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; Sequence 12, Application US/10054225
; Patent No. 6623931
; GENERAL INFORMATION:
; APPLICANT: Saint Under Children's Research Hospital
; APPLICANT: Atkinson, Robyn M
; TITLE OF INVENTION: Diagnostic Assay for Antibiotic Tolerance
; APPLICANT: Atkinson, Robyn M
; TITLE OF INVENTION: Diagnostic Assay for Antibiotic Tolerance
; RIER REPERENCE: 30.01-0022
; CURRENT APPLICATION UNBERS: US/10/054,225
; CURRENT PILING DATE: 2001-11-13
; SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                 Score 14.2; DB 1; Length 20;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                      Query Match 1.3%; Score 14.2; I
Best Local Similarity 84.2%; Pred. No. 1e+C
Matches 16; Conservative 0; Mismatches
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ORGANISM: Streptococcus pneumoniae
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                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CRGANISM: Chlamydia pneumoniae
US-09-198-452A-6581
                                                                                                  TYPE: DNA; Chlamydia pneumoniae; ORCANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 84.2%
Matches 16; Conservative
                           NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 5166
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 60
US-09-198-452A-6581
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US-10-054-225-12
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489 ATTGAATTTCTTAGAACTC 507

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STATE: PA
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PCT-US94-07770-94
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APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: SUKUMAR, Saraswati
APPLICANT: SUKUMAR, Saraswati
APPLICANT: BOOLSY, William C.
APPLICANT: DOOLSY, William C.
APPLICANT: DOOLSY, William C.
TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
FILE REFERENCE: JHU1630-1
CURRENT APPLICATION NUMBER: US/10/059,579A
FILE REPERENCE: JHU1630-1
CURRENT APPLICATION NUMBER: US 09/771,357
FRIOR FILLING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 136
SOFTWARE: PATENT APPLICATION NUMBER: US/10/1,357
FRIOR FILLING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 136
SOFTWARE: PATENT APPLICATION NUMBER: US/10/1,357
SEQ ID NO ?9
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84.2%; Pred. No. 1e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.3%; Score 14.2; DB 1; Length 20;
84.2%; Pred. No. 1e+02;
tive 0; Mismatches 3; Indels
                   Sequence 310, Application US/09543771B
Fatent No. 6780609
GENERAL INFORMATION:
APPLICANT: Carulli, John P.
APPLICANT: Little, Randall D.
APPLICANT: Little, Randall D.
TITLE OF INVENTION: High bone mass gene of 11q13.3
FILE REPERENCE: 032796-014
CURRENT APPLICATION NUMBER: US/09/543,771B
CURRENT APPLICATION NUMBER: 2000-04-05
                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/229,319
PRIOR FILING DATE: 1999-01-13
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: US 60/071,449
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 641
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 310
LENGTH: 20
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Patent No. 6835541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: PCR sense primer
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Matches 16; Conservative
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
-09-543-771B-310/c
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US-10-059-579A-79
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RESULT 66

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Sequence 94, Application PC/TUS9407770
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett and APPLICANT: Russell T. Boggs
ITILE OF INVENTION: Oligonucleotide Modulation of TITLE OF INVENTION: Protein
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 460, Application US/08119492B
Patent No. 561648B
GENERAL INFORMATION:
APPLICANT: Sullivan, Sean M.
APPLICANT: Draper, Kenneth G.
APPLICANT: Brinchowh, Dan T.
ITLE OF INVENTION: REGOTME TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF IL-5
                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT/US94/07770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
APPLICATION NUMBER: 08/089,996
FILING DATE: July 9, 1993
APPLICATION NUMBER: 08/199,779
FILING DATE: February 22, 1994
ATYONEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434 AGAGGAGATGATTTTAGCT 452
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 AGAGAAGAGGATTTTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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Matches 16; Conserv
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US-08-319-492B-460
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US-09-422-978-4185/C
US-09-422-978-4185/C

Sequence 4185, Application US/09422978

Sequence 4185, Application US/09422978

Sequence 4185, Application US/09422978

Sequence 4185, Application US/09422978

GENERAL INFORMATION:
APPLICANT: Chumakov, IIya
APPLICANT: Blumenfeld, Marta
APPLICANT: UNWABER: US/09/422,978

CURRENT FILING DATE: 1999-04-21

EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER PELING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 4185

LENGTH:: 20
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GENERAL INCORPATION.

APPLICANT: Cohen, Daniel

APPLICANT: Chumenfeld, Marta

FILE REFERENCE: GENSET.020CP1

CURRENT PREJIGNON NUMBER: US (09/422,978

CURRENT FILING DATE: 1999-04-21

EARLIER FILING DATE: 1999-04-21

EARLIER FILING DATE: 1998-11-23

EARLIER FILING DATE: 1998-11-3

EARLIER FILING DATE: 1998-11-3

EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NOS: 11796
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LOCATION: 1..20

LOCATION: 1..20

COTHER INFORMATION: upstream amplification primer 99-13853 for SEQ 251,

US-09-422-978-4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
; OTHER INFORMATION: upstream amplification primer 99-5186 for SEQ 1619, US-09-422-978-5553
                                                                                                                                                       Gaps
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1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                           Query Match 1.3%; Score 14; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-422-978-5624; Sequence 5624, Application US/09422978; Patent No. 6537751
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH
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1. Sequence 5553, Application US/09422978

1. Sequence 5553, Application US/09422978

2. Sequence 5553, Application US/09422978

3. Patent No. 6537751

3. Patent INFORMATION:

3. APPLICANT: Chumakov, IIya

4. APPLICANT: Blumenfeld, Marta

APPLICANT: Chumakov, IIya

7. TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

7. TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

7. TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

7. TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

7. TITLE OF INVENTION: Biallelic markers US 00/92/298, 850

EARLIER PLING DATE: 1999-10-20

7. EARLIER PLING DATE: 1999-11-23

7. EARLIER PLING DATE: 1999-04-21

7. NUMBER OF SEQ ID NOS: 11796

7. EARLIER PLING DATE: 1999-04-21

7. NUMBER OF SEQ ID NOS: 11796

7. EARLIER PLING DATE: 1999-04-21

7. NUMBER OF SEQ ID NOS: 11796

7. EARLIER DATE OF NOS: 11796
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                                                                                                                                                                                         COUNTRY:

ZIP: U.S.A.
MEDIUM TYPE: G. D. Diskette, 1.44 Mb
MEDIUM TYPE: G. S. Diskette, 1.44 Mb
MEDIUM TYPE: G. S. Diskette, 1.64 Mb
MEDIUM TYPE: BM Compatible
COMPUTER: IBM Compatible
COMPUTER: Word Perfect 5.1
CURRENT APPLICATION DATA: US/08/319,492B
FILING DATE: October 7, 1994
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 08/008,895
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warblucy, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/276
TELECOMMUNICATION INFORMATION:
                                                633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNE. (213) 485-17.
TELEPHONE: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 46
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 TGACTTTTCTTATG 136
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PRGANISM: Homo Sapiens
PEATURE:
NAME/KEY: primer_bind
LOCATION: 1..18
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                                                                                                                Los Angeles
California
                                                                                                                                                                          U.S.A.
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US-08-319-492B-460
                                                            STREET: 6
STREET: S
CITY: LOB
STATE: Ca
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RESULT 73
US-08-219-842-12/c
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                                                                                                                                                                                                                                                                                                                                US-09-665-615B-156/C

Sequence 156, Application US/09665615B

Patent No. 6653133

GRENERAL INFORMATION:
APPLICANT: Watt, Jacqueline
APPLICANT: Watt, Jacqueline
TITLE OF INVENTION: Antieense Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0502
CURRENT APPLICATION NUMBER: US/09/665,615B
CURRENT FILING DATE: 1909-04-12
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 179
SOFTWARE: PatentIN Ver. 2.0
LENGTH: 20
NAME/KEY: primer_bind

| LOCATION: 1..20

| OTHER INFORMATION: upstream amplification primer 99-5681 for SEQ 1690,

US-09-422-978-5624
                                                                                                                                                                   Gaps
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Sequence 55, Application US/10172911

Patent No. 6743909

GENERAL INCORNATION:

APPLICANT: Lear M Cowsert

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF PTPN12 EXPRESSION

FILE REPERENCE: PTS-0016

CURRENT APPLICATION NUMBER: US/10/172,911

CURRENT FILING DATE: 2002-06-17

NUMBER OF SEQ ID NOS: 123

SEQ ID NO 55

LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.3%; Score 14; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                 Ouery Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.18+02;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-665-615B-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-172-911-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                               324 CTGTTATTCTTGCT 337
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Gaps
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Sequence 12, Application US/08219842

Patent No. 5565323

GENERAL INFORMATION:
APPLICANT: Parker, W. D.
TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
TITLE OF INVENTION: for Alzheimer's Disease
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/08451096
Patent No. 5760205
GENERAL INFORMATION:
APPLICANT: Parker, W. D.
APPLICANT: Herrnstadt, Corinna
TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
TITLE OF INVENTION: For Alzheimer's Disease
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.2%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 1.2e+02; Live 0; Mismatches 2; Indel8
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,842
FILING DATE: 30-MAR-1994
CLASSIFICATION: 43-
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REFREENCE/DOCKET NUMBER: 9-AG 9504
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       562 TGGGTTTTTAATACCT 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 TGGTTTTTCTAATACCT 1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.23
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 74
US-08-451-096-12/c
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RESULT 76
US-08-413-740A-140/C
US-08-413-740A-140/C

Sequence 140, Application US/08413740A

Patent No. 6171859

Patent No. 6171859

Patent No. 6171859

APPLICANT: HERRNSTADT, CORINNA

APPLICANT: PARKER, WILLIAM D.

APPLICANT: MILLER, SCOTT W.

TITLE OF INVENTION: Diagnosis, Therapy and Cellular and

TITLE OF INVENTION: Diagnosis, Therapy and Cellular and

TITLE OF INVENTION: Defects

NUMBER OF SEQUENCES: 206

CORRESPONDENCE ADDRESS: 206

CORRESPONDENCE ADDRESS: Renyon

STREET: 1025 Connecticut Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,740A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEE: Kenyon & Kenyon
: 1025 Connecticut Avenue, N.W.
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: 08/413,740
FILING DATE: 30 Mar 1995
APPLICATION NUMBER: US 08/410,658
FILING DATE: 24 MARCH 1995
APPLICATION NUMBER: US 08/397,808
FILING DATE: 3 Mar 1995
APPLICATION NUMBER: US 08/219,842
FILING DATE: 30 MARCH 1994
ATTORNEY/AGENT INFORMATION:
NAME: TOFFENET, Judich L.
NAME: TOFFENET, Judich L.
REGISTRATION NUMBER: 39,048
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
TELEPHONE: 202-429-176
TELEPHONE: 202-429-176
TELEPHONE: ADS-429-176
TELEPHONE: ADS-429-176
TELEPHONE: ADS-429-176
TELEPHONE: ADS-429-176
TELEPHONE: ADS-429-176
TELEPHONE: ADS-429-176
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COUNTRY: USA
COUNTRY: USA
ZIP. 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-1995
NR: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: other nucleic acid HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 30-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BONDAM, DAVIG B.
REGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34297
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Best Local Similarity 88.2
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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US-08-810-599-64
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VB-6810-599-64/c

VB-6810-599-64/c

Sequence 64, Application US/08810599

FRETENT WO. 596798

FRETENT WO. 596798

FRETENT WO. 596798

APPLICANT PARKER, W. Davis

APPLICANT PAHY. Boin

TITLE OF INVENTION: Methods for Detecting Mitochondrial Mutations

TITLE OF INVENTION: Methods for Althelmer's Disease and Methods for Detecting Mitochondrial Mutations

TITLE OF INVENTION: Of Mitochondrial Nucleic Acid

NUMBER OF SEQUENCES: 8-2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kenyon & Kenyon

STREET: 1025 Connecticut Avenue, N.W., Suite 600

CITT: Washington

STREET: D.C.

COUNTRY: US

CONTRY: READBLE FORM:

CONTRY: READBLE FORM:

CONTRY: READBLE FORM:

MEDIUM TIPLE OF ORDERS: SOURCES: 0.1 for Windows

CONTRY: READBLE FORM:

CONTRY: US

CONTRY
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                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,096
FILING DATE:
CLASSIFICATION NUMBER: US 08/219,842
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/219,842
FILING DATE: OF OWER-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathyn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
REFERENCE/OFFET N
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Query Match 1.2%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 1.2e+02; Matches 15; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                  17 regririrciaaraccr
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                                 US-08-413-740A-151
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          ANTI-SENSE:
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| Sequence 151, Application US/08413740A
| Pattent No. 61718B
| Pattent No. 61718B
| GENERAL INFORMATION:
| APPLICANT: HERRNSTADT, CORINNA
| APPLICANT: PARKER, WILLIAM D.
| APPLICANT: DAVIS, ROBERT
| APPLICANT: MILLER, SCOTT W.
| TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
| TITLE OF INVENTION: Defects
| TITLE OF INVENTION: Defects
| TITLE OF SEQUENCES: 206
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                       Query Match 1.2%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 1.2e+02; Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W.
CITY: Washington
STRYE: 1025
COUNTRY: USA
ZIP: 20036-5405
COUNTRY: USA
ZIP: 20036-5405
COUNTRY: USA
ZIP: 20036-5405
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,740A
FILING DATE: 30-MAR-1995
CLASSIFICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: 98/413,740
FILING DATE: 30-MAR-1995
CLASSIFICATION NUMBER: 34297
ATTORNEY/AGENT INFORMATION:
AMERICATION NUMBER: 34297
FILING DATE: 30-MAR-1995
CLASSIFICATION NUMBER: 34297
FELEPROMENT (202) 429-0796
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TVPR: nucleic acid
                                                                                                                                                                                                                             MOLECULE TYPE: other nucleic acid HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: other nucleic acid HYPOTHETICAL: NO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          562 TGGGTTTTTTAATACCT
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STRANDEDNESS: double
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US-08-413-740A-140
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RESULT 78
US-08-413-740A-185/c
| Sequence 185, Application US/08413740A|
| Sequence 185, Application US/08413740A|
| Sequence 185, Application US/08413740A|
| Patent No. 6171859
| GENERAL INFORMATION:
| APPLICANT: PARKER, WILLIAM D.
| APPLICANT: MILLER, SCOTT W.
| APPLICANT: MILLER, SCOTT W.
| TITLE OF INVENTION: Diagnosis, Therapy and Cellular and TITLE OF INVENTION: Defects
| NUMBER OF SEQUENCES: 206
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Kenyon & Kenyon & Kenyon |
| CTTLE OF INVENTION: Defects |
| NUMBER OF SEQUENCES: 206
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Kenyon & Kenyon |
| CTTLE OF INVENTION: DEFECTS |
| MUMBER OF SEQUENCES: 206
| CORRESPONDENCE ADDRESS: ADDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY:

STATE: DC
CONDUTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUT
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Animal Models for Diseases Associated With Mitochondrial
Defects
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APPLICANT: HANZEL, David R.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/205, PRIOR PLILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-36
PRIOR APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.2%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 1.2e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: PATENTION NUMBER: US/08/413,740A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION HATA:
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: 08/413,740
FILING DATE: 30-MAR-1995
CLASSIFICATION HAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: BONDAM, DAVIG B.
REGISTRATION NUMBER: 2105/7
REFERENCE/DOCKET NUMBER: 2105/7
TELEPHONE: (202) 429-1776
TELEPHONE: (202) 429-1776
TELEPHONE: (202) 429-1776
TELEPHONE: (202) 429-1776
TELEPHONE: CAPACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                 SEEE: Kenyon & Kenyon
F: 1025 Connecticut Avenue, N.W.
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.2
Query Match
Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                              TITLE OF INVENTION: An TITLE OF INVENTION: DE NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ANTI-SENSE: N
US-08-413-740A-188
                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
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                                                                                                                                                                                                                                                                                                                                                                                                Diagnosis, Therapy and Cellular and
Animal Models for Diseases Associated With Mitochondrial
Defects
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08413-740A-188/C
US-08413-740A-188, Application US/08413740A
; Sequence 188, Application US/08413740A
; Patent No. 6171859
; GENERAL INFORMATION:
    APPLICANT: PARKER, WILLIAM D.
    APPLICANT: PARKER, WILLIAM D.
    APPLICANT: PARKER, WILLIAM D.
    APPLICANT: MILLER, SCOTT W.
    APPLICANT: MILLER, SCOTT W.
    TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,740A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04063
PILING DATE: 30-MAR-1995
CLASSIFICATION NUMBER: 08/413,740
PILING DATE: 30-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 34297
REFERENCE/DOCKET NUMBER: 34297
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFPXX: (202) 429-1776
TELEFPXX: (202) 429-177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: DC
COUNTRY: USA
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
MATI-SENSE: NO
US-08-413-740A-186
                                                                                                                                                                                              Sequence 186, Application US/08413740A
Patent No. 6171859
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: HERRNSTADT, CORINNA
APPLICANT: PARKER, WILLIAM D.
APPLICANT: DAVIS, ROBERT
APPLICANT: MILLER, SCOTT W.
TITLE OF INVENTION: Dagnosis, T)
TITLE OF INVENTION: Animal Model,
TITLE OF INVENTION: Defects
NUMBER OF SEQUENCES: 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               563 GGGTTTTTAATACCTT 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 GGTTTTTCTAATACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            double
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STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1022
                                                                                                                                                    RESULT 79
US-08-413-740A-186/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Gaps

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Patent No. 6686188
SEQ ID NO 2564
LENGTH: 17
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PCT-US95-04063-140/c
                                                                                                                                                                                     , ORGANISM: Homo
US-09-866-108A-2564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-866-108A-6749
                                                                                                                                              TYPE: DNA
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US-09-866-108A-2564/C

Sequence 2564, Application US/09666108A

PARELLOWIT: GV. Yizhong

APPLICANT: GV. Yizhong

APPLICANT: GV. Yizhong

APPLICANT: FRIN, Wensheng

APPLICANT: FRIN, Wensheng

APPLICANT: FRIN, Wensheng

APPLICANT: GHANNON, MARK

ITILE OF INVENTION: MYCSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

TITLE OF INVENTION: MYCSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

TITLE OF INVENTION: MARK

TITLE OF INVENTION: MYCSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

TITLE OF INVENTION: MARK

TITLE OF INVENTION: MYGSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

TITLE OF INVENTION: MYGSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: ABOMICA-

CURRENT APPLICATION NUMBER: US/09/866,108A

PRIOR PELING DATE: 2001-05-26

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                   PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PRIOR SPEICATION NUMBER: PCT/US01/00663
PRIOR PLING DATE: 2001-01-30
PRIOR PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.2%; Score 13.8; DB 1;
88.2%; Pred. No. 1.2e+02;
ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Acomica Sequence Listing Engine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                745 GCAGCTGCCACCTTATG 761
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2000-09-27
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Best Local Similarity 88.2°
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CORGANISM: Homo sapiens
US-09-866-108A-2563
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APPLICANT: SHANNON, Mark

APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYGIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ABONICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT PILING DATE: 2001-05-25

PRIOR PPLICATION NUMBER: US 60/207,456

PRIOR PPLICATION NUMBER: GB 24263.6

PRIOR PLILING DATE: 2000-10-00-04

PRIOR PLILING DATE: 2000-10-00-04

PRIOR PLILING DATE: 2001-00-03-7

PRIOR PLILING DATE: 2001-00-03-7

PRIOR PLILING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR
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                                                                                                                                                                                  Gaps
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                                                                                                      Length 17;
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                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.2%; Score 13.8; DB 1;
88.2%; Pred. No. 1.2e+02;
iive 0; Mismatches 2;
                                                                                                  1.2%; Score 13.8; DB 1;
88.2%; Pred. No. 1.2e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6749, Application US/09866108A
Patent No. 6686188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               836 AGGAAGGCCGGGGTGGA 852
                                                                                                                                                                                                                                                         744 GGCAGCTGCCACCTTAT 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGGAAGGCCGTGGAGGA 17
                                                                                                                                                                                                                                                                                                                                    17 GÉCAGCTGCCGCCTTCT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: GI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
                                                                                       Query Match
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Conservative
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CORGANISM: Homo sapiens
US-09-866-108A-6749
sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 15; Conserv
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PCT-US95-04063-185/C

PCT-US95-04063-185/C

Sequence 185, Application PC/TUS9504063

GENERAL INFORMATION:
APPLICANT: BERNSTADT, CORINNA
APPLICANT: BARKER, WILLIAM D.
APPLICANT: MILLER, SCOTT W.
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
TITLE OF INVENTION: Defects
NUMBER OF SEQUENCES: 206
CORRESPONDENCE 206
CORRESPONDENCE ACHYON & Kenyon
STREET: 1025 Connecticut Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.2%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 1.2e+02; tive 0; Mismatches 2; Indels
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ZIP: 20036-5405

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIT Release #1.0, Version #1.30
SOFTWARE: PATEMIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REBERRENCE/POCKET WUMBER: 2105/7
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202) 429-0796
TELEFRAX: (202) 429-0796
TELEFRAX: (202) 429-0796
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARES PATEMIT PC-DOS/MS-DOS
SOFTWARE: PATEMIT Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 2105/7
REPERBNCE/DOCKET NUMBER: 2105/7
RELEFANT (202) 429-1776
TELEFANX: (202) 429-1776
TELEFANX: (202) 429-176
TELEFANX: (202) 429-176
TELEFANX: (202) 429-176
TELEFANX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 185
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 562 TGGGTTTTTTAATACCT 578
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Best Local Similarity 88.28
Matches 15; Conservative
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STATE: DC
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PCT-US95-04063-151
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PCT-USSS-04063-151/C
Sequence 151, Application PC/TUS9504063
Sequence 151, Application PC/TUS9504063
Sequence 151, Application
Sequence 151, Application
Sequence 151, Application
APPLICANT: PARKER, WILLIAM D.
APPLICANT: DAVIS, ROBERT
APPLICANT: DAVIS, ROBERT
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
TITLE OF INVENTION: Defects
TITLE OF INVENTION: Defects
NUMBER OF SEQUENCES: 206
CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon
CORRESPONDENCE ADDRESS:
                                                                             APPLICANT: PARKER, WILLIAM D.
APPLICANT: PARKER, WILLIAM D.
APPLICANT: PARKER, WILLIAM D.
APPLICANT: PAILER, SCOTT W.
TITLE OF INVENTION: Disagnosis, Therapy and Cellular and
TITLE OF INVENTION: Disagnosis, Therapy and Cellular and
TITLE OF INVENTION: Defects
TITLE OF INVENTION: DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 20036-5405
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: BATCHCIIN Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
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1025 Connecticut Avenue, N.W.
                                      Sequence 140, Application PC/TUS9504063 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: BONDAM, David B.
REFERENCE/DOCKET NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2105/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-176
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TTPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 88.2
Matches 15, Conservative
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COMPUTER READABLE FORM:
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HYPOTHETICAL: NC
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STATE:
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PCT-US95-04063-188/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HERRNETADT, CORINNA
APPLICANT: PARKER, WILLIAM D.
APPLICANT: PARKER, WILLIAM D.
APPLICANT: DAVIS, ROBERT
TAPLICANT: MILLER, SCOTT W.
TITLE OF INVENTION: Disgnosis, Therapy and Cellular and
TITLE OF INVENTION: Defects
NUMBER OF SEQUENCES: 206
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                 Length 17;
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                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1025 Connecticut Avenue, N.W.
CITY: Washington
STATE: DC
COMPUTER: DC
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REFERENCE/DOCKET NUMBER: 2105/7
TELECOMMUNICATION INFORMATION:
TELECHOME: (202) 429-176
TELECHOME: (202) 429-176
TELERRATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: MOLDALCA COUNDER:
TYPE: MOLDALCA CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: MOLDALCA CHARACTERISTICS:
TYPE: MOLDAL
                                                                                                                                                                                                                                                                         Score 13.8; DB 1;
Pred. No. 1.2e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 87
PCT-US95-04063-186/c
; Sequence 186, Application PC/TUS9504063
; GENERAL INFORMATION:
                        , vroLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US95-04063-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 TGGTTTTTCTAATACCT 1
                                                                                                                                                                                                                                                                         Query Match
1.2%;
Best Local Similarity 88.2%;
Matches 15; Conservative
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Matches 15, Conservative
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US95-04063-186
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RESULT

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Sequence 188 Application PC/TUS9504063
GENERAL INFORMATION:
APPLICANT: HERRNSTADT, CORINNA
APPLICANT: DAVIS, ROBERT
APPLICANT: MILLER, SCOTT W.
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
TITLE OF INVENTION: Defects
NUMBER OF SEQUENCES: 206
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADD
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Sequence 23, Application US/08219842

Patent No. 5465323

GENERAL INFORMATION:
APPLICANT: Parker, W. D.
APPLICANT: Parker, W. D.
TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
TITLE OF INVENTION: for Alzheimer's Disease
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.2%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 1.2e+02; Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA

ZIP: 20036-5405

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04063

FILING DATE: 30-MAR-1995

CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: other nucleic acid HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REPERENCE/DOCKET NUMBER: 2105
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 429-1776
INFORMATION FOR SEQ ID NO: 188:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 563 GGGTTTTTTAATACCTT 579
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
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US-08-219-842-23/c
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Length 18; Indels

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APPLICANT: Chao, Yu-Chan
TITLE OF INVENTION: Hz-1 VIRUS PERSISTENCE-ASSOCIATED
TITLE OF INVENTION: GENE 1 (pag1) PROMOTER, USES
TITLE OF INVENTION: THEREFOR, AND COMPOSITIONS
TITLE OF INVENTION: THEREFROM
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS: ADDRESSE: QUITIE, MOITIE & Safford, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,350
FILING DATE: 18-APR-1996
CLASSIFICATION: 4355
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2;
                                                                                                                                   NAME/KEY: misc_difference
| LOCATION: replace[1, "")
| OTHER INFORMATION: /note= "N = fluorescein"
| US-08-451-096-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Curtis, Morris & Safford, P.C. STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, William F.
REGISTRATION NUMBER: 28,029
REFERENCE/DOCKET NUMBER: 516450-2008
REFERENCE/DOCKET NUMBER: 516450-2008
TELECHNINGATION INFORMATION:
TELECHNING (212) 840-3333
TELECHNI: (212) 840-3333
TELECHNI: (212) 840-313
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-634-350-23/c
; Sequence 23, Application US/08634350
; Patent No. 5911982
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; MOLECULE TYPE: DNA (genomic)
US-08-634-350-23
                                                                                                                                                                                                                                                                                                                                                                                             562 IGGGTTTTTTAATACCT 578
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rypE: nucleic acid
STRANDEDNESS: single
TOPOLGY: linear
FRATURE:
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APPLICANT: Chao, 1
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US-00-451-096-23/C
US-00-451-096-23/C
Sequence 23, Application US/08451096
Sequence 23, Application US/08451096
Sequence 23, Application US/08451096
Sequence 24, Application US/08451096
Sequence 25, Application US/08451096
Sequence 26, W. D.
TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
TITLE OF INVENTION: For Alzheimer's Disease
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
STREET: 4370 La Jolla Village Drive, Suite 700
STREET: California
COUNTRY: USA
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                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
SUSTRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,842
FILING DATE: 30-MAR.1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-AG 9504
TELEPRATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRAX: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,096
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
1.2%; Score 13.8; DB 1;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | NAME/KEY: misc_difference
| LOCATION: replace(1, "")
| OTHER INFORMATION: /note= "N = fluorescein"
| US-08-219-842-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 08/219,842
FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-AG 9504
TELECOMMUNICATION INFORMATION:
TELECHONE: (619) 535-901
TELERAX: (619) 535-904
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       562 IGGGTTTTTAATACCT 578
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ö Gaps ö Query Match 1.2%; Score 13.8; DB 1; Length 18; Best Local Similarity 88.2%; Pred. No. 1.2e+02; Matches 15; Conservative 0; Mismatches 2; Indels

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APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Chonesteld, Marta
APPLICANT: Chumarker, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
TITLE REPERBENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT PILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER PILING DATE: 1998-11-23
EARLIER PILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-10-20
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
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Patent No. 6537751

GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ilya

TITLE OF INVENTION:
Billelic markers for use in constructing a high density...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: upstream amplification primer 99-8576 for SEQ 2107 US-09-422-978-6041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/422, 978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298, 850
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1999-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-67
EARLIER FILING DATE: 1998-11-67
NUMBER OF SEQ ID NOS: 11796
                      Sequence 4732, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                905 AGCCTCAACATTTCCTA 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             942 AATCTGAAGCCCCACTC 958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.2
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: primer_bind LOCATION: 1..18
US-09-422-978-4732/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-422-978-6041
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 4732
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; LOCATION: 1..18 - A. OTHER INFORMATION: downstream amplification primer 99-4448 for SEQ 3487, in complemed US-09-4422-978-11352
      Sequence 11352, Application US/09422978

Sequence 11352, Application US/09422978

Sequence 11352

GENERAL INFORMATION:

APPLICANT COhen, Daniel

APPLICANT: Chumakov, Ilya

TITLE OF INVENTION: Blallelic markers for use in constructing a high density...

FILE REPRENCE: GENSET.020CP1

CURRENT APPLICATION NUMBER: US/09/422,978

CURRENT APPLICATION NUMBER: US 09/298,850

EARLIER PELING DATE: 1999-10-20

EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER PILING DATE: 1998-11-23

EARLIER PILING DATE: 1998-11-23

EARLIER PILING DATE: 1998-11-34

SARLIER PILING DATE: 1998-11-36

SARLIER PILING DATE: 1998-11-38

EARLIER PILING DATE: 1998-11-38

SEALIER PILING DATE: 1998-11-38

EARLIER PILING DATE: 1998-11-38

SEALIER PILING DATE: 1998-11-38

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APPLICANT: Robbins, Joan M.
APPLICANT: Tritz, Richard
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: SKIN AND EYE DISEASES
FILE REPRENCE: 480124.407
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT PILING DATE: 2000-10-25
SUFTWARE OF SEQ ID NOS: 4523
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 649
LENGTH: 19
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88.2%; Pred. No. 1.2e+02;
tive 0; Mismatches 2;
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; OTHER INFORMATION: Cdk6 ribozyme binding site
US-09-696-791-649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 649, Application US/09696791; Patent No. 6770633
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Best Local Similarity 88.2
Matches 15; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo Sapiens
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US-09-422-978-11352/c
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US-09-696-791-649/c
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RESULT 96 US-09-696-791-1039/c

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448 TAGCTGGGAGCAGTG 462
        SEQUENCE CHARACTERISTICS:
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TOPOLOGY: 1
US-08-311-760A-354
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Sequence 1039, Application US/09696791

Batent No. 6770633

GENERAL INFORMATION:

APPLICANT: Robbins, Joan M.

APPLICANT: Tritz, Richard

TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE

TITLE OF INVENTION: SKIN AND EYE DISEASES

FILE REFERENCE: 480124.407

CURRENT FILING DATE: 2000-10-25

NUMBER OF SEQ ID NOS: 4523

SOFTWARE PATELLY OF THE TREATMENT OF PROLIFERATIVE

TITLE OF INVENTION: SKIN AND EYE DISEASES

FILE REPERENCE: 480124.407

CURRENT FILING DATE: 2000-10-25

NUMBER OF SEQ ID NOS: 4523
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US-08-311-760A-354/C
US-08-311-760A-354/C
Sequence 354, Application US/08311760A
Sequence 354, Application US/08311760A
Selent No. 5559706
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Newton, Roads
APPLICANT: Newton, Roads
TITLE OF INVENTION:
TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
TITLE OF INVENTION: PLASMA LIPOPROTEIN
TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
STREET: 633 West Fifth Street
STREET: 633 West Fifth Street
STREET: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.2%; Score 13.8; DB 1; Length 19; Best Local Similarity 88.2%; Pred. No. 1.2e+02; Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: Cdk8 ribozyme binding site
US-09-696-791-1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: ENORAGE

COMPUTER: IBM COMPATIBLE

COMPUTER: IBM COMPATIBLE

COMPUTER: TEST COMPATIBLE

COMPUTER: STORAGE

COMPUTER: STORAGE

COMPUTER: STORAGE

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COMPUTER: STORAGE

APPLICATION NUMBER:

RILING APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 354:
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ORGANISM: Homo sapiens
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LENGTH: 19
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Best Local Similarity 93.3%; Pred. No. 1.40+02;
Matches 14; Conservative 0; Mismatches 1; Indel8
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Sequence 354, Application US/08774310

Patent No. 5877022

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Newton, Roger S.
APPLICANT: Ramharack, Randy
TITLE OF INVENTION: REDAYME TREATMENT OF DISEASES
TITLE OF INVENTION: PLASMA LIPOPROTEIN
TITLE OF INVENTION: PLASMA LIPOPROTEIN
TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                       Query Match
1.2%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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CALF: 9700'1

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage COMPUTER: 1EM COMPACIBLE COMPUTER: 1EM COMPACIBLE COMPUTER: 1EM COMPACIBLE COMPUTER: 1EM COMPACIBLE COMPUTER: 1EM P.C. DOS 5.0 SOFTWARE: FASTESQ VERSION 1.5 CURRENT APPLICATION DATA: December 23, 1996 PRIOR APPLICATION NUMBER: 08/311,760 APPLICATION NUMBER: 08/311,760 APLICATION NUMBER: 32,327 REGISTRATION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 223/229 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION OF THE TE
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STREET: 633 West Fifth Street
STREET: Suite 4700
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
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STRANDEDNESS: single
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STATE: California
COUNTRY: U.S.A.
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APPLICANT: Draper, Kenneth
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                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Jarvis, Thale
APPLICANT: Jarvis, Thale
ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCES: 2627
CORRESPONDENCES: 1000 & Lyon
STREET: 633 West Pifth Street
STREET: 631 West Pifth Street
STREET: California
CUTY: LOS Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: storage
COMPUTER: IBM COMPACTED:
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
BRIOR APPLICATION NUMBER: 08/192,943
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: PEDRUARY 7, 1994
APPLICATION NUMBER: 07/997,132
FILING DATE: December 7, 1994
APPLICATION NUMBER: 07/997,132
FILING DATE: AUGUST 26, 1992
ATORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 30/035
TELEFPAX: (213) 989-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: SLORAGE
                                                                                                                                                       US-08-373-124A-1915/c
; Sequence 1915, Application US/08373124A
; Patent No. 5646042
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; Sequence 1915, Application US/08435628
; Patent No. 5817796
; PARERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 ACTGGCATATTTCTT 288
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    16 TAGCTGGGAACAGTG
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McGwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stochedo, Jaim
APPLICANT: Stochedo, Jaim
ITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions ReTITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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APPLICANT: McSwigeh, James
APPLICANT: McSwigeh, James
APPLICANT: McSwigeh, James
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSE: 140n & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
CITY: Los Angeles
STRTE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOCTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: Mord Perfect 5.1
CURRENT APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/373,124
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/986,132
FILING DATE: PEDPLUARY 7, 1994
APPLICATION NUMBER: 07/986,132
FILING DATE: BAY 18, 1994
APPLICATION NUMBER: 07/986,422
APPLICATION NUMBER: 07/986,422
FILING DATE: BAY 18, 1994
APPLICATION NUMBER: 07/986,422
FILING DATE: BAY 18, 1994
APPLICATION NUMBER: 07/986,132
FILING DATE: AUGUST 18, 1994
APPLICATION NUMBER: 32, 327
FILING DATE: AUGUST 18, 1994
APPLICATION NUMBER: 32, 327
FILING DATE: AUGUST 18, 1994
APPLICATION NUMBER: 32, 327
FILING DATE: AUGUST 18, 1994
APPLICATION NUMBER: 32, 327
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APPLICATION NUMBER: 32, 327
FILING DATE: AUGUST 18, 1994
APPLICATION NUMBER: 32, 327
FILING DATE: AUGUST 18, 1994
APPLICATION NUMBER: 32, 327
FILING DATE: AUGUST 18, 1994
APPLICATION NUMBER: 304/35, 506
ATTORNEY AGENT INFORMATION: RESTERMATION: NUMBER: 204/35, 327
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10.09-371-712B-4443/C

1 Sequence 4443, Application US/09371772B

1 Patent No. 6566127...
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INFORMATION FOR SEQ ID NO: 1915:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
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STRANDEDNESS: single
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RESULT 104
US-09-866-108A-6288
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Sequence 2567, Application US/09866108A

Parent No. 6666188

Sequence 2567, Application US/09866108A

Parent No. 6666188

APPLICANT GJ, Yizhong

APPLICANT HANEL, David K.

APPLICANT RELNG DATE: 2000-05-05

CURRENT FILNS DATE: 2000-05-05

PRIOR FILING DATE: 2000-05-05

PRIOR PLILOG DATE: 2000-05-05

PRIOR PLILOG DATE: 2000-05-07

PRIOR PLILOG DATE: 2000-05-07

PRIOR PLILOG DATE: 2000-05-07

PRIOR PLILOG DATE: 2000-09-07

PRIOR PLILOG DATE: 2001-01-00

PRIOR PLILOG DATE: 2001-01-30

PRIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.2%; Score 13.4; DB 1; Length 17; Best Local Similarity 93.3%; Pred. No. 1.4e+02; Matches 14; Conservative 0; Mismatches 1; Indels
FILE REFERENCE: MBHBOO, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-28
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin Version 3.0
SEQ ID NO 4443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          626 GITITATICICAGCA 640
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CORGANISM: Homo sapiens
US-09-866-108A-2567
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-371-772B-4443
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CURRENT FILING DATE: 1001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PAPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-010-04

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PILING PILING DATE: 2001-01-30

PRIOR PILING PILING DATE: 2001-01-30

PRIOR PILING PILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                 GENERAL INC. SUGGLER
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yongquag
APPLICANT: APIN, Sharron G.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: ABOMICA-7
CURRENT APPLICATION INVENTER: US/09/866,108A
CURRENT PILING DATE: 2010-05-25
CURRENT PILING DATE: 2010-05-26
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93.3%; Pred. No. 1.4e+02;
tive 0; Mismatches 1;
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; Sequence 6288, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: PENN, Sharron G.
APPLICANT: PENN, Sharron G.
APPLICANT: RANK, David K.
APPLICANT: RANK, David K.
APPLICANT: SHANK, David K.
APPLICANT: SHANK, Wensheng
; APPLICANT: SHANNON, Mark
                                                                                                                                                                                                                                                      Sequence 6287, Application US/09866108A Patent No. 6686188
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743 AGGCAGCTGCCACCT 757
                                                                          15 AGGCAGCTGCCGCCT 1
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Best Local Similarity
Matches 14; Conserv
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SEQ ID NO 41
LENGTH: 18
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                                                     CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT PILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PLICATION NUMBER: US 60/207,456

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-010-04

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30
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APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-06-36
PRIOR PILING DATE: 2000-06-49
PRIOR PILING DATE: 2000-09-70
PRIOR PILING DATE: 2000-09-70
PRIOR PAPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-70
PRIOR PAPLICATION NUMBER: PCT/USO1/00666
PRIOR PRILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 CCGGGCCGTGGCAGG 35
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Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108A-6288
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US-09-866-108A-6289
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Patent No. 627433.

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SEQUENCE APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Splawski, 1gor
TITLE OF INVENTION: MITATIONS IN THE KCNEI GENE ENCODING HUMAN mink WHICH
TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
TITLE OF INVENTION: KCNEI AS AN LQT GENE
FILE REPERENCE: 2323-131
CURRENT APPLICATION NUMBER: US/09/135,020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Splawski, igor
TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KYLQT1 WHICH CAUSES JERVELL
TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
FILE REFERENCE: 2323-128
CURRENT APPLICATION NUMBER: US/09/135,021A
CURRENT APPLICATION NUMBER: 08/874,655
EARLIER PILING DATE: 1999-06-13
EARLIER PILING DATE: 1999-06-13
EARLIER APPLICATION NUMBER: 60/094,477
EARLIER APPLICATION NUMBER: 60/094,477
EARLIER APPLICATION NUMBER: 2000-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver: 2.0
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PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 6289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1;
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EARLIER APPLICATION NUMBER: 08/921,068
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; ORGANISM: Homo sapiens
US-09-866-108A-6289
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Matches 14; Conserv
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TITLE OF INVENTION: MUTATIONS IN THE KCNEI GENE ENCODING HUMAN mink WHICH
TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
TITLE OF INVENTION: KCNEI AS AN LQT GENE
FILE REFERENCE: 2323-131
CURRENT APPLICATION NUMBER: US/09/44,871
CURRENT PILING DATE: 1999-11-22
EARLIER APPLICATION NUMBER: 08/921,068
EARLIER PILING DATE: 1996-08-17
EARLIER PILING DATE: 1996-08-17
EARLIER PILING DATE: 1996-10-29
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Sequence 6, Application US/09662402A

Patent No. 6420117

GENERAL INFORMATION:
APPLICANT: Weesler, Suean R

APPLICANT: Casa, Alexandra M

TITLE OF INVENTION: METHORS OF USE
TITLE OF INVENTION: METHORS OF USE

FILE REFERENCE: 235.00230101

CURRENT APPLICATION NUMBER: US/09/662,402A

CURRENT FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PatentIN Ver. 2.1

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 6

LENGTH: 18
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide primer
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93.3%; Pred. No. 1.4e+02;
tive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 93.3
Matches 14; Conservative
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US-09-444-871-43
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US-09-597-735-43
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US-09-662-402A-6
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US-09-662-402A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 1.2%; Score 13.4; DB 1; Length 18; Local Similarity 93.3%; Pred. No. 1.46+02; Indels hes 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENDERAL INFURMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Curran, Mark E.
APPLICANT: Curran, Mark E.
APPLICANT: Curran, Mark E.
APPLICANT: Curran, Mark E.
APPLICANT: Landes, Gregory M.
APPLICANT: Burn, Timothy C.
APPLICANT: Splawski, Igor
TITLE OF INVENTION: KYLQTI - A LONG QT SYNDROME GENE
TITLE OF INVENTION: KYLQTI - A LONG QT SYNDROME GENE
TITLE OF INVENTION: KYLQTI - A LONG QT SYNDROME GENE
TITLE OF INVENTION: KYLQTI - A LONG QT SYNDROME GENE
TITLE OF INVENTION: KYLQTI - A LONG QT SYNDROME GENE
TITLE OF INVENTION: KYLQTI - A LONG QT SYNDROME GENE
TITLE OF INVENTION NUMBER: 60/094,477
PRIOR APPLICATION NUMBER: 08/921,068
PRIOR APPLICATION NUMBER: 08/921,068
PRIOR PILING DATE: 1996-10-29
PRIOR PILING DATE: 1996-10-29
PRIOR PILING DATE: 1996-10-29
PRIOR FILING DATE: 1996-10-20
NUMBER OF SEQ ID NOS: 116
                                               EARLIER FILING DATE: 1997-08-29;
EARLIER APPLICATION NUMBER: 08/739,383
EARLIER FILING DATE: 1996-10-29
EARLIER APPLICATION NUMBER: 60/019,014
EARLIER APPLICATION NUMBER: 60/094,477
EARLIER FILING DATE: 1995-12-29
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 43
LENGTH: 18
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US-09-444-871-43
; Sequence 43, Application US/09444871
; Patent No. 6323026
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Sanguinetti, Michael C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-135-010A-43; Sequence 43, Application US/09135010A; Patent No. 6277978
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Best Local Similarity 93.3%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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LENGTH: 18
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48 GCCGCGCCCCAGIT 62
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Sequence 43, Application US/09444295

Sequence 43, Application US/09444295

Sequence 43, Application

6442644

GENERAL INFORMATION

APPLICANT: Sanguinecti, Michael C.

TITLE OF INVENTION: MUTATIONS IN THE KCNEI GENE ENCODING HUMAN mink WHICH

TITLE OF INVENTION: MCANER: US/09/444,295

FILE REFERENCE: 1232-131

CURRENT FILING DATE: 1999-08-17

PRIOR PELICATION NUMBER: 09/135,020

PRIOR PELICATION NUMBER: 09/21,068

PRIOR PELICATION NUMBER: 06/019,014

PRIOR PELING DATE: 1998-08-17

PRIOR PELING DATE: 1998-01-29

PRIOR PELING DATE: 1998-07-29

PRIOR PELING DATE: 1998-07-29

NUMBER OF SEQ ID NOS: 114

SOFTWARE: Patentin Ver: 2.0

SEQ ID NO 43

LENGTH: 18
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APPLICANT: Sanguinetti, Michael C.
APPLICANT: Curran, Mark E.
APPLICANT: Landes, Gregory M.
APPLICANT: Landes, Gregory M.
APPLICANT: Splawski, 1907
APPLICANT: Splawski, 1907
TITLE OF INVENTION: VINDER: US/09/597,735
TITLE REFERENCE: 2323-133
FILE REFERENCE: 2323-133
CURRENT APPLICATION NUMBER: US/09/597,735
CURRENT FILING DATE: 1998-08-19
EARLIER APPLICATION NUMBER: 09/135,010
EARLIER APPLICATION NUMBER: 08/094,477
EARLIER PILING DATE: 1998-08-29
EARLIER PILING DATE: 1997-08-29
EARLIER PILING DATE: 1997-08-29
EARLIER PILING DATE: 1997-08-29
EARLIER PILING DATE: 1997-08-29
EARLIER PILING DATE: 1995-10-29
EARLIER PILING DATE: 1995-10-29
EARLIER PILING DATE: 1995-10-29
EARLIER PILING DATE: 1995-11-22
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 43
LENGTH: 18
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CORGANISM: Homo sapiens
US-09-444-295-43
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; ORGANISM: Homo sapiens
US-09-597-735-43
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Pred. No. 1.4e+02;
0; Mismatches 1; Indels
                            GENERAL INFOGRATION:
APPLICANT: Reating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Curran, Mark E.
APPLICANT: Landes, Gregory M.
APPLICANT: Connors, Timothy D.
APPLICANT: Connors, Timothy C.
APPLICANT: Blurn, Timothy C.
APPLICANT: SPLORER: 08/09/597,732
CURRENT APPLICATION NUMBER: 08/09/477
PRIOR APPLICATION NUMBER: 08/09/1068
PRIOR FILING DATE: 1996-10-29
PRIOR FILING DATE: 1997-108-29
PRIOR FILING DATE: 1997-102-29
PRIOR FILING DATE: 1995-10-29
PRIOR FILING DATE: 1995-12-22
NUMBER: OF SEQ ID NOS: 116
; Sequence 43, Application US/09597732
; Patent No. 6451534
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Best Local Similarity 93.3
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-09-597-732-43
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ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
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1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indel8
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; Sequence 2, Application US/09816814
; Sequence 2, Application US/09816814
; Patent No. 6818466
; Patent No. 6818466
; GENERAL INFORMATION:
APPLICANT: Goronzy, Cornelia M.
APPLICANT: Wayand, Cornelia M.
TITLE OF INVENTION: RHEUMATOID ARTHRITIS MARKERS
; TITLE OF INVENTION: RHEUMATOID
; CURRENT APPLICATION UNMER: US/09/816,814
; CURRENT APPLICATION UNMER: 2001-03-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 93.3%; Pred. No. 1.46+02;
Matches 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WESULT 11.2
US-09-338-907-372/C
Sequence 372, Application US/09338907
Sequence 372, Application US/09338907
Sequence 372, Application US/09338907
Sequence 372, Application US/09338907
Settlicant INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: BROUGHELET, US/09/338, 907
CURRENT APPLICATION NUMBER: 08/996, 306
EARLIER FILING DATE: 1998-09-09
EARLIER FILING DATE: 1998-09-09
EARLIER APPLICATION NUMBER: 09/218, 207
EARLIER APPLICATION NUMBER: 09/218, 207
SOFTWARR: PARENT. PR
PRIOR APPLICATION NUMBER: 60/019,014
PRIOR FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: primer for PCR US-09-816-814-2
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                       2 GCCGCGCCCCCAGTT 16
                                                                                                                                                                                                                                                                                                                                                            48 GCCGCGCCCCAGTT 62
                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                               US-09-597-731-43
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US-09-422-98-5744

Sequence 5744, Application US/09422978

Sequence 5744, Application US/09422978

Sequence 5745, Application US/09422978

Sequence 573751

APPLICANT: Chora, Daniel

APPLICANT: Chumakov, IIya

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE: GENSET.020CP1

CURRENT APPLICATION NUMBER: US/09/422,978

CURRENT FILING DATE: 1999-10-20

EARLIER PILING DATE: 1999-10-20

SEALIER PELING DATE: 1998-11-23

EARLIER PILING DATE: 1998-11-23

EARLIER PILING DATE: 1998-04-21

SEALIER RILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 5744
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; OTHER INFORMATION: upstream amplification primer 99-6557 for SEQ 1810,
US-09-422-978-5744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                     ; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-4677 for SEQ 1561,
US-09-422-978-5495
                                                                                                                                                                            Gaps
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                                                                                                                            Length 18;
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APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Curran, Mark B.
APPLICANT: Curran, Mark B.
APPLICANT: Comors, Timothy D.
APPLICANT: Burn, Timothy C.
APPLICANT: S133-133
FURRENT APPLICATION NUMBER: US/09/597,731
CURRENT APPLICATION NUMBER: 09/135,010
PRIOR FILING DATE: 1998-08-17
PRIOR PLILING DATE: 1998-08-17
PRIOR PLILING DATE: 1999-08-29
PRIOR FILING DATE: 1996-10-29
                                                                                                                                                                            Indels
                                                                                                                      Query Match
1.2%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1;
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Patent No. 6582913
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                                                                                                                                                                                                                                  1060 CTTTCCAGTGGCTAA 1074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 116
US-09-597-731-43
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                 NAME/KEY: misc_feature; NAME/KEY: misc_feature; NAME/KEY: 1.19 ; OCHER INFORMATION: upstream amplification primer for SEQ 251, SEQ 328 US-09-338-907-372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: 1..19
OTHER INFORMATION: upstream amplification primer for SEQ 251, SEQ 328
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Patent No. 6399370
GENERAL INFORMATION:
APPLICANT: WILSON, James M
APPLICANT: GOLDWAN, Mitchell
APPLICANT: STOLZENBERG, Ethan D
APPLICANT: ANDERSON, Mark
APPLICANT: ANDERSON, Mark
APPLICANT: ZASLOFP, Michael
APPLICANT: CASLOFP, MICHAEL
APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                   Query Match
1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-18-207-372/c

Sequence 372, Application US/09218207

Patent No. 6346381

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Bougueleret, Lydie

TITLE REPERENCE: GENSET, 018CP1

CURRENT APPLICATION NUMBER: US/09/218, 207

CURRENT FILING DATE: 1997-12-22

EARLIER FILING DATE: 1997-12-22

EARLIER PILING DATE: 1998-09-09

NUMBER OF SEQ ID NOS: 578

SOFTWARE: Patent.pm

SEQ ID NO 372

LENGTH: 19
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CURRENT APPLICATION NUMBER: US/09/228,302
CURRENT FILING DATE: 1999-01-12
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PRIOR FILING DATE: 1996-08-22
PRIOR APPLICATION NUMBER: US 60/027,334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 TCAAATGGGGAGCCT 365
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ORGANISM: Homo Sapiens
FEATURE:
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ORGANISM: Homo Sapiens
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Sequence 4387, Application US/09422978

Fatent No. 6537751

GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Chen, Daniel
APPLICANT: Chumakov, IIya
TITE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-04-21
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-04-21
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Sequence 11326, Application US/09422978

Sequence 11326, Application US/09422978

Sequence 11326, Application US/09422978

Sequence 11326, Marta

APPLICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Chumakov, 11ya

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE: GRNSET.020CP1

FURRENT PAPLICATION NUMBER: US/09/422,978

CURRENT PILING DATE: 1999-10-20

EARLIER APPLICATION NUMBER: US 09/298,850
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; OTHER INFORMATION: upstream amplification primer 99-1481 for SEQ 453,
US-09-422-978-4387
                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
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                                                                                                                                                                                                                                                                                                                                                                                         Length 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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93.3%; Pred. No. 1.4e+02;
tive 0; Mismatches 1;
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PRIOR FILING DATE: 1996-10-01
PRIOR APPLICATION NUMBER: US 08/915,011
PRIOR FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 2: 31
LENGTH: 19
                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           954 CACTCTGGACCCAGG 968
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                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 93.33
Matches 14; Conservative
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ORGANISM: Homo Sapiens
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US-09-422-978-4387/c
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                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Guntaka, Ramareddy V.
APPLICANT: Guntaka, Attilla
APPLICANT: Kovacs, Attilla
APPLICANT: Kovacs, Attilla
APPLICANT: Kandala, Jagannadhachari
TITLE OF INVENTION: OLLAGEN GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Boulevard, Suite 400
CITY: Kansas City
STATE: MO
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.2%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 1.5e+02; tive 0; Mismatches 3; Indels
                                                                                              Length 19;
                                                                                                                                      Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,547
FILING DATE:
                                                                                          Query Match
1.2%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1;
                    FRATURE:
COTHER INFORMATION: Cdc25 hs ribozyme binding site
US-09-696-791-3671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COllins, John M.
REGISTATION UNDER: 26,262
REFERENCE/DOCKET NUMBER: 2412:
TELEPHONE: 816-474-9050
                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/08802547
Patent No. 5780611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 CICCCCCATCCCCATIT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 18 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crececercerein 1
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                        238 CTATGACTCAGATGC 252
                                                                                                                                                                                                                         CTATCACTCAGATGC 16
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Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: YES
POSITION IN GENOME:
UNITS: bp
US-08-802-547-12
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 126
US-08-800-751-34/C
                                                                                                                                                                                                                                                                                                       RESULT 125
US-08-802-547-12/c
                                                                                                                                                                                                                                                                                                                                                                          ; Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
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                                                                                                                                                                                                                                         NAME/KEY: primer_bind
LOCATION: 1..19
OTHER INFORMATION: downstream amplification primer 99-4233 for SEQ 3461, in compleme
US-09-422-978-11326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3671, Application US/09696791
; Sequence 3671, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
APPLICANT: Tritz, Richard
; TITLE OF INVENTION: SKIN AND EYE DISBASES
; TITLE OF INVENTION: SKIN AND EYE DISBASES
; TITLE OF INVENTION: SKIN AND EYE DISBASES
; TITLE OF INVENTION: 281N AND EYE DISBASES
; TITLE OF INVENTION: 281N AND EYE DISPASES
; TITLE OF INVENTION: 480124.407
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3671
; LENGTH: 19
; TUTLE OF TOWN AND EYE DISPASES
; SOFTWARE: PATENTIN VER. 2.0
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US-09-818-780-80/C

Sequence 80, Application US/09818780

Sequence 80, Application US/09818780

Sequence 80, Application US/09818780

SERVERAL INFORMATION:

APPLICANT: McHenry, Charles

TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III HOLOENZYME

TILE REFERENCE: 1794.0031004

CURRENT APPLICATION NUMBER: US/09/818,780

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 98

NUMBER OF SEQ ID NOS: 98

SEQ ID NO 80

LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; PEATURE:
OPERATOR: reverse/antisense ATG primer #P133-A1237
US-09-818-780-80
                                                                                                                                                                                                                                                                                                                                                               Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                          Query Match
1.2%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1;
      ; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER FILING DATE: 1998-11-24
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   835 CAGGAAGGCCGGGGT 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    394 CATTITCCTTACAAT 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 CATTTGCCTTACAAT 18
                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
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REFERENCE/DOCKET NUMBER: BNRIAS 100
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; POSITION IN GENOME:
; UNITS: bp
US-08-712-357-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Kalamazoo
STATE: MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-525-849C-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/08712357
; Sequence 12, Application US/08712357
; GENERAL INFORMATION:
    APPLICANT: Guntaka, Ramareddy V.
    APPLICANT: Weber, Karl T.
    APPLICANT: Kandala, Jagannadhachari
    TITLE OF INVENTION: OLICOMERS WHICH INHIBIT
    TITLE OF INVENTION: EXPRESSION OF COLLAGEN GENES
    NUMBER OF SEQUENCES: 12
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: HOVEY, Williams, Timmons & Collins
    STREET: 2405 Grand Boulevard, Suite 400
    CITY: Kansas City
    CONTENTION: MISSOURI
                                                               APPLICANT: 170, Kiyoshi
APPLICANT: 170, Kiyoshi
APPLICANT: 170, Kiyoshi
APPLICANT: YAMAKI, Toshifumi
APPLICANT: YAMAKI, Teruo
APPLICANT: TSURUOKA, Takeshi
TITLE OF INVENTION: NOVEL NITRILE HYDRATASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STRATE: VIGILIAE
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIND NATE: PATENTIN NATES:
APPLICATION NUMBER: US/08/800,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-027004
FILING DATE: 14-FEB-1996
ATTORNEY/AGENT THORMATION:
NAME: TEGKIN, RODMATION:
NAME: TEGKIN, RODMATION:
TELEPHONE: (703) 836-6201
TELEPHONE: (703) 836-6201
INPORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESCRIPTION: /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: other nucleic acid
Sequence 34, Application US/08800751
Patent No. 5807730
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 CTGCCCGGCCGTGGCAG 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-712-357-12/c
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APPLICANT: Pederson, Finn S
APPLICANT: Lund, Anders H
APPLICANT: Lowmand, Jette
APPLICANT: Lowmand, Jette
APPLICANT: Jorgensen, Poul
APPLICANT: Jorgensen, Poul
APPLICANT: Jorgensen, MITTLE OF INVENTION: SYSTEM FOR SAID VECTOR, A REPLICATION
TITLE OF INVENTION: TRANSFECTED WITH SAID VECTOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,357
FILING DATE:
NAME: COLLINS, John M.
REGISTRATION NUMBER: 26262
TELEPHONE: (816) 474-9050
TELEPHONE: (816) 474-9050
TELEPHONE: (816) 474-9057
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
"vor. nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 49007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,849C
FILING DATE: 08-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Gordon W. Hueschen
STREET: 715 The "H" Building, 310 East Michigan
STREET: Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.2%; Score 13.2; DB 1;
83.3%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08525849C; Patent No. 5866411; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 CICCCCCATCCCCCATIT 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hueschen, Gordon W.
REGISTRATION NUMBER: 16,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 crececerecrecrir
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Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
TOPOLOGY: linear
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Gaps

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Indels

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3; Mismatches

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Matches 12; Conservative
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APPLICANT: Federson, Finn S

APPLICANT: Lund, Anders H

APPLICANT: Lowmand, Jette

APPLICANT: Lowmand, Jette

APPLICANT: Jouch, Mogens

TITLE OF INVENTION: A RETROVIRAL VECTOR, A REPLICATION

TITLE OF INVENTION: TRANSFECTED WITH SAID VECTOR

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 13.2; DB 1; Length 18; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Gordon W. Hueschen
STREET: 715 The "H" Building, 310 East Michigan
STREET: Avenue
STR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRICA PRICATION:
APPLICATION NUMBER: US/08/525,849
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: HUESCHOM, GOTGON W.
REGISTRATION NUMBER: 16,157
REFERENCE/DOCKET NUMBER: BNRIAS 100
TELECOMMUNICATION:
TELEPHONE: 616-382-0030
TELEPRAX: 616-382-0030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 129
US-08-749-4995A-3
'Sequence 3, Application US/08749495A
'Patent No. 5886166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 TCCACGCCATCTCCCCCA 209
                                                              TELEPHONE: 616-382-0030
TELEFAX: 616-382-0030
TELEFAX: 616-382-2030
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
GOOLOGY: linear
MOLECULE TYPE: LENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.2%;
                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.23
Dest Local Similarity 66.73
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Virginia
COUNTRY: United States
ZID: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENTIA PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,818
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.2%; Score 13.2; DB 1;
83.3%; Pred. No. 1.5e+02;
cive 0; Mismatches 3;
                                                                                                                         GENERAL INFORMATION:
APPLICANT: ITO, Kiyoshi
APPLICANT: YAMAT, Toshifumi
APPLICANT: YAMAT, Toshifumi
APPLICANT: TSURUOKA, Miyuki
APPLICANT: TSURUOKA, Miyuki
APPLICANT: NAKAMURA, Takeshi
TITLE OF INVENTION: NOVEL NITRILE HYDRATASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
APPLICATION NUMBER: JP 8-027004
FILING DATE: 14-FEB-1996
ATTORNEY/AGET INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37, Application US/09205204
Patent No. 5958772
GENERAL INFORMATION
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/800,751
                                                                                                                                                ; Sequence 34, Application US/08990818
; Patent No. 5910432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTATION NOWBER: 0280
REFERENCE/DOCKET NUMBER: 0280
TELECOMMUNICATION INFORMATION:
TELEPAN: (703) 836-6620
TELEFAX: (703) 836-620
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 CTGCCCGGGCCGTGGCAG 34
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192 TCCACGCCATCTCCCCCA 209
                             1 UCCCCGGCAUCUCCACCA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.2
Best Local Similarity 83.3
Matches 15; Conservative
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                                                                                                                  RESULT 130
US-08-990-818-34/C
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APPLICANT: Akong, Anthony
APPLICANT: Akong, Anthony
APPLICANT: Akong, Michael
APPLICANT: Harpold, Michael
APPLICANT: Velicelebi, Ganul
APPLICANT: Brust, Paul
TITLE OF INVENTION: AUTOMATED ANALYSIS EQUIPMENT AND ASSAY
TITLE OF INVENTION: METHOD FOR DETECTING CELL SURFACE PROTEIN FUNCTION USING SAME
NUMBER OF SEQUENCES: 4
CORRESSPONDENCE ADDRESS:
ADDRESSEB: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
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      1.2%; Score 13.2; DB 1; Length 18; 66.7%; Pred. No. 1.5e+02; ive 3; Mismatches 3; Indels
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Pred. No. 1.5e+02;
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COUNTRY: USA
ZIP: 92101-2926

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPOLIALIA
OPERATING SYSTEM: DOS
SOFTWARE: FASTEN DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/434,511
FILING DATE: 04-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/24,985
FILING DATE: 18-DEC-1995
APPLICATION NUMBER: 07/812,254
FILING DATE: 18-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seldman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
TELEBRONE: 619-238-9999
                                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/08434511; Patent No. 6057114
                                                                                                                                  192 TCCACGCCATCTCCCCCA 209
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                                                                                                                                                                      18 GTTCATGAATTCAAGGTG
                                                                         12; Conservative
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SEQUENCE CHARACTERISTICS:
LENGHH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3
Matcheë 15; Conservative
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                            Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                         US-08-434-511-2/c
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               Query Match
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APPLICANT: Lex M. COWBERT
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-1 EXPRESS
FILE REFERENCE: RTS-0020
FURENT PERIOTON UNMBER: US/09/205,204
CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 47
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     us-u9-169-078-3
; Sequence 3, Application US/09169078
; Patent No. 603712
; GENERAL INFORMATION:
    APPLICANT: Lund, Anders H
    APPLICANT: Lund, Anders H
    APPLICANT: Lund, Anders H
    APPLICANT: Lund, Anders H
    APPLICANT: Duch, Mogens
    TITLE OF INVENTION: SYSTEM FOR SAID VECTOR, A REPLICATION
    TITLE OF INVENTION: TRANSFECTED WITH SAID VECTOR
    TITLE OF INVENTION: TRANSFECTED WITH SA
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APPLICATION NUMBER: US/09/169,078
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.2%; Score 13.2; DB 1;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-204-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
PPLICATION NUMBER: US 08/525,849
FILING DATE: 08-52P-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hueschen, Gordon W.
REGISTRATION NUMBER: 16,157
REPERENCE/DOCKET NUMBER: 16,157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-382-2030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 49007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               974 TTGATGAGATCCAAAGGA 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 Trgargagarrcaaggra 1
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                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: tRNA US-09-169-078-3
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GENERAL INCRMATION:
GENERAL INCRMATION:
APPLICANT: Botetein, David A.
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Levine, Arnold J.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Poy, Margert Ann
APPLICANT: Pennica, Diane
APPLICANT: Pennicant Dian
                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonuclectide used for screening of products having
OTHER INFORMATION: ECORI site adjacent to initiation codon of human
OTHER INFORMATION: HM1 coding region
US-08-229-150-2
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Pred. No. 1.5e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 18;
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1.2%; Score 13.2; DB 1;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3;
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Patent No. 6387657
US-09-182-145-131
CURRENT FILING DATE: 1994-04-18
EARLIER APPLICATION NUMBER: 07/812,254
EARLIER FILING DATE: 1991-12-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-182-145-131
; Sequence 131, Application US/09182145B
; Patent No. 6387657
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                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 137
US-09-422-978-5708
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Sequence 2, Application US/08229150
Patent No. 6127130:
Patent Patent Patent No. 6127130:
Pate
                                                                                                             Sequence 3, Application US/09169248

Sequence 3, Application US/09169248

Patent No. 6107478

GENERAL INFORMATION:
APPLICANT: Loud, Anders H
APPLICANT: Loumad, Jette
APPLICANT: Loumad, Jette
APPLICANT: Loumad, Jette
APPLICANT: Duch, Mogens
TITLE OF INVENTION: SYSTEM FOR SAID VECTOR, A REFLICATION
TITLE OF INVENTION: TRANSFECTED WITH SAID VECTOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gordon W. Hueschen
STREET: 715 The "H" Building, 310 East Michigan
STREET: Avenue
CITY: Kalamazoo
STREET: Avenue
STREET: M. Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/169,248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFTCATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/525,849
FILING DATE: 08-5EP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hueschen, Gordon W.
REGISTRATION NUMBER: 16,157
REFERENCE/DOCKET NUMBER: BNRIAS 100
TELECOMMUNICATION:
TELEPHONE: 616-382-0030
TELEFAX: 616-382-2030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 TCCACGCCATCTCCCCCA 209
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1 UCCCCGGCAUCUCCACCA 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: MI
COUNTRY: USA
ZIP: 49007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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STRANDEDNESS: sing
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 135
US-08-229-150-2/c
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                                                                                                                                               US-09-169-248-3
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; Sequence 4, Application PC/TUS9105625
; GENERAL INFORMATION
; APPLICANT: Harpold, Michael M.
; APPLICANT: Brust, Raul
; TITLE OF INVENTION: ASSAY METHODS AND COMPOSITIONS FOR DETECTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                       APPLICANT: Bancroft, F. Carter
APPLICANT: Filss, Maikiko
APPLICANT: Filss, Maikiko
APPLICANT: Taylor Clelland, Catherine L.
TITLE OF INVENTION: PROIACTIN REGULATORY ELEMENT BINDING
TITLE OF INVENTION: PROIACTIN REGULATORY ELEMENT
TITLE OF INVENTION: PROIACTIN REGULATORY ELEMENT
CURRENT APPLICATION NUMBER: US/09/533,494A
CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FREESE for Mindows Version 3.0
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Barbara Jordan
APPLICANT: Alain Charest
TITLE OF INVENTION: Methods and Products Related to
TITLE OF INVENTION: Genotyping and DNA Analysis
FILE REFERENCE: M0656/7045 (HCL/MAT)
CURRENT APPLICATION NUMBER: US 60/101,757
PRIOR APPLICATION NUMBER: US 60/101,757
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22283
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 691
SOFTWARE: PSELSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 13.2; DB 1;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13.2; DB 1;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                        ; Sequence 29, Application US/09533494A
; Patent No. 6586581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-404-912-16/c
; Sequence 16, Application US/09404912
; Patent No. 6703228
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Best Local Similarity 83.33
Matches 15; Conservative
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Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: John Landers
APPLICANT: David Houseman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-404-912-16
                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Human
US-09-533-494A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, 1 ya
TITLE OF INVENTION: Blallelic markers for use in constructing a high density...
FILE REPERBNEE: GENER: 10200P1
CURRENT PILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER PILING DATE: 1999-44-21
EARLIER FILING DATE: 1999-41-23
EARLIER PILING DATE: 1999-11-23
EARLIER PILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER PILING DATE: 1998-4-21
NUMBER: OF SEQ ID NOS: 11796
                                                                   APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Marta
APPLICANT: Blunefeld, Marta
APPLICANT: Blunefeld, Marta
APPLICANT: Chumakov, 11ya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET-1020CP1
CURRENT APPLICATION NUMBER: US (09/422,978
CURRENT PAPLICATION NUMBER: US 09/298,850
EARLIER PILING DATE: 1999-04-21
EARLIER PILING DATE: 1999-04-21
EARLIER PILING DATE: 1998-11-23
EARLIER PILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: primer_bind
LOCATION: 1..18
OTHER INFORMATION: upstream amplification primer 99-6298 for SEQ 1774,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.2%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
Sequence 5708, Application US/09422978 Patent No. 6537751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9959, Application US/09422978 Patent No. 6537751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        871 TCCATGCTATTAAAAGTG 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 ATCCCCCATTTCATTGCC 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.33
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-422-978-5708
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US-09-422-978-9959
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 5708
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US-08-657-884-16/C
US-08-657-884-16/C
Sequence 16, Application US/08657884
Sequence 16, Application US/08657884
Sequence 16, Application US/08657884
Sequence 10. 5858918
GENERAL INFORMATION:
APPLICANT: SCHEBIBER, ALAN D.
APPLICANT: PARK, JONG-GU
TITLE OF INVENTION: METHODS OF INHIBITING PHAGOCYTOSIS
TITLE OF INVENTION: METHODS OF INHIBITING PHAGOCYTOSIS
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US.A.
ZIP: 22201-4714
COMPUTER: FLADABLE FORM:
MEDIUM TYBE: FLODPY disk
COMPUTER: PARABLE FORM:
COMPUTER: 1BM PC COMPATIBLE
COMPUTER: PARABLE POSS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURSIFICATION NUMBER: US/08/657,884
FILING DATE: 07-JUN-1996
CLASSIFICATION: NECESSIFICATION: 424
ATTORNEY/AGTENT INDOMETER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 144

US-09-158-980-16/C

; Sequence 16, Application US/09158980
; Patent No. 624247
; GENERAL INFORMATION:
    APPLICANT: SCHREIBER, ALAN D.
    APPLICANT: PARK, JONG-GU
    TITLE OF INVENTION:
    NUMBER OF SEQUENCES: 31
    NUMBER OF SEQUENCES: 31
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: NIXON & VANDERHYE P.C.
    STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
    CITY: ARLINGTON
    STATE: VIRGINIA
    COMPUTER: US-14
    COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IP POPOS/MS-DOS
    OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 16;
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1.2%; Score 13; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNET FLATION:
NAME: WILSON, MARY J.
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 555-4
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 816-4100
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
18 GTTCATGAATTCAAGGTG
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             AND EVALUATING THE INTRACELLULAR TRANSDUCTION OF AN EXTRACELLULAR SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.2%; Score 13.2; DB 1; Length 18; Best Local Similarity 83.3%; Pred. No. 1.5e+02; Matches 15; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HARPOLD, MICHAEL M.;BRUST, PAUL
TITLE OF INVENTION: ASSAY METHODS AND COMPOSITIONS USEFUL
FOR MEASURING THE TRANSDUCTION OF AN INTRACELLULAR SIGNAL
NUMBER OF SEQUENCES: 5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/563,751
FILING DATE: 07-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | NAME/KEY: misc feature
| LOCATION: 7..12
| OTHER INFORMATION: /function= "EcoRI restriction
| OTHER INFORMATION: recognition sequence"
| OTHER INFORMATION: /label= EcoRI
| PCT-US91-05625-4
                TITLE OF INVENTION: AND EVALUATING THE INTRACES
TITLE OF INVENTION: OF AN EXTRACELLULAR SIGNAL
NUMBER OF SEQUENCES:
ADDRESSEE: Fitch Even Tabin & Flannery
STREET: 135 So. LaSalle Street, Suite 900
CITY: Chicago
CITY: Chicago
CITY: USA
ZIP: G0603
ZIP: G0603
CONDITRY: USA
ZIP: FICOPA disk
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                 MEDIUM TITE: FIGURY ABDIUM TITE: FIGURY ABDIUM TITE: FIGURY ABDIUM TITE: FIGURY ABDICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05625
FILING DATE: 19910807
CLASSIFICATION: 48 07/563,751
PRIOR APPLICATION: 40 07/563,751
PRIOR APPLICATION: 40 07/563,751
PRIOR APPLICATION: 40 07/563,751
PILING DATE: 07-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERRICE/DOCKET NUMBER: 33,779
REFERRICE/DOCKET NUMBER: 33,779
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 619-552-0095
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              695 GTTCATGTAGTCACGGTG 712
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MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5401629-3/c
;Patent No. 5401629
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RESULT 142

SEQ ID NO:3

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NUMBER OF SECURNCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSER: NIXON & VANDERHYE P.C.
STRRET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
CITY: ARLINGTON
CONDUTE: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
CONDUTER: VIGALIA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OMPUTER: IBM PC Compatible
OMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/811,492
FILING DATE: 19-Jul-2001
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/811,492
FILING PATE: 19-Jul-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/09811492
Patent No. 6638764
GENERAL INFORMATION:
APPLICANT: SCHREIBER, ALAN D.
APPLICANT: SCHREIBER, ALAN D.
TITLE OF INVENTION: METHODS OF INHIBITING PHAGOCYTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.2%; Score 13; DB 1; Length 16; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 13; Conservative 0; Mismatches 0; Indels
SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/657,884
PILING DATE: 07-07N-1996
ATTORNEY AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFRENCE/DOCKET NUMBER: 555-46
TELECOMMUNICATION:
                                                                                                                       PRIOR ADPLICATION DATA:
APPLICATION NUMBER: 08/657,884
PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 555-46
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 16 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-158-980-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 AGACATGGCGGGC 79
                                                                            FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-811-492-16/c
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GENERAL INFORMATION:
APPLICANT: Kurnit, David M.
APPLICANT: Kurnit, David M.
APPLICANT: Chiang, Pei Wen
APPLICANT: Wing, Chang, Nei Wen
APPLICANT: Wing, Chang J.
TITLE OF INVENTION: METHOD FOR DETERMINING THE COPY NUMBER OF A NUCLEIC ACID SEQUENC:
FILE REPERENCE: 06498/004001
TITLE OF INVENTION: MUMBER: 10/09/014,065
CURRENT FILING DATE: 1998-01-27
EARLIER APPLICATION NUMBER: US 08/434,474
EARLIER FILING DATE: 1995-05-04
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                   Gaps
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APPLICANT: Weiss, Arthur
APPLICANT: Weiss, Arthur
APPLICANT: Irving, Brian A.
APPLICANT: Roberts, Margo R.
APPLICANT: Roberts, Margo R.
APPLICANT: Roberts, Margo R.
APPLICANT: Roberts, Margo R.
APPLICANT: Asbo, Kristina
TITLE OF INVENTION: Chimeric Chains for Receptor
TITLE OF INVENTION: Associated Signal Transduction Pathways
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hearbert Hohbach, Test, Albritton &
ADDRESSEE: Hearbert Stehr, Hohbach, Test, Albritton &
ADDRESSEE: Hearbert Stehr, Hohbach, Test, Albritton &
ADDRESSEE: Capon Francisco
STATE: CA
COUNTRY: USA
ZIP: 9411-4187
COMPUTER: ISM PC compatible
OOMPUTER: IBM PC compatible
OOMPUTER: IBM PC compatible
OOMPUTER: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/988,194A
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                                                                                                           1.2%; Score 13; DB 1; Length 16;
100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13; DB 1; Lengtn 10, Pred. No. 1.7e+02; Pred. no. 1.7e+02; Indels
                    MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 147
US-07-988-194A-6
Sequence 6, Application US/07988194A
Patent No. 5159046
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     RESULT 146
US-09-014-065-4/c
; Sequence 4, Application US/09014065
; Patent No. 6033884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.2%; Scc
Best Local Similarity 100.0%; Pi
Matches 13; Conservative 0;
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                                                                                                      Query Match
Best Local Similarity 100.0
Matches 13; Conservative
TOPOLOGY: linear
                                                                                                                                                                                                                 67 AGACATGGCGGGC 79
                                                                                                                                                                                                                                              16 AGACATGGCGGGC 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-014-065-4
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US-09-811-492-16
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LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.1%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 148
US-08-757-024-750
; Sequence 750, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
APPLICANT: NYOS. JONATHAN W.
TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA ADDRESSED:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELIZER, PARK & GIBSON STREET: P.O. Drawer 34009
CITY: Charlotte
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Thoppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Thoppy disk
CONFINENT APELICATION DATA:
APPLICATION NUMBER: US/08/757,024
FILING DATE: 26-NOV-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAMM: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5218-41
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELEFAX: 919-881-3175
FILING DATE: December 9, 1992
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I.
REGISTRATION NUMBER: 20015
REFRENCE/DOCKET NUMBER: A-55107-1 CELL-0051
TELECHONE: 415-781-1989
TELEPAN: 415-398-3249
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 GGGAGACATGGCGGGC 79
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TELERAX: 575102
INFORMATION FOR SEQ ID NO: 75
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 AGTICGGGAGACAIGG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 87.5%
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
US-07-988-194A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-757-024-750
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Us-08-282-76C-35, Application US/08582776C

Sequence 35, Application US/08582776C

Sequence 35, Application US/08582776C

Sequence 35, Application US/0858276C

Sequence 35, Application US/0858276C

GENERAL INFORMATION W. I.

APPLICANT: Briese, Thomas

APPLICANT: Schnesenin, Anette

APPLICANT: Schnesenin, Anette

APPLICANT: Schnesenin, Anette

TITLE OF INVENTION: Bystem Diseases Viral Sequences,

TITLE OF INVENTION: Diagnostics and Therapeutics for Central Nervous

TITLE OF INVENTION: System Diseases

NUMBER OF SEQUENCES: 61

CORRESONDENCE ADDRESS:

ADDRESSEE: Fulbright & Jaworski, L.L.P.

STREET: 865 South Figuence Street, 29th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1%; Score 12.8; DB 1;
87.5%; Pred. No. 1.8e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 90017-2576
COUNTRY: USA
ZIP: 90017-2576
COUNTRY: USA
ZIP: 90017-2576
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BE PC compatible
COMPUTER: ASCIL DOS TEXT
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
PILING DATE: 04-JAN-1996
CLASSIFICATION: 435
PRICA PAPLICATION DATA:
APPLICATION NUMBER: US 08/369,822
FILING DATE: 06-JAN-1995
PRICA PAPLICATION DATA: 39-944
REDIENTRY NUMBER: US 08/34,831
PILING DATE: 06-JAN-1995
PILING DATE: 06-JAN-1995
PILING DATE: 06-JAN-1995
PILING DATE: 06-JAN-1995
ATTORNEY-AGENT INFORMATION:
NAME: CHURCHILL, MATGARER A.
REGISTRATION NUMBER: 39-944
REPERENCE/DOCKET NUMBER: 1279-194CZ
TELESCOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 150
US-08-611-587-16/c
; Sequence 16, Application US/08611587
; Patent No. 615091
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 213/660-4518
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
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14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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US-08-582-776C-35
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Weiss, Arthur
Irving, Brian A
Roberts, Margo R
Zeebo, Krisztina
TITLE OF INVENTION: CHIMERIC CHAINS FOR RECEPTOR ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1%; Score 12.8; DB 1; Length 16;
87.5%; Pred. No. 1.8e+02;
ive 0; Mismatches 2; Indels
APPLICANT: PANDOLFO, MASSIMO
APPLICANT: MONTERMINI, LAURA
APPLICANT: MOLTO, MARIA D.
APPLICANT: MOLTO, MARIA D.
APPLICANT: Campuzano, Victoria
APPLICANT: Cossee, Mireille
TITLE OF INVENTION: Direct Diagnosis of Friedreich Ataxia
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             18: Fulbright & Jaworski L.L.P. Patent Dept.
1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,587
FILING DATE: US/08/611,587
FILING DATE: US/08/611,587
ATTONEX/AGENT INPORMATION: 436
ATTONEX/AGENT INPORMATION: NAME: Brashears-Macatee, Sarah J. REGISTRATION NUMBER: 38,087
REGISTRATION NUMBER: 38,087
TELEPROMOVICATION INFORMATION:
TELEPROMOVICATION INFORMATION:
TELEPRAK: 713-651-5246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: ______/desc = "oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 51
CORRESPONDENCB ADDRESS:
ADDRESSEE: CELL GENESYS, INC.
STREET: 322 Lakeside Drive
CITY: Foster City
STATE: California
                                                                                                                                                                                                                                                                                                  ZIP: 77010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08479737
Patent No. 6319494
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 713-651-5246
TELEX: 76-2829
INPORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 cceseaacascceces 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 87.53
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
POSITION IN GENOME:
UNITS: DD
                                                                                                                                                                                             ADDRESSEE: Fulk
STREET: 1301 MC
CITY: Houston
                                                                                                                                                                                                                                                                                      u.s.
                                                                                                                                                                                                                                                              STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , US-08-611-587-16
                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 151
US-08-479-737-6
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: LOWEY THE COMPUTER: COMPUTER: EN PC COMPUTER: EN PC COMPUTER: SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/716,319 FILING DATE: 21.NO. RE38028-2000 CLASSIFICATION: CURKOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/770,234
PILING DATE: 19-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 0295.56516
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
CORGANISM: Pasteurella haemolytica
STRAIN: Serotype 1/pD70
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-716-319-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER AND WITCOFF, LTD.
STREET: 1001 G STREET, NW
CITY: WASHINGTON
TELEPHONE: 609-409-3035
TELEFAX: 413-254-2245
TELEX: CIDEX: <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 egecegekrececece 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 GGGAGACATGGCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 87.59
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 154
US-09-716-319-2
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Sequence 750, Application US/09093972C
Patent No. 6825174
GENERAL INFORMATION:
APPLICANT: Nyce, Jonathan W.
TITLE OF INVENTION: E TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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CORRESPONDENCE ADDRESS:
ADDRESSES: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STREET: 7 Clarke Drive
COUNTRY: USA
ZIP: 08512
COMPUTER: New Jersey
COUNTRY: USA
ZIP: 08512
COMPUTER: BMP C compatible
COMPUTER: BMP 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.1%; Score 12.8; DB 1; Length 16; Best Local Similarity 87.5%; Pred. No. 1.8e+02; Matches 14; Conservative 0; Mismatches 2; Indels
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REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00672
TELECOMMUNICATION INFORMATION:
                                                     APPLICATION NUMBER: US 07/988,194
FILING DATE: 09-DEC-1992
APPLICATION DATE:
APPLICATION DATE:
BEDLICATION DATE: US 07/627,643
FILING DATE: 14-DEC-1990
PRIOR APPLICATION DATE: 12-DEC-1991
ATTORNEY AGENT INFORMATION:
NAME: KRUPEN, KAREN I
REGISTRATION NUMBER: 34,647
REPRINCE/DOCKET NUMBER: CELL5.5
TELEPHONE: (415)349-7392
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: NUCLEIC CALABORY
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: NUCLEIC CALABORY
STRANDENNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGTTTGGGAGACAGGG 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-093-972C-750
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Sequence 478, Application US/08435634
Patent No. 5731295
                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
Query Match 1.1%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 1.8e+02; Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.1%; Score 12.8; DB 1; Length 17;
87.5%; Pred. No. 1.8e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                   RESULT 155
US-08-390-850-478/C
i Sequence 478, Application US/08390850
i Patent No. 5612215
i GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
APPLICANT: McSwiggen, James
APPLICANT: Gustofson, John
APPLICANT: Gustofson, John
TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
NUMBER OF SEQUENCES: 1151
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08390,850
FILING DATE: February 17, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/354,920
FILING DATE: December 13, 1994
APPLICATION NUMBER: 07/589,848
FILING DATE: No. 5612215ember 12, 1993
APPLICATION NUMBER: 07/589,848
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 32,327
REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                       323 CCTGTTATTCTTGCTC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      904 GAGCCTCAACATTTCC 919
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Best Local Similarity 87.54
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY:
US-08-390-850-478
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RESULT 156 US-08-435-634-478/c

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PREDICANT: Drager; knumeth G.
APPLICANT: Barcap: wanta a preparation with a preparation of a properation of a preparation of a preparation of a preparation of
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Gaps
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Best Local Similarity 56.2%; Pred. No. 1.88+02;
Matches 9; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 159
US-08-758-306-631/C
Sequence 631, Application US/08758306
Fatent No. 5807743
Sequence 631, Application US/08758306
Fatent No. 5807743
Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: RELACENTY TREATMENT OF DISEASES
TITLE OF INVENTION: TREATMENT OF DISEASES
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
NUMBER OF SEQUENCES: 1379
CORRESPONDENCE ADDRESS:
ADDRESSED: LYON & LYON
ADDRESSED: LYON & LYON
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2026
COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Pastes 4 Version 1.5
CURRENT APPLICATION NUMBER: US/08/758,306
FILING DATE: December 3, 1996
CLASSIFICATION NUMBER: WING APPLICATION DATA:
PRIONEY APPLICATION DATA:
FILING DATE: FILING DATE:
FILING DATE: FILING DATE:
FILING DATE: FILING DATE:
ATTORNEY AGENT INFORMATION:
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/758,306
FILING DATE: December 3, 1996
CLASSIFICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
ATTORNEY/AGEN INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 212/132
REFERENCE/DOCKET NUMBER: 212/132
REFERENCE/DOCKET NUMBER: 212/132
RELEFRAX: (213) 489-1600
TELLEFAX: (213) 480-1600
TELLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32,327
R: 212/132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               918 CCTAGAGCCTTATTAG 933
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REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||:||| ||: ::||
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US-08-758-306-577
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1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
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Sequence 577, Application US/08758306

Sequence 578, Application US/08758306

Sequence 577, Application US/08758306

Sequence 577, Application US/08758306

SERIESAL INFORMATION: METHOD AND REAGENT FOR THE TITLE OF INVENTION: TREATHERY OF DISEASES

TITLE OF INVENTION: TREATHERY OF DISEASES

TITLE OF INVENTION: ASSOCIATED WITH TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION

NUMBER OF SEQUENCES: 1379

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: 634 West Fifth Street

STREET: California

COUNTRY: U.S.A.

COUNTRY: U.S.A.

ZIP: 9071-206
                                                  TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
TITLE OF INVENTION: GAWAA-CHAIN EXPRESSION
NUMBER OF SEQUENCES: 1379
CORRESPONDENCE 1379
CORRESPONDENCE LYON & LYON
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: LOS ANGELES
ZIP: 90071-2066
ZIP: 90071-2066
COMPUTER: Galifornia
COMPUTER: Galifornia
COMPUTER: Galifornia
COMPUTER: Galifornia
COMPUTER: BADABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 18M Compatible
OORFWARE: FastSeq Version 1.5
COMPUTER: IBM Compatible
OOFFWARE: FastSeq Version 1.5
COMPUTER: BASTSERION DATA:
APPLICATION NUMBER: 19,996
CLASSIFICATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
RELEPHONE: (213) 955-0440
TELLEFAR: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1073 AAACCACTTAACCTCT 1088
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US-08-758-306-65
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US-08-757-024-731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08770234
; Sequence 2, Application US/08770234
; Patent No. 5840556
; GENERAL INFORMATION:
    APPLICANT: BRIGGS, ROBERT E.
    APPLICANT: TATUM, FRED M.
    TITLE OF INVENTION: WACLINE STRAINS OF PASTEURELLACEAE
    NUMBER OF SEQUENCES: 7
    CORRESPONDENCE ADDRESS: 7
    STREET: 1001 G STREET, NW
    CITY: WASHINGTON
    STATE: DC
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                       Query Match
1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USAL
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,234
FILING DATE: 19-DEC-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARMATION:
NAME: KAGAN, SARMATION:
TRIEFRENCE/DOCKET NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 0295.56516
TELECOMMUNICATION INFORMATION:
TELEPRAX: 202 508 9100
TELECOMMUNICATION INFORMATION:
TELEPRAX: 202 508 9109
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pasteurella haemolytica
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEX: 6-3510
TELEX: 6-3510
TELEX: 6-3510
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               serotype 1/pD70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                   ; TOPOLOGY:
US-08-758-306-631
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1.8e+02; Indels
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIION TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/757,024
FILING DATE: 26-NOV-1996
CLASSIFICATION S14
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D:
REGISTRATION NUMBER: 31,665
REFRENCE/POCKET NUMBER: 5218-41
TELEPHONE: 919-881-3140
TELEPHONE: 919-881-315
                                                                  GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: Nyce, Jonathan W.
TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA NUMBER OF SEQUENCES: 952
CORRESPONDENCE ADDRESS:
ADDRESSE: BELL, SELTER, PARK & GIBSON STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6025339th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Nyce, Jonathan W.
TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
NUMBER OF SEQUENCES: 952
CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6025339th Carolina
COUNTRY: USA
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1.1%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-757-024-731
; Sequence 731, Application US/08757024
; Patent No. 6025339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 749, Application US/08757024
; Patent No. 6025339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 GGGAGACATGGCGGGC 79
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STRANDEDNESS: single
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US-08-757-024-749
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
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CORGANISM: Homo sapiens
US-09-474-432B-578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: RNA
CORGANISM: Homo sapiens
US-09-474-432B-368
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US-09-474-432B-578
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US-09-442-143A-40/C
Sequence 40. Application US/09442143A
Patent No. 6403089
GENERAL INFORMATION:
APPLICANT: Levy. Gary
APPLICANT: Levy. Gary
TITLE OF INVENTION: Methods of Modulating Immune Coagulation
FILE REPRENCE: 9579-14
CURRENT APPLICATION NUMBER: US/09/442,143A
CURRENT FILING DATE: 1999-11-15
PRIOR PLILING DATE: 1997-05-17
PRIOR PLILING DATE: 1997-06-17
PRIOR APPLICATION NUMBER: US 60/061,684
PRIOR PLILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 60/061,684
PRIOR PLILING DATE: 1997-10-10
SOFTWARE: Patentin version 3.1
SEQ ID NO 40
LINGTH. 17
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,024
FILING DATE: 26-NOV-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFRENCE/POCKET NUMBER: 31,665
REFRENCE/POCKET NUMBER: 31,665
REFRENCE/POCKET NUMBER: 31,665
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEX: 575102
TELEX: 575102
TELEX: 575102
INFORMATION FOR SEQ ID NO: 749:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 Dase pairs
TYPE: nucleic acid
STRANDEDIESS: single
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%2-09-4744432B-368
Sequence 368, Application US/09474432B
Patent No. 6528640
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.;
APPLICANT: Beigelman, Leo
APPLICANT: Burgin, Alex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 CICCCCCATCCCCCAT 217
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: DNA (genomic) US-08-757-024-749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 GGGAGACATGGCGGGC 79
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APPLICANT: Rarpeisky, Alex
APPLICANT: Rarpeisky, Alex
APPLICANT: Adamic, Jasenka
APPLICANT: Adamic, Jasenka
APPLICANT: Sweedler, David
TILE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleour TILE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleour TILE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleour TILE REFRENCES MBHBOO 831-B (247/276)
FILE REFRENCES MBHBOO 831-B (247/276)
FRICK APPLICATION NUMBER: US 60/064, 866
FRICK APPLICATION NUMBER: US 09/186,675
FRICK APPLICATION NUMBER: US 09/186,675
FRICK APPLICATION NUMBER: US 09/301,511
FRICK APPLICATION NUMBER: US 09/301,511
FRICK APPLICATION NUMBER: US 09/301,511
FRICK PILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1526
SEQ ID NOS: 1526
SEQ ID NO 368
SEQ ID NO 368
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APPLICANT: Beigelman, Leo
APPLICANT: Bergelman, Leo
APPLICANT: Bergelman, Leo
APPLICANT: Bergelsky, Alex
APPLICANT: Rarpelsky, Alex
APPLICANT: Karpelsky, Alex
APPLICANT: Swedler, David
APPLICANT: Number: US(09/474,432B
CURRENT FILING DATE: 1997-11-05
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1536
SEQ ID NOS: 1536
SEQ ID NO 578
LEMCHEN 177
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US-09-371-772B-6171/C

Sequence 6111, Application US/09371772B

Sequence 6121, Application US/09371772B

Sequence 6121, Application US/09371772B

Sequence 6127, Application US/09371772B

Sequence 6127, Application US/09371772B

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ravico, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stacobedo, Jaime

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Pactor Receptor

TITLE OF INVENTION: UNWBER: US/09/371,772B

CURRENT FILING DATE: 1999-08-10

PRIOR APPLICATION NUMBER: US 60/005,974

PRIOR FILING DATE: 1995-10-08

PRIOR APPLICATION NUMBER: US 08/584,040
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| Sequence 3, Application US/09589560B
| Sequence No. 6605451.
| Patent No. 6605451.
| Patent No. 6605451.
| APPLICANT: Marmaro, Jeffery M.
| APPLICANT: Marmaro, Jeffery M.
| APPLICANT: Gerdes, John C.
| APPLICANT: Gerdes, John C.
| APPLICANT: Gerdes, John C.
| TILLE OF INVENTION MEthods and Devices for Multiplexing Amplification Reactions FILE REFERENCE: XTR005
| CURRENT APPLICATION NUMBER: US/09/589,560B
| CURRENT FILING DATE: 2000-06-06
| NUMBER OF SEQ ID NOS: 84
| SOFTWARE: PatentIn version 3.2
| SEQ ID NO 3
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     87.5%; Pred. No. 1.8e+02;
ive 0; Mismatches 2;
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87.5%; Pred. No. 1.8e+02;
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SOFWARE: Patentin version 3.0
SEQ ID NO 6171
LENGTH: 17
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                                14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-371-772B-6171
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  Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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US-09-371-772B-6170/c

Sequence 6170, Application US/09371772B

Sequence 6170, Application US/09371772B

Sequence 6170, Application US/09371772B

Sequence 6170, Application

Restrict No. 6556127

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Racoco, Pam

APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime

APPLICANT: Escobedo, Jaime

APPLICANT: McWaygen, Jim

APPLICANT: McWaygen, Jim

APPLICANT: McWaygen, Jim

APPLICANT: McWaygen, Jim

APPLICANT: Nethod and Reagent for the Treatment of Diseases or Conditions Re

TILLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TILLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

CURRENT FILING DATE: 1999-08-10

PRIOR FILING DATE: 1999-08-10

PRIOR FILING DATE: 1999-01-026

NUMBER OF SEQ ID NOS: 14225

SOFTWARE: PatentIn version 3.0

SEQ ID NO 6170

LENGTH: 17
                                                                                                                                                                                                                           APPLICANT: Beryelmen, Deck
APPLICANT: Beryelmen, Deck
APPLICANT: Burgin, Alex
APPLICANT: Rarpeisky, Alex
APPLICANT: Rarpeisky, Alex
APPLICANT: Adamic, Jasenka
APPLICANT: Sweedler, David
APPLICANT: Sweedler, David
APPLICANT: Sumen, Shawn
ITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
FILE REFERENCE: MBHB00-831-B (247/276)
CURRENT APPLICATION NUMBER: US 60/064,866
FILE REFERENCE: HOWER: US 60/064,866
FRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-04-29
FRIOR FILING DATE: 1999-04-28
NUMBER: PROM APPLICATION NUMBER: US 09/301,511
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1526
SOFTWARE: Patentin version 3.0
SEQ ID NO 579
TRANGTH: 17
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68.8%; Pred. No. 1.8e+02;
htive 3; Mismatches 2;
                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
                                                                                                                    Sequence 579, Application US/09474432B
Patent No. 6528640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 AGCCTGCGGCCTTGTG 376
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     GGAGCUGGCGGCCUUG 17
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Best Local Similarity 68.8
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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                                                                         RESULT 166
US-09-474-432B-579
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Beigelman, Leo
APPLICANT: Beigelman, Leo
APPLICANT: Beaudry, Amber
APPLICANT: Admin, Jasenka Matulic
APPLICANT: Sweedler, Dave
APPLICANT: Sweedler, Dave
APPLICANT: Sumen, Slawn
ITILE OF INVENTION: Nuclectide Triphosphate and their Incorporation into Oligonucleo
ITILE OF INVENTION: Nuclectide Triphosphate and their Incorporation into Oligonucleo
FILE REFERENCE: MBHB00-831-C (249/073)
FILE REFERENCE: MBHB00-831-C (249/073)
FILE REFERENCE: 1999-12-29
FRICH APPLICATION NUMBER: 09/474,432
FRICH APPLICATION NUMBER: 09/186,675
FRICH APPLICATION NUMBER: 09/186,675
FRICH APPLICATION NUMBER: 60/083,727
FRICH STILING DATE: 1998-04-29
FRICH STILING DATE: 1998-04-29
FRICH STILING DATE: 1998-04-29
FRICH STILING DATE: 1997-11-05
NUMBER OF SEQ ID NOS: 1524
SOFFWARE: PATENTIN VETSION 3.0
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APPLICANT: GL, Yizhong
APPLICANT: Shannon, Mark
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
TITLE OF INVENTION: NOVEL
TILE REFERENCE: MDHMORP-8
CURRENT APPLICATION NUMBER: US/09/827,998
CURRENT PILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Abomica Sequence Listing Engine
Patent No. 6656700
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68.8%; Pred. No. 1.8e+02;
                                                                                  Query Match
1.1%; Score 12.8; DB 1;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 12; Conservative 2; Mismatches 2;
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; Patent No. 6656700
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 172
US-09-476-387-578
; Sequence 578, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
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Best Local Similarity 68.8
Matches 11; Conservative
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ORGANISM: Homo sapiens
US-09-476-387-578
, ORGANISM: Homo sapiens
US-09-476-387-577
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LENGTH: 17
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Sequence 577, Application US/09476387

Patent No. 6617438

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Rarpelsky, Abex

APPLICANT: Rarpelsky, Alex

APPLICANT: Rarpelsky, Alex

APPLICANT: Rarpelsky, Alex

APPLICANT: Sweedler, Dave

APPLICANT: Wensiler, 1040

FILE REFERENCE: MHBNO-831-C(1249/073)

FILE REFERENCE: MHBNO-831-C(1249/073)

FILE REPERENCE: MHBNO-831-C(1249/073)

FILE REPERENCE: MHBNO-831-C(1249/073)

FRIOR PELING DATE: 1999-04-04

PRIOR PELING DATE: 1999-04-29

PRIOR PELING DATE: 1999-04-29

PRIOR PELING DATE: 1998-11-04

PRIOR PELING DATE: 1998-11-05

PRIOR PELING DATE: 1998-11-05

PRIOR PELING DATE: 1997-11-05

NUMBER OF SEQ ID NOS: 1524

SOFTWARE: PATENTH VERSION 3.0

SEQ ID NO 577

LENGTH: 17
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                       US-09-476-387-367
Sequence 367, Application US/09476387
Patent No. 6617438
GENERAL INFORMATION:
APPLICANT: Riboxyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Beigelman, Leo
APPLICANT: Beigelman, Leo
APPLICANT: Sweedler, Dave
CURRENT APPLICATION NUMBER: 09/9474,432
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/186,675
PRIOR FILING DATE: 1999-10-04
PRIOR APPLICATION NUMBER: 60/064,866
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 60/064,866
PRIOR APPLICATION NUMBER: 60/064,866
PRIOR APPLICATION NUMBER: 60/064,866
PRIOR APPLICATION NUMBER: 60/064,866
PRIOR FILING DATE: 1999-04-29
PRIOR PRIOR PRIOR DATE: 1999-04-29
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81.2%; Pred. No. 1.8e+02;
tive 1; Mismatches 2; Indels
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Best Local Similarity 81.2'
Matches 13; Conservative
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CORGANISM: Homo sapiens
US-09-476-387-367
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Sequence 516, Application US/09827998

Sequence 516, Application US/09827998

Patent No. 6656700

APPLICANT: Shanon, Mark

TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

FILE REFERENCE: MDAMORR-8

CURRENT APPLICATION NUMBER: US/09/827,998

CURRENT FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

NUMBER OF SEQ ID NOS: 1881

SOFTWARE: Acomica Sequence Listing Engine

PACTION NO 516

TENTING NO 516
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APPLICANT: GT, Yanggang
APPLICANT: T, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: CHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE TITLE OF INVENTION: MYOSIN-LIKE GENE CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT APPLICATION TOWNER: 2001-05-25
                                                                                                                                                                                                   Gaps
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                                                                                                                                          Query Match
1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.1%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 1.8e+02; Matches 14; Conservative 0; Mismatches 2; Indels
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-07
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-09-866-108A-2562/c
Sequence 2562, Application US/09866108A
Patent No. 6686188
                                                                                                                                                                                                                                               310 TGCCTTTGGATTTCCT 325
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CORGANISM: Homo sapiens
US-09-827-998-516
                                              TYPE: DNA
CORGANISM: Homo sapiens
US-09-827-998-515
SEQ ID NO 515
LENGTH: 17
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PRICE FILING DATE: 2001-01-05

PRICE FILING DATE: 2001-01-01

PRICE FILING DATE: 2001-01-01

PRICE FILING DATE: 2001-01-01

PRICE FILING DATE: 2001-01-01-01

PRICE PARTICATION NUMBER: PCT/USD1/0665

PRICE PARTICATION NUMBER: PCT/USD1/0666

PREDICATION NUMBER: PCT/USD1/0666

PREDICATION NUMBER: PCT/USD1/0666

PREDICATION NUMBER: PCT/USD1/0666

PRICE PARTICATION NU
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US-09-866-108A-6748
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ilarity 87.5%; Pred. No. 1.88+02;
Conservative 0; Mismatches 2; Indels
                    Query Match
1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.00-09-866-108A-6748
; Sequence 6748, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 TGCTGGGATGTGCCTT 150
                                                         135 TGCTGGGATGTGCCTT 150
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CORGANISM: Homo sapiens
US-09-866-108A-6309
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Matches 14; Conservat
, ORGANISM: Homo sapiens
US-09-866-108A-6308
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APPLICANT: SHANNON, MARK
APPLICANT: SHANNON, MARK
TITULE OF INVERTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITULE REFERENCE: ADGUNCA-7
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2
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APPLICANT: PENN, Sharton G.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE OF INVENTION: WOSIN-LIKE GENE EXPRESSED CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT APPLICATION DATE: 2001-05-25
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCI/US01/00666
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
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Patent No. 6686188
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PENN, Sharron G.
HANZEL, David K.
RANK, David R.
CHEN, Wensheng
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US-09-866-108A-7017
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APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: GLEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPRESENCE: ALGOHICA-7
CURRENT APPLICATION NUMBER: US 60/207, 456
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR PILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
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                    PRIOR PILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00668
PRIOR PLICATION NUMBER: PCT/US01/00668
PRIOR PILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00668
PRIOR PILING DATE: 2001-01-30
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1.1%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2;
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Patent No. 6686188
SEQ ID NO. 7017
LENGTH: 17
PCT/US01/00667
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2.09-866-108A-7017/c
; Sequence 7017, Application US/09866108A
; Patent No. 6686188
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APPLICATION NUMBER:
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APPLICANT: SHANNON, MARK

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE REPERENCE: ADOILOA-7

CURRENT PILING DATE: 2001-05-25

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30
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SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6686188
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1.1%; Score 12.8; DB 1; Length 1
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Best Local Similarity 0: Mismatches 2; Indels
                                                               Indels
Score 12.8; DB 1;
Pred. No. 1.8e+02;
0; Mismatches 2;
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; Sequence 7018, Application US/09866108A
; Patent No. 6686188
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US-09-866-108A-7967/c
; Sequence 7967, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
                                                                                                                               743 AGGCAGCTGCCACCTT 758
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   1.1%;
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
Query Match
Best Local Similarity 87.5
Matches 14; Conservative
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US-09-866-108A-7018
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US-09-866-108A-8291/c
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US-09-66-108A-7968/C

Sequence 7968, Application US/09866108A

Sequence 7968, Application US/09866108A

Sequence 7968, Application US/09866108A

GENERAL INPORMATION:

APPLICANT: GU, Yizhong

APPLICANT: GI, Yonggang

APPLICANT: HANZEL, David R.

APPLICANT: HANZEL, David R.

APPLICANT: RENN, Sharron G.

APPLICANT: RANK, David R.

APPLICANT: RANK, David R.

APPLICANT: RANK, David R.

APPLICANT: RANK, David R.

APPLICANT: SHANNON, MARE.

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

TITLE OF INVENTION: WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

TITLE OF INVENTION: WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

TITLE OF INVENTION: WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REPERENCE: ACOULG-5-25

CURRENT FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-27

PRIOR PILING DATE: PURPLE PURPLE PILING DATE: PURPLE PILING DATE: PURPLE PILING DATE: PURPLE PILING DATE: PURPLE PURPLE PILING DATE: PURPLE P
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                            APPLICANT: 91, Youggang
APPLICANT: 91, Youggang
APPLICANT: PRNN, Sharron G.
APPLICANT: HANZEL, David R.
APPLICANT: SHANNON, MAKE
TITLE OF INVENTION: WOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERSENCE: AEONICA-7
CURRENT PILING DATE: 2001-05-26
PRIOR PLING DATE: 2000-10-26
PRIOR APPLICANTION NUMBER: GB 24263.6
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLI
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CORGANISM: Homo sapiens
US-09-866-108A-7967
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Best Local Similarity
Matches 14; Conserv
GU, Yizhong
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PREMERAL INO.6861148

APPLICANT: NO. 6861148

APPLICANT: PENN, Sharron G. APPLICANT: TI. Yongang APPLICANT: PENN, Sharron G. APPLICANT: PENN, Sharron G. APPLICANT: PENN, Sharron G. APPLICANT: PENN, Sharron G. APPLICANT: RANK, David K. APPLICANT: RANK, David K. APPLICANT: RANK, David K. APPLICANT: SHANKON, MARK BEREKESED IN HUMAN HEART AND MUSCLE TILE OF INVENTION: WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE FILE OF INVENTION: WOMER: US/09/866,108A CURRENT PILING DATE: 2000-105-26 FRIOR APPLICATION NUMBER: US 60/207,456 FRIOR APPLICATION NUMBER: US 60/207,456 FRIOR APPLICATION NUMBER: US 60/207,456 FRIOR APPLICATION NUMBER: US 60/207,666 FRIOR APPLICATION NUMBER: US 60/207,666 FRIOR APPLICATION NUMBER: US 60/207,666 FRIOR PILING DATE: 2000-10-1-30 FRIOR PILING DATE: 2001-01-30 FRIOR FILING DATE: 2
                             PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR TILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PRESENT PROPER PROPER POSTO NUMBER: PCT/USO1/00663
PRIOR PRESENT APPLICATION NUMBER: PCT/USO1/00663
PRIOR PRESENT APPLICATION NUMBER: PCT/USO1/00663
PRIOR PRIOR PILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/USO1/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00664
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Patent No. 6686188
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CORGANISM: Homo sapiens
US-09-866-108A-7968
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LENGTH: 17
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CURRENT FILING DATE: 2001-05-25
FRIOR PAPLICATION NUMBER: US 60/207,456
FRIOR PELING DATE: 2000-05-25
FRIOR APPLICATION NUMBER: US 60/207,456
FRIOR APPLICATION NUMBER: US 60/206,359
FRIOR APPLICATION NUMBER: GB 24263.6
FRIOR APPLICATION NUMBER: PCT/US01/00666
FRIOR FILING DATE: 2000-09-27
FRIOR PILING DATE: 2001-01-30
FRIOR APPLICATION NUMBER: PCT/US01/00667
FRIOR APPLICATION NUMBER: PCT/US01/00667
FRIOR APPLICATION NUMBER: PCT/US01/00669
FRIOR APPLICATION NUMBER: PCT/US01/00669
FRIOR PILING DATE: 2001-01-30
FRIOR PILING DATE: 2001-01-30
FRIOR PLING DATE: 2001-01-30
FRIOR APPLICATION NUMBER: PCT/US01/00668
FRIOR PLING DATE: 2001-01-30
FRIOR FILING DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SHANNON, MARK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                  1.1%; Score 12.8; DB 1; Length 17; 87.5%; Pred. No. 1.8e+02;
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1.1%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                         0; Mismatches
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Patent No. 6686188
SEQ ID NO 8292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 185
2.09-866-108A-8292/c
; Sequence 8292, Application US/09866108A
; Patent No. 6686188
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; Sequence 351, Application US/09720435A
; Patent No. 6803187
                                                                                                                                                                                                                                                                                                                        475 TCTGATTACAGTGCAT 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                           17 rcreacaacacar
                                                                                                                                                                              Query Match 1.1
Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RANK, David R. CHEN, Wensheng
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-8291
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US-09-866-108A-8292
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APPLICANT: Stuyver, Lieven
TITLE OF INVENTION: Method for detection of drug-selected mutations in the protease
TITLE OF INVENTION: gene
TITLE OF INVENTION: gene
TITLE OF INVENTION: gene
TITLE OF INVENTION: gene
CURRENT APPLICATION NUMBER: US/09/720,435A
CURRENT APPLICATION NUMBER: US/09/720,435A
CURRENT APPLICATION NUMBER: PT/FEP99/04317
PRIOR APPLICATION NUMBER: 98870143.9
PRIOR FILING DATE: 1998-06-22
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 529
SOFTWARE: Patentin version 3.2
SEQ ID NO 351
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TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
TITLE OF INVENTION: COMPOSITION, FOR SEASON AITH
BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
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US-09-902-563-40/c
; Sequence 40, Application US/09902563
; Patent No. 6805863
; CANERAL INFORMATION:
; APPLICANT: Levy, Gary
: TITLE OF INVENTION:
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-37
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 09/442,143
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1%; Score 12.8; DB 1;
87.5%; Pred. No. 1.8e+02;
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Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Aids-associated retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Conservative
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Best Local Similarity
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US-09-093-972C-731
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Length 17;
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US-08-403-634-21

Sequence 21. Application US/08403634

Sequence 21. Application US/08403634

Patent No. 5674748

TITLE OF INVENTION: NOVEL HUMAN CYCLIN-DEPENDENT

TITLE OF INVENTION: OF USING THE SAME

TITLE OF SEQUENCES: 31

CORRESPONDENCE ADDRESS: ADDRESSE: ModCock, Washburn, Kurtz, Mackiewicz & ADDRESSEE: No. 5674748Tis

STREET: One Liberty Place, 46th floor

CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1%; Score 12.8; DB 1;
87.5%; Pred. No. 1.8e+02;
tive 0; Mismatches 2;
                                          FILING DATE: 7-June-1995
APPLICATION NUMBER: US 08/757,024
FILING DATE: 26-11-1996
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
FILING DATE: 30-January-1998
                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00672
TELECOMMUNICATION INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US_08/472,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 749:
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REGISTRATION NUMBER: 33,229
REPERBENCE, DOCKET NUMBER: TUU-1482
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR PELICATION DATA:
APPLICATION NUMBER: US 08/208,575
FILING DATE: 08-MAR-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                       TELEPHONE: 609-409-3035
TELERA: 413-254-9245
TELEX: «ONKNOWN»
INFORMATION FOR SEQ ID NO: 749:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
Matches 14; Conserv
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APPLICANT: Nyce, Jonathan W.
TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
TITLE OF INVENTION: & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
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1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
                                CUMPINY: USA

CLOWINTY: USA

CLOWITER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IN PC Compatible

CURRENT APPLICATION NUMBER: US/09/093,972C

FILING DATE: 09-Jun-1998

FILING DATE: 7-June-1995

APPLICATION NUMBER: US 08/472,527

FILING DATE: 26-11-1996

APPLICATION NUMBER: US 08/472,527

FILING DATE: 7-June-1995

APPLICATION NUMBER: US 08/472,527

FILING DATE: 7-June-1996

APPLICATION NUMBER: US 08/472,527

FILING DATE: 7-June-1998

ATTOMBER: US 09/016,464
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/093,972C
FILING DATE: 09-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: BPI-00672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 731:
US-09-093-972C-731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 749, Application US/09093972C Sequence No. 6825174 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 609-409-3035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 7 Clarke Drive
CITY: Cranbury
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 731:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 413-254-9245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 GGGAGACATGGCGGGC 79
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CORRESPONDENCE ADDRESS:
STATE: New Jersey
                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-093-972C-749
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Gaps

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RESULT 192
US-08-816-693A-25/c
; Sequence 25, Application US/08816693A
; Patent No. 5874241
  1 TTAACCTCTGTGGCTG 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-212-771-42/C
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                             셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Attie, Kenneth
APPLICANT: Carlsson, Lena
APPLICANT: Gesundheit, Neil
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
TITLE OF INVENTION: Treatment of Partial Growth Hormone Insensitivity Syndrome
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                       Query Match
1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,580 FILING DATE: 06-JUN-1995 CLASSIFICATION: 5.14 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/410452 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/410452 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/224982 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/224982 PRIOR APPLICATION NUMBER: 08/224982 PRILING DATE: APPRICATION NUMBER: 08/224982 ATTORNEY AGENT INFORMATION:

NUMBER: ARRANGE ARRAY INFORMATION:

NUMBER: ARRAY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: P0884P1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 41s/225-1896
TELEFAX: 41s/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: Galifornia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34, Application US/08468580
Patent No. 5824642
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     792 TGCTTGGAGAGGCAGA 807
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INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 bases
                                                                                                                                                                                                                                                                                                                                                                              2 rccrrccagaagcaga 17
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
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Best Local Similarity 87.59
Matches 14, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hasak, Janet E. REGISTRATION NUMBER:
                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                         ; TOPOLOGY: linear;
; MOLECULE TYPE: cDNA
US-08-403-634-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Patent No. 5958773

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Lex M. Cowsert

TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION

FILE REFERENCE: RTS-0034

CURRENT APPLICATION UNDERS: US/09/212,771

CURRENT PILING DATE: 1998-12-16

NUMBER OF SEQ ID NOS: 47

LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 18;
                                                                                                                    CORRESPONDENCES: 53 CORRESPONDENCES: 53 CORRESPONDENCES: 53 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Dreesler, Rockey, Milnamow & Katz STREET: Two Prudential Plaza, Suite 4700 CITY: Chicago STATE: Illinois COUNTRY: USA ZIP: 60601 COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,693A
GENERAL INFORMATION:
APPLICANT: Takahashi, Joseph S
APPLICANT: Turek, Fred W
APPLICANT: Pinco, Lawrence H
APPLICANT: Turek Clock Gene and Gene Product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 1.1%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2;
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OTHER INFORMATION: Antisense Oligonucleotide
US-09-212-771-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: NO. 5874241thrup, Thomas
REGISTRATION NUMBER: 33,268
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1048 CAACTTCCTTATCTTT 1063
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 312-616-5400
TELEPAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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US-08-757-024-711
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                                             Gaps
                                                                                                                                                                                                       Sequence 39, Application US/09213768
; Sequence 39, Application US/09213768
; Patent No. 598564
; Patent No. 598564
; Garbral Invorwaring
; APPLICANT: Lex M. Cowsert
; APPLICANT: Lex M. Cowsert
; TILE OF INVENTION: ANTISENSE MODULATION OF SENTRIN EXPRESSION
; TILE REFERENCE: RTS-006;
; CURRENT APPLICATION NUMBER: US/09/213,768
; CURRENT APPLICATION NUMBER: US/09/213,768
; URMBER OF SEQ ID NOS: 47
; SEQ ID NO 39
; LENGTH: 18
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1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 74, Application US/09161244

Sequence 74, Application US/09161244

Patent No. 6004814

GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Cowest, Lex M.
TITLE OF INVENTION: ANTISENSE MODULATION OF CD71 EXPRESSION
FILE REFERENCE: RTS-0007

CURRENT APPLICATION UNDER: US/09/161,244

CURRENT FILING DATE: 1998-09-25

NUMBER OF SEQ ID NOS: 91

SEQ ID NO 74
Query Match 1.1%; Score 12.8; DB 1; Length 18; Best Local Similarity 87.5%; Pred. No. 1.8e+02; Andels Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
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ilarity 87.5%; Pred. No. 1.8e+02;
Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Antisense Oligonucleotide US-09-161-244-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Antisense Oligonucleotide US-09-213-768-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 196
US-09-255-888-35/c
'Sequence 35, Application US/09255888
'Patent No. 6013787
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 ATTTCATTGCCAAAAG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Arcrcagreccaaaad 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 ATTTCTTCACTACTGG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                              661 ATTATGTTACTCAAAT 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 Arracricacrecies 1
                                                                                                                   |||||||| ||||||
16 ATTATGTTGTTCAAAT 1
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US-09-161-244-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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87.5%; Pred. No. 1.8e+02;
Live 0; Mismatches 2; Indels
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD4 EXPRESSION
TITLE REPERENCE: RTS-0041
CURRENT APPLICATION NUMBER: US/09/255,888
CURRENT FILING DATE: 1999-02-23
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 35
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 197

US-08-757-024-711

Sequence 711, Application US/08757024
; Betent No. 6025339
; GENERAL INFORMATION:
APPLICANT: Nyce, Jonathan W.
TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA NUMBER OF SEQUENCES: 952
CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON STREET: P.O. Drawer 34009
; CITY: Charlotte
STATE: No. 6025339th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIP: 28234
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPOTER: IBM PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,024
FILING DATE: 26-NOV-1996
CLASS/FICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: SIDLEY, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5218-41
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELECOMMONICATION 1NFORMATION:
TELECOMMONICATION 1NFORMATION:
TELECOMMONICATION 1NFORMATION:
TELECOMMONICATION 1NFORMATION:
TELECOMMONICATION 1NFORMATION:
TELECOMMONICATION 1NFORMATION:
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87.5%; Pred..No. 1.8e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                            FEATURE: OTHER INFORMATION: Antisense Oligonucleotide US-09-255-888-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 TGACTTTTCTTATGCT 138
                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 GGGAGACATGGCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 575102
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 87.5
Matches 14; Conservative
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Best Local Similarity
Matches 14; Conserv
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: S1bley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5218-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEX: 575102
INFORMATION FOR SEQ ID NO: 748:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1048 CAACTTCCTTATCTT 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear _ MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGCGGCATGGCGGGC 16
26-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 GGGAGACATGGCGGGC
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Best Local Similarity 87.5
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
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US-08-885-291-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-757-024-748
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1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                               Sequence 730, Application US/08757024
Fatent No. 6025339
GENERAL INFORMATION:
APPLICANT: NVCe, Jonathan W.
TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA NUMBER OF SEQUENCES: 952
CORRESPONDENCE ADDRESS:
ADDRESSE: BELL, SELTZER, PARK & GIBSON STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: Wo. 6025339th Carolina
COUNTRY: USA
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Sequence 748, Application US/08757024

Sequence 748, Application US/08757024

Patent No. 6025339

TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
NUMBER OF SEQUENCES: 952

CORRESPONDENCE ADDRESS:

ADDRESSE: BELL, SELL, SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/757,024

FILING DATE: 26-NOV-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INPORMATION:

NAME: Sibley, Kenneth D.

REGISTRATION NUMBER: 31,665

REPERENCE/DOCKET NUMBER: 5218-41

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-881-3175

INFORMATION FOR SEQ ID NO: 730:

SEQUENCE CRARACTERISTICS:

LENGTH: 18 base pairs

LENGTH: 18 base pairs
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,024
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: single
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Sequence 21, Application US/08913441B
Sequence 21, Application US/08913441B
Patent No. 5152612
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. 6162612el Human Cyclin-Dependent Kinase-Like Proteins and
TITLE OF INVENTION: Methods of Using The Same
TITLE OF INVENTION: Methods of Using The Same
TITLE OF INVENTION: NUMBER: US/08/913,441B
CURRENT APPLICATION NUMBER: US/08/913,441B
PRIOR APPLICATION NUMBER: US/403,634
PRIOR PLING DATE: 1995-03-14
PRIOR APPLICATION NUMBER: PCT/US96/03557
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Length 18;
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1.1%; Score 12.8; DB 1; Length 1
87.5%; Pred. No. 1.8e+02;
tive 0; Mismatches 2; Indels
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1.Sequence 25, Application US/08885291A

1.Sequence 25, Application US/08885291A

1.Sequence 25, Application US/08885291A

1.Sequence 25, Application US/08885291A

1.Sequence No. 6057125

1.Sequence No.
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87.5%; Pred. No. 1.8e+02;
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Best Local Similarity
Matches 14; Conserv
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; Sequence 56, Application US/08643212
; Patent No. 6207640
; Patent No. 6207640
; GENERAL INFORMATION:
APPLICANT: Attie, Kenneth
APPLICANT: Carlsson, Lena
APPLICANT: Gesundheit, Neil
APPLICANT: Goddard, Audrey
TITLE OF INVENTION: Treatment of Partial Growth Hormone
TITLE OF INVENTION: Insensitivity Syndrome
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-08-913-4418-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.1%; Score 12.8; DB 1; Length 18; Best Local Similarity 87.5%; Pred. No. 1.8e+02; Matches 14; Conservative 0; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/643,212

FILING DATE: 03-MAY-1996

FILING PATE: 07-APR-1994

ATTORNEY/AGENT INFORMATION:

MANNEY ATTORNEY/AGENTION:

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REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: 4-61292-2
REFERENCE/DOCKET NUMBER: 4-61292-2
TELEPHONE: (415) 781-1989
TELER: 910 2772-99
TERER: 910 27
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US-08-643-212-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          792 TGCTTGGAGAGGCAGA 807
                                                       PRIOR FILING DATE: 1996-03-14
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 87.5%
Matches 14; Conservative
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US-08-643-212-56
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US-09-496-694B-116
US-09-496-694B
Sequence 116, Application US/09496694B
Patent No. 6335194
GENERAL INFORMATION
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Lex M. Coweart
TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
FILE REFERENCE: 15PH-0439
CURRENT PILING DATE: 1990-02-02
PRIOR PILING DATE: 1990-04-05
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 249
SEQ ID NO 116
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 18;
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                                                                                   APPLICANT: Takahashi, Joseph S.
APPLICANT: Takahashi, Joseph S.
APPLICANT: Turek, Fred W.
APPLICANT: Pinto, Lawrence H.
TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
FILE REFERENCE: 0290-5
CURRENT FILING DATE: 2000-02-03
CURRENT FILING DATE: 1997-06-30
PRIOR PELICATION NUMBER: 08/816,693
PRIOR FILING DATE: 1997-06-30
PRIOR FILING DATE: 1997-06-31
NUMBER OF SEQ ID NOS: 55
SOFWARE: Patentin Ver. 2.0
SOFWARE: Patentin Ver. 2.0
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US-09-496-672-25/c; Sequence 25, Application US/09496672; Parent No. 6291429; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               953 CCACTCTGGACCCAGG 968
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Query Match
                                                                                                         LENGTH:
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Parent No. 6448059

GENERAL INFORMATION:
APPLICATT: HOU, Ya-Ming

TITLE OF INVENTION: Methods And Compositions For Inhibition Of tRNA Activities
FILE REFERENCE: USFP-0229

CURRENT APPLICATION NUMBER: US 60/026,768

CURRENT PILING DATE: 1996-09-13

PRIOR FILING DATE: 1996-09-13

PRIOR APPLICATION NUMBER: US 86/026,094

PRIOR APPLICATION NUMBER: US 86/928,362

PRIOR APPLICATION NUMBER: US 08/928,362

NUMBER OF SEO ID NOS: 15

SOFTWARE: PatentIn version 3.1
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                                                                          APPLICANT: Baker, Brenda F.
APPLICANT: Cowsert, Lex M.
APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION FILE REFERENCE: ISPH-0321
CURRENT APPLICATION NUMBER: US/09/167,109
CURRENT FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 228
SEQ ID NO 184
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Batent No. 6472154

GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INFORTENCE: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.1%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                 PERTURE:
; OTHER INFORMATION: antisense sequence US-09-167-109-184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; OTHER INFORMATION: Yeast D stem-loop
US-09-506-768-2
             Sequence 184, Application US/09167109
Patent No. 6399297
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 GTCGGGAACTGGCATA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                454 GGAGCAGTGGTAGCAC 469
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Best Local Similarity 75.0°
Matches 12; Conservative
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US-09-167-109-184
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LENGTH: 18
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### GENERAL INFORMATION:
### GENERAL INFORMATION:
### GENERAL INFORMATION:
### GENERAL INFORMATION:
### APPLICANT: Blumenfeld, Marta
### TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
### CURRENT APPLICATION NUMBER: US/09/422,978
### CURRENT APPLICATION NUMBER: US 60/298,850
### EARLIER PILING DATE: 1999-04-21
### EARLIER PILING DATE: 1999-11-23
### EARLIER PILING DATE: 1999-11-23
### EARLIER PILING DATE: 1998-04-21
### EARLIER PILING DATE: 1998-11-35
### EARLIER PILING DATE: 1998-11-36
### EARLIER PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Chumakov, Ilya

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REPERRNE: GENERT. 020CP1

CURRENT APPLICATION NUMBER: US/09/422,978

CURRENT FILING DATE: 1999-04-20

EARLIER APPLICATION NUMBER: US 09/298,850

EARLIER APPLICATION NUMBER: US 09/298,050

EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER APPLICATION NUMBER: US 60/109,732
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OTHER INFORMATION: upstream amplification primer 99–21079 for SEQ 1190,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                  1.1%; Score 12.8; DB 1;
87.5%; Pred. No. 1.8e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.1%; Score 12.8; DB 1;
87.5%; Pred. No. 1.8e+02;
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CURRENT APPLICATION NUMBER: US/09/475,947A CURRENT FILING DATE: 1999-12-31 NUMBER OF SEQ ID NOS: 346 SOFWARE: Patentin Ver. 2.1 SEQ ID NO 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-422-978-5124/c
; Sequence 5124, Application US/09422978
; Patent No. 6537751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCAGCAGCAGCCCCAG 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 GCAGCCGCGCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 AGTTCGGGAGACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 87.5
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: primer_bind LOCATION: 1..18
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                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-422-978-5124
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; OTHER INFORMATION: Primer US-09-571-985C-21
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Query Match
Best Local Similarity 87.5
Matches 14; Conservative
                                         Query Match 1.1;
Best Local Similarity 77.8
Matches 14; Conservative
US-09-856-662-80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Robbins, Joan M.
APPLICANT: Triz, Richard
TITLE OF INVENTION: SKIN AND EVE DISEASES
TITLE OF INVENTION: SKIN AND EVE DISEASES
TITLE OF INVENTION: SKIN AND EVE DISEASES
TITLE OF INVENTION: 18/09/696,791
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4204
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                              ; LOCATION: 1..18 ... OTHER INFORMATION: upstream amplification primer 99-49 for SEQ 3526, US-09-422-978-7460
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| Sequence 80, Application US/09856662
| Sequence 80, Application US/09856662
| Sequence 80, Application US/09856662
| Patent No. 6790616
| GENERAL INFORMATION:
| APPLICANT: MORIBE, Toyoki et al. |
| TILLE REFERENCE: 0032-0261P |
| FILLE REFERENCE: 0032-0261P |
| CURRENT FILLING DATE: 2001-05-24 |
| PRIOR PILLING DATE: 1998-11-26 |
| NUMBER OF SEQ ID NOS: 130 |
| SEQ ID NO 80 |
| LENGTH: 18 |
| LENGTH: 18 |
| LENGTH: 18 |
| LENGTH: NA
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
             EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 7460
LENGTH: 18
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US-09-696-791-4204/C
US-09-690ence 4204, Application US/09696791
; Patent No. 6770633
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                          308 TCTGCCTTTGGATTTC 323
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                                                                                                                                TYPE: DNA
ORGANISM: Homo Sapiens
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Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                          Length 18;
1.1%; Score 12.8; DB 1; Length 18; 77.8%; Pred. No. 1.8e+02;
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               3; Indels
                                                                                                                                                                                                                           1.1%; Score 12.8; DB 1;
87.5%; Pred. No. 1.8e+02;
tive 0; Mismatches 2;
              1; Mismatches
                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Aids-associated retrovirus
US-09-720-435A-349
                              811 CGCTGAAGCAGGCCTCTC 828
                                                                                                                                                                                                                                                          370 CCTTGTGTTGGCAGGC 385
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                      18 ccrrarcrraacaggc 3
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Query Match
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                                                                                                                                                  Sequence 711, Application US/09093972C

Patent No. 6825174

GENERAL INFORMATION:

APPLICANT: Nyce, Jonathan W.

TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION

& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/093,972C
FILING DATE: 09-Jun-1998
CLASSIFICATION NUMBER: US/09/093,972C
APPLICATION NUMBER: US/08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US/08/472,527
FILING DATE: 26-11-1996
APPLICATION NUMBER: US/08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US/08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US/08/472,527
FILING DATE: 30-January-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Amzel, Viviana
REGISTRATION NOMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00672
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 711:
US-09-093-972C-711
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US-09-093-972C-730
Sequence 730, Application US/09093972C
Patent No. 6825174
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
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STRANDEDNESS: single
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TCCTTGGAGAAGCAGA 17
                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 996
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 GGGAGACATGGCGGGC 79
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New Jersey
COUNTRY: USA
  TGCTTGGAGAGGCAGA
                                                                                                               RESULT 214
US-09-093-972C-711
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Sequence 748, Application US/09093972C

Patent No. 6825174

GENERAL INFORMATION:

APPLICANT: Nyce, Jonathan W.

IITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION

& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH

BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
APPLICANT: Nyce, Jonathan W.
TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
& TREATMENT OF DISSASES & CONDITIONS ASSOCIATED WITH
BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
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COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,972C
FILING DATE: 09-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
PRIOR APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 09/016,464
FILING DATE: 7-June-1998
ATTORNEY/AGENT INFORMATION:
AND ATTORNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1%; Score 12.8; DB 1; Length 18; 87.5%; Pred. No. 1.8e+02;
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ADDRESSE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                           NUMBER OF SEQUENCES: 996
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00672
TELECOMMINICATION INFORMATION:
TELEPHONE: 609-409-3035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 730:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,
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LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 413-254-9245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 730:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 GGGAGACATGGCGGGC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 descederarescedes 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                           CITY: Cranbury
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Conservative
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Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-093-972C-730
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US-09-093-972C-748
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Gaps

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RESULT 218
PCT-USS5-03731-34
PCT-USS5-03731-34
Sequence 34, Application PC/TUS9503731
Sequence 34, Application PC/TUS9503731
Sequence 34, Application PC/TUS9503731
GENERAL INFORMATION:
TITLE OF INVENTION: Treatment of Partial Growth Hormone Insensitivity Syndrome TITLE OF INVENTION: Treatment of Partial Growth Hormone Insensitivity Syndrome TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 219
US-08-785-750-2/c
Squence 2.8 Application US/08785750
; Sequence 2.8 Application US/08785750
; Patent No. 5846528
; GENERAL INFORMATION:
APPLICANT: PODSAKOFF, GREGORY M.
APPLICANT: RUBTZMAN, GARY J.
TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING
TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
; UNMERS OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
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1.1%; Score 12.8; DB 1; Length 18; 87.5%; Pred. No. 1.8e+02; tive 0; Mismatches 2; Indels
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87.5%; Pred. No. 1.8e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   884PlPCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
PRICASIFICATION DATA:
PRICA APPLICATION DATA:
APPLICATION NUMBER: 08/224982
FILING DATE: 07-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hassk, Janet E.
REGISTRATION NUMBER: 28,616
REPERENCE/DOCKET NUMBER: 884PIPPTELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1080 TTAACCTCTCTGGGTG 1095
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                                                                                                                                                  953 CCACTCTGGACCCAGG 968
                                                                                                                                                                                                   1 CCACTCTGGGACCAGG 16
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
                        Query Match
Best Local Similarity 87.5%
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 18 bases
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Best Local Similarity
Matches 14; Conserv
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PCT-US95-03731-34
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Sequence 116, Application US/09918186A

Patent No. 6838283

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Elizabeth J. Ackermann

APPLICANT: Elizabeth J. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                     CURLER REPLACED FORCH
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: 09-Jun-1998
CLASSIFICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 08/757,024
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 08/757,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 08/757,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 09/016,464
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 09/016,464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGIETRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00672
RELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEPKX: 413-254-9245
TELEPKX: 413-254-9245
INFORMATION FOR SEQ ID NO: 748:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: Antisense Oligonucleotide US-09-918-186A-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 748:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 GGGAGACATGGCGGC 79
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                        ZIP: 08512
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-918-186A-116
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CORRESPONDENCE ADDRESS:
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Sequence 1, Application US/08588355

Patent No. 5858351

Patent No. 5858351

PAPLICANT: RESIER, PAUL D.

APPLICANT: RESIER, PAUL D.

APPLICANT: KURTZMAN, GARY J.

TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE

TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE

TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO WUSCLE

TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE

TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE

TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE

TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE

TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE

TITLE OF INVENTION: A ASSOCIATES

STREET: 90 MIDDLEFIELD ROAD, SUITE 200

STATE: CACOUNTRY: USA

COMPUTER: READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: BADABLE FORM:

MEDIUM TYPE: PLODS/MS-DOS

SOFTWARE: PATENTION DATA:

MEDICATION NUMBER: US/08/588,355

FILING DATE: 18-JAN-1996

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/588,355

FILING DATE: 18-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-UDS/MS-LDS
CURRENT APPLICATION DATA:
PEPLICATION NUMBER: US/08/785,750
FILING DATE: 16-JAN-1997
CLASSIFCATION: 514
PRICATION NUMBER: US/08/355
FILING DATE: 18-JAN-1996
APPLICATION NUMBER: US/08/88,355
FILING APPLICATION THOMAS.
APPLICATION NUMBER: US/08/588,355
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NUMBER: MCCRACKEN, THOMAS.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009.21
TELECOMMUNICATION NUMBER: 08.548
REFERENCE/DOCKET NUMBER: 08.548
REFERENCE/DOCKET
STREET: 90 MIDDLEFIELD ROAD, SUITE 200 CITY: MENLO PARK
                                                                                                                                                            ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               740 TGTAGGCAGCTGCC 753
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Best Local Similarity 92.94
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 TGCAGGCAGCTGCC 1
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APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                 USA
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Sequence 1, Application US/08812102

| Sequence 1, Application US/08812102
| Patent No. 5952221
| GENERAL INFORMATION:
| APPLICANT: COLOSI, PETER C. APPLICANT: YOSHIDA, UJN
| APPLICANT: YOSHIDA, UJN
| APPLICANT: MIZUNO, MASAAKI
| APPLICANT: MIZUNO, MASAAKI
| APPLICANT: OKADA, HIDEHO
| TITLE OF INVENTION: GENE THERAPY FOR THE TREATMENT OF SOLID
| TITLE OF INVENTION: TUMORS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
| NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Colosi, Peter
TITLE OF INVENTION: Adenovirus Helper-Free Systems for Producing
TITLE OF INVENTION: Adenovirus Helper-Free Systems for Producing
TITLE OF INVENTION: Recombinant AAV Virions Lacking Oncogenic Sequences
FILE REFERENCE: 2555.2.2
CURRENT APPLICATION NUMBER: US/09/116,780
CURRENT FILING DATE: 1998-07-16
EARLIER APPLICATION NUMBER: 08/745,957
EARLIER APPLICATION NUMBER: 06/006,402
EARLIER APPLICATION NUMBER: 06/006,402
EARLIER FILING DATE: 1995-11-09
WUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide US-09-116-780-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.1%; Score 12.4; DB 1; Best Local Similarity 92.9%; Pred. No. 2.1e+02; Matches 13; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.1%; Score 12.4; DB 1; Best Local Similarity 92.9%; Pred. No. 2.1e+02; Matches 13; Conservative 0; Mismatches 1;
ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOWAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-
TELECOMMUNICATION INFORMATION:
TELEFONE: (550) 325-7812
TELEFAX: (650) 325-7812
TELEFAX: (650) 325-7812
TELEFAX: (650) 325-7812
TELEFAX: 14 base pairs
TYPE: nucleic acid
MOLECULE TYPE: DNA (genomic)
US-08-588-355-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-116-780-5/c; Sequence 5, Application US/09116780; Patent No. 5945335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            740 TGTAGGCAGCTGCC 753
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FILING DATE: 18-JAM-1996
ATTORNEY/AGENT INFORMATION:
NAME: WCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009.20
TELECOMMUNICATION INFORMATION:
TELEFHOME: (415) 325-7812
TELEFHOME: (415) 325-7812
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDBINSS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08745957
Patent No. 6004797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 327-3400
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-323
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-784-757-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          740 TGTAGGCAGCTGCC 753
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-745-957-1/C
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US-08-784-757-1/c

Sequence 1, Application US/08784757

Sequence 1, Application US/08784757

Patent No. 5962313

Patent No. 5962313

APPLICANT: RESSLER, PAUL D.

APPLICANT: BYRNE, BARRY J.

APPLICANT: BYRNE, BARRY J.

APPLICANT: WINTENTON: METHODS FOR DELIVERING DNA TO MUSCLE

TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE

TITLE OF INVENTION: CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRION NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: ROBINS & ASSOCIATES

STREET: 90 MIDDLEFIELD ROAD, SUITE 200

CITY: MENLO PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PROC COMPALIBLE
COMPUTER: DA PC COMPALIBLE
COMPUTER: DA PC COMPALIBLE
COMPUTER: DA PC COMPALIBLE
COMPUTER: DA PC COMPALIBLE
COMPUTER: DA COMPATION DATA:
APPLICATION NUMBER: US/08/784,757
FILING DATE: 16-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/588,355
                                                                                                                                                                                COMPUTER PAGES

COMPUTER PROBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US (08/812,102
FILING DATE: 05-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/013,209
FILING APPLICATION NUMBER: US 60/013,209
FILING APPLICATION NUMBER: US 60/013,209
ATYONEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOWAS P.
REGISTRATION NUMBER: 38,548
REGISTRATION NUMBER: 38,548
REGISTRATION NUMBER: 38,548
REGISTRATION NUMBER: 38,548
REGISTRATION NUMBER: 0800-0008
TELEPHONE: (415) 325-7823
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
LENGTH: 14 base pairs
LENGTH: 14 base pairs
                          ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CALIFERNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            740 TGTAGGCAGCTGCC 753
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                                                                                                                   STATE: CALI
COUNTRY: US
ZIP: 94025
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Gaps
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Best Local Similarity 92.9%; Pred. No. 2.16+02;
Matches 13; Conservative 0; Mismatches 1; Indels
Ouery Match 1.1%; Score 12.4; DB 1; Length 14; Best Local Similarity 92.9%; Pred. No. 2.1e+02; Matches 13; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
ACCESSORY FUNCTIONS FOR USE IN
TITLE OF INVENTION: ACCESSORY FUNCTIONS FOR USE IN
TITLE OF INVENTION: ACCESSORY FUNCTION PRODUCTION
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE
CITY: PALO ALTO
STRYE: CALIFORNIA
COUNTY: USA
ZIP: 94301
COMPUTER: ISH PC COMPATION
MEDIUM TYPE: Floppy disk
COMPUTER: ISH PC Compatible
COMPUTER: ISH PC Compatible
COMPUTER: DETENT RELABLE FORM:
MEDIUM TYPE: PLOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATION SYSTEM: US/08/745,957
FILING DATE: 09-NOV-1996
CLASSIFICATION NUMBER: US 60/006,402
FILING DATE: 09-NOV-1995
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 09107
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USA
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Pred. No. 2.1e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                  ADDRESSER: PERNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
CUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER: BIOSPY disk
COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BIM PC COMPALIABLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,789A
FILING DATE: NAW 21, 1996
CLASSIFICATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 18,872
REGISTRATION SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LEEROTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-646-789A-83/C

Sequence 83, Application US/08646789A

Fatent No. 60228A

Patent No. 60228A

PAPLICANT: Peyman, John A.

TITLE OF INVENTION: REGULATION OF GENE EXPRESSION NUMBER OF SEQUENCES: 101

CORRESPONDENCE ADDRESS:

ADDRESSE: PENNIE & EDMONDS

STREET: 1155 Avenue of the Americas

CITY: New York

COWNTRY: US.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
                                                                                                            US-08-646-789A-13/C
Sequence 13, Application US/08646789A
Sequence 13, Application US/08646789A
SEMENAL INFORMATION:
APPLICANT: Peyman, John A.
TITLE OF INVENTION: REQUIATION OF GENE EXPRESSION NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.1%;
740 TGTAGGCAGCTGCC 753
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Best Local Similarity 92.9°
Matches 13, Conservative
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COMPUTER: IRW PC COMPATING
OPERATION STSTEM: PC-DES/MS-LOS
STSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09205337
Sequence 2, Application US/09205337
Patent No. 632598
GENERAL INFORMATION:
APPLICANT: PODSAKOFF, GREGORY M.
APPLICANT: KURTZMAN, GARY J.
RINTZMAN, METADDS OF TREATING ANEMIA USING
TITLE OF INVENTION: METADDS OF TREATING ANEMIA USING
TITLE OF INVENTION: METADDS OF TREATING ANEMIA USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                        Score 12.4; DB 1; Length 14;
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTATE: PLOSPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release
APPLICATION UMBER: US/09/205,337
FILING DATE: 04-Dec-1998
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION

PLIASLICATION NUMBER: 08/785,750

FILING DATE: «Unknown.)

ATTORNEY/AGBNT INFORMATION:

ATTORNEY/AGBNT INFORMATION:

RAME: MCCRACKEN, THOMBER: 38,548

REGISTRATION NUMBER: 38,548

REFERENCE/DOCKET NUMBER: 0800-0009.21

TELLECONTUNICATION INFORMATION:

TELLEPAX: (415) 325-7812

TELLEPAX: (415) 325-7813

INFORMATION FOR SEG ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-309-042-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   740 TGTAGGCAGCTGCC 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94025
COMPUTER READABLE FORM:
                                                                                                                                                              Query Match 1.1%;
Best Local Similarity 92.9%;
Matches 13; Conservative (
                                                                                                                                                                                                                                                             740 TGTAGGCAGCTGCC 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                     14 ridcaddcaddriddd 1
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 229
US-09-406-362-1/c
                                                                                                                                                                                                                                                                                                                                                                                                       US-09-205-337-2/c
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RESULT 230
US-09-755-734-1/c
US-09-755-734-1/c
US-09-755-734-1/c
Sequence 1. Application US/09755734
Fatent No. 6391858
Fatent No. 6391868
FATEN BARN 10.
FAPRIL BARN 10.
FARRY 1.
KURTZMAN, GARY 1.
KURTZMAN, GARY 3.
FITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
                                                                APPLICANT: PODSAKOFF, GREGORY M.

KESSLER, PAUL D.

BYRNE, BARY J.

KURTZMAN, GARY J.

TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE

TITLE OF LELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1%; Score 12.4; DB 1; 92.9%; Pred. No. 2.1e+02; tive 0; Mismatches 1;
                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOWAS P.
REGISTRATION NUMBER: 38,548
REPERENCE/DOCKET NUMBER: 0800-0009.20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PASTENT: Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/406,362
FILING DATE: 28-Sep-1999
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION: «UNKNOWN»
PRIOR APPLICATION NUMBER: US/784,757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (415) 325-7812
Sequence 1, Application US/09406362
Patent No. 6335011
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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                                                                                                                                                                                                                                                                                                               STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-406-362-1
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COMPUTER REALIZE FORPY

COMPUTER: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: Bateniin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/755,734

FILING DATE: 04-Jan-2001

CLASSIFICATION: cUnknown>

PRIOR APPLICATION ON WEBER: 08/588,355

FILING DATE: cunknown>

ATORNEY/AGENT INFORMATION:

NAME: MCCRACKEN, THOMAS P.

REGISTRATION NUMBER: 38,548

REGISTRATION NUMBER: 38,548

TELEPHONE: (550) 325-7812

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 14;
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MEDIUM TYPES: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PACENTIN Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/406,363

FILING DATE: 28-58p-1999

CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

REPLICATION DATA:

APPLICATION TOWNS-

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09406363
Patent No. 6482633
GENERAL INPORMATION:
APPLICANT: COLOSI, PETER C.
TITLE OF INVENTION: RECOMBINANT AAV VIRION PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.1%; Score 12.4; DB 1;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MCCRACKEN, THOMAS P.
REGIGSTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0007
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
BADDRESSER: REED & ROBINS ILP
STREET: 285 HAMILTON AVENUE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           740 TGTAGGCAGCTGCC 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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Sequence 1, Application US/09649890
Patent No. 6531456
GENERAL INPORMATION:
APPLICANT: VOSHIDA, DIN
MIZUNO, MASAAKI
OKADA, HIDEHO
TITLE OF INVENTION: GENE THERAPY FOR THE TREATMENT OF SOLID
TUMORS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
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                                                                                                                                                                                                         Length 14;
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                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                       Score 12.4; DB 1;
Pred. No. 2.1e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/812,102
FILING DATE: 05-MAR-1997
APPLICATION NUMBER: US 60/013,209
FILING DATE: 06-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
REGISCTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/649,890
FILING DATE: 28-Aug-2000
CLASSIFICATION: <UNKNOWT>
                                                                                         TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-406-363-1
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TELEPHONE: (415) 325-7812
TELEFAX: (415) 325-7823
(415)327 - 3231
                                                     LENGTH: 14 base pairs
                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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               INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                     740 TGTAGGCAGCTGCC 753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: MENLO PARK STATE: CALIFORNIA
                                                                                                                                                                                                 Query Match
Best Local Similarity 92.94
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                        14 recadecaderiece 1
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TELEFAX:
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US-09-69-204-1/c
US-09-69-10-204A-1/c
Sequence 1, Application US/09969204A
Sequence 1, Application US/09969204A
Sequence 1, Application US/09969204A
Sequence 1, Application US/0969204A
Sequence 1, Application US/09669204A
SESSIER, PAUL D.
BYRE, BARRY J.
SETILE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
TITLE OF INVENTIONS
VIRIONS
VIRIONS
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  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORMY

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARCHIL Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/969,204A
FILING DATE: 01-Oct-2001
CLASSIFICATION NUMBER: US/99/406,362
FILING DATE: 28-Sep-1999
APPLICATION NUMBER: US/99/406,362
FILING DATE: CURNOWN-
FILING DATE: CURNOWN-
ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOWAS P.
REGISTRATION NUMBER: 38,548
REGISTRATION NUMBER: 38,548
REGISTRATION NUMBER: 38,548
REPERENCE/DOCKET NUMBER: 0800-0009.20
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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92.9%; Pred. No. 2.1e+02;
Live 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-969-204A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 234
US-08-182-968A-118
Sequence 118, Application US/08182968A
Patent No. 5610054
Patent No. 5610054
APPLICANT: Draper, Kenneth G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94025
COMPUTER READABLE FORM:
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                                               740 TGTAGGCAGCTGCC 753
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         Matches 13; Conservative
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Best Local Similarity
Matches 13; Conserv
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TITLE OF INVESTION: WIRTHOW AND REAGENT FOR TITLE OF INVESTION: WIRTHOW AND REAGENT FOR TITLE OF INVESTION: WIRTHOW AND REAGENT FOR TITLE OF INVESTION: WIRTHOW AND WIRTHOUS CONTRESS:

ADDRESSIE: 631 WOR F 1/4th Street
STREET: 631 WOR F 1/4th Street
STREET: 631 WOR F 1/4th Street
GTTY: 10.8 ADGIL=8

CONTYTES REALABLE FOON: STREET: 10.1 FOON STREET: 10.1
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RESULT 237
US-08-435-628-94
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Sequence 94, Application US/08373124A

Sequence 94, Application US/08373124A

Fatent No. 5646042

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Braper, Kenneth

APPLICANT: McSwiggen, James

APPLICANT: Jarvis, Thale

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND

TITLE OF INVENTION: CANCER USING RIBOZYMES

NUMBER OF SEQUENCES: 2627

CORRESPONDENCES: 2627

CORRESPONDENC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 12.4; DB 1;
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTY: 0.5.A.

ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: atorage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PEFFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION NUMBER: 08/45,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/986,422
FILING DATE: MAUGHT 17, 1992
ATTORNEY/AGENT INFORMATION:
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/182,968A
FILING DATE: 13-JANUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/882,888
FILING DATE: 14-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 205/277
REFERENCE/DOCKET NUMBER: 205/277
REPERENCE/DOCKET NUMBER: 206/277
REPERENCE/TOCKET NUMBER: 206/277
TELECOMMUNICATION INFORMATION:
TELEFANK: (213) 985-0440
TELERA: 67-3510
INPORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
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STRANDEDNESS: single
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US-08-182-968A-119
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REPERENCY CONCETN UNRESH. 209 (035)

TELEGRAM: (121) 955-5440

TELEGRAM: (121) 955-9440

TELEGRA
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Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 6; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BROWDY AND NEIWARK STREET: 419 Seventh Street, N.W., Suite 300 STATE: 419 Seventh Street, N.W., Suite 300 STATE: D.C. COUNTRY: USA
                Joseph Martin Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATIOS SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774,306A
FILING DATE: December 26, 1996
PRIOR APPLICATION NUMBER: 09/182,968
FILING DATE: May 14, 1994
APPLICATION NUMBER: 07/862,888
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/227
TELECOMMUTICATION INFORMATION:
TELECHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-08-667-939A-10
Sequence 10, Application US/08667939A
Sequence 10, Sp9166
Patent No. 5998166
Patent No. 5998166
THILE OF INVENTION:
THILE OF INVENTION:
THILE OF SEQUENCES: 25
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          683 ACTIGITITGGCIGT 696
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1 ACUGGUUUGGCUGU 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-774-306A-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                 Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20004
             US-08-774-306A-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 240
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                                                                                                                                                                                                            1.1%; Score 12.4; DB 1; Length 15; 50.0%; Pred. No. 2.18+02; trive 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 238
US-08-774-306A-118
Sequence 118, Application US/08774306A
TITLE OF INVENTION: METHOD AND REAGENT FOR TITLE OF INVENTION: VIRUS REPLICATION NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon STREET: Gailfornia COUNTX: Los Angeles
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
COUNTX: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: S. Diskette, 1.44 Mb
MEDIUM TYPE: S. Diskette, 1.44 Mb
MEDIUM TYPE: BLOOMPAR: Word Perfect 5.1
CURPUTER: December 26, 1996
PILING DATE: December 26, 1996
PILING DATE: December 26, 1996
PILING DATE: May 14, 1992
ATTORNER' MADTH: MAY 14, 1992
ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
RESERENCE/DOCKET NUMBER: 32,33/27
RESERENCE/DOCKET NUMBER: 32,33/27
RESERENCE/DOCKET NUMBER: 223/27
FELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    683 ACTTGTTTGGCTGT 696
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TELEFAX: (213) 955-044(
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0
Matches 7; Conservative
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-94
                                                                                                                                                                                                                                                                                                                                                                                      |:||||:|:|:|
1 CUGGAAUUGUUGCU 14
                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0%
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: Bir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-774-306A-118
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TOPOLOGY: linear
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                                                     OPERATING SYSTEM: PC-LUCS/MS-LUCS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996
PRIOR APPLICATION NUMBER: US 08/433,123
PILING DATE: 03-MAY-1995
ATORNEY AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUC-2A
TELEPHONE: 202-628-5197
TELEPHONE: 202-639-737-3528
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LEUGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER I.
REGISTRATION NUMBER: LUO-2A
TELECCHMONICATION INFORMATION:
TELECCHMONICATION INFORMATION:
TELEPHONE: 202-628-5397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 241

US-08-667-939A-21/C

Sequence 21, Application US/08667939A

Patent No. 5998166

GENERAL INFORMATION:

APPLICANT: LUO, Shun

TITLE OF INVENTION:

CORRESPONDENCE ADDRESS:

ADDRESSER: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             455 GAGCAGTGGTAGCA 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 92.93
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-667-939A-10
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                                                            Length 15;
                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Kohn & Associates
30500 No. 6057111thwestern Highway, Suite 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 48334

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/284,782
                                                          Score 12.4; DB 1;
Pred. No. 2.1e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                            Sequence 13, Application US/09284782
Patent No. 6057111
GENERAL INFORMATION:
APPLICANT: ENTERPRISES, LTD., QBI
APPLICANT: Yehiely, Fruma
APPLICANT: Efimova, Elena
APPLICANT: Efimova, Elena
APPLICANT: Elmac, Paz
TITLE OF INVENTION: GENE IDENTIFICATION METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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; Patent No. 6132966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INPORMATION:
NAME: MONTGOMERY, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 0164:
TELECOMMUNICATION INFORMATION:
TELEPRA: (248) 539-5050
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                            455 GAGCAGTGGTAGCA 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 30500 NC. CITY: Farmington Hills STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              841 GGCCGGGGTGGATC 854
                                                        Query Match
Best Local Similarity 92.99
Matches 13; Conservative
                                                                                                                                                               15 GAGCAGTGGCAGCA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 435
; MOLECULE TYPE: CDNA
US-08-667-939A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                            RESULT 242
US-09-284-782-13/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 243
US-09-064-156A-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-284-782-13
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Gaps
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US-09-081-646-526

j Sequence 526, Application US/09081646
j Sequence 526, Application US/09081646
j Patent No. 6333152
j GENERAL INFORMATION:
j APPLICANT: Kinzler, Kenneth
j APPLICANT: Zhang, Lin
h APPLICANT: Zhang, Lin
j APPLICANT: Zhang, Lin
j TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
j TITLE OF INVENTION: Cancer Cells
j TITLE OF INVENTION: Cancer Cells
j TITLE OF INVENTION: Cancer Cells
j TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
j TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
j TITLE OF INVENTION: Cancer Cells
j TITLE APPLICATION WUMBER: 08/09/081,646
j CURRENT FILING DATE: 1998-05-20
j EARLIER PRILING DATE: 1997-05-21
j NUMBER OF SEQ ID NOS: 871
j SOFTWARE: FastSEQ for Windows Version 3.0
j SOFTWARE: FastSEQ for Windows Version 3.0
j SEQ ID NO 526
j LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.1%; Score 12.4; DB 1; Length 15; Best Local Similarity 50.0%; Pred. No. 2.18+02; Matches 7; Conservative 6; Mismatches 1; Indels
                             MEDIUM TYPE: storage
COMPUTER: IBM COMPALIALE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT PAPPLICATION DATA:
APPLICATION DATA: BY 1998
FILING DATE: APTIL 21, 1998
FILING DATE: December 26, 1996
FILING DATE: December 26, 1996
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: January 13, 1994
APPLICATION NUMBER: 23, 23, 78
FILING DATE: MAY 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REFERENCE/DOCKET NUMBER: 234/083
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                977 ATGAGATCCAAAGG 990
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Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
EDNESS: single
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COCGANISM: Homo sapiens
US-09-081-646-526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nuc-
STRANDEDNESS: 81H9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-064-156A-119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 244
US-06-064-156A-119
Sequence 119, Application US/09064156A
Patent No. 613296
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD AND REAGENT FOR TITLE OF INVENTION: METHOD AND REAGENT FOR TITLE OF INVENTION: INHIBITING HEPATITIS C TITLE OF INVENTION: URBISITING HEPATITIS C TITLE OF INVENTION: VIRUS REPLICATION INDRESCORRESPONDENCES: 498
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 634 West Fifth Street
STREET: California
COUNTRY: U.S.A.
                  APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HERATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 498
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 Weat Fifth Street
STREET: 631 Weat Fifth Street
STREET: SMILE 4700
CITY: Los Angeles
STRRET: SMILE 4700
COMPUTER: BADDABLE FORM:
MEDIUM TYPE: Storage
MEDIUM TYPE: Storage
MEDIUM TYPE: STORAGE
COMPUTER: LBM Compatible
COMPUTER: MAD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/74,306
FILING DATE: December 26, 1994
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 32,327
REGISTRATION NUMBER: 33,327
REGISTRATION NUMBER: 33,327
REGISTRATION NUMBER: 33,327
REGISTRATION NUMBER: 33,327
REFERENCE CARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-064-156A-118
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LENGTH: 15 base pairs
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                   20004
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1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels
                                                            GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: Acswiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: OP VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: LUO, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                STREET: Sulte 4,00
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.

ZIP: 90071-206E
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: BLORAGE IS OF SOFTWARES WORD PERFECT 5.1
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIPTCATION NUMBER: 60/005,974
FILING DATE: OCCOPORE 56, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRANCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELLEFAX: (213) 955-0440
TELLEFAX: (213) 955-0440
TELLEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 8484:
SEQUENCE CHARACTERISTICS:
LIENGTH: 15 base pairs
5-08-584-040-8484
Sequence 8484, Application US/08584040
Patent No. 6346398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 247
US-08-433-123-10
Sequence 10, Application US/08433123
Patent No. 6444789
                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1015 GAAGCATCATCATA 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/433,123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,123
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-433-123-21/c

Sequence 21, Application US/08433123

Sequence 21, Application US/08433123

Patent No. 6444789

APPLICANT: LOO, Shun

TITLE OF INVENTION:

NUMBER OF SEQUENCES:

ADDRESSE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 12.4; DB 1;
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.1%; Score 12.4; D
Best Local Similarity 92.9%; Pred. No. 2.1e
Matches 13; Conservative 0; Mismatches
               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                        FILING DATE:
CLASSIFICATION: 514
ATTORNEY, AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFRERENCE/POCKET NUMBER: LUO=:
TELECHONE: 202-628-5197
TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25,618
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TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BROMDY, ROGET L.
REGISTRATION UNMER: 25,6
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                       TELERAX: 202-737-5520
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            455 GAGCAGTGGTAGCA 468
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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US-07-696-793A-18
US-07-696-793A-18
is equence 18, Application US/07696793A
gequence 18, Application US/07696793A
general information:
General information:
APPLICANT: Nasarabadi, Shanavaz L.
APPLICANT: Nasarabadi, Shanavaz L.
TITLE OF INVENTION: Methods and Reagents for Gamma Globin TITLE OF INVENTION: TYPING
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cetus Corporation
STREET: 1400 Fifty-Third Street
CITY: Emeryville
STATE: Callifornia
COUNTRY: U.S.A.
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                                                                                                                                                                                                     Query Match 1.1%; Score 12.4; DB 1; Length 15; Best Local Similarity 78.6%; Pred. No. 2.1e+02; Matches 11; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S....

ZIP: 94608
COMPUTER RADABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage computer: Apple Macintosh 6.0.5
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NOTA:
APPLICATION WHASE: US/07/696,793A
FILING DATE: 19910507
CLASSIFICATION 19435
PRICA APPLICATION DATA:
APPLICATION NUMBER: SEPLICATION NUMBER: SEPLICATION NUMBER: 32704
REGISTRATION NUMBER: 32704
REGISTRATION NUMBER: 2598
REFERENCE/DOCKET NUMBER: 2598
TELECOMMUNICATION:
TELEPHONE: (415) 420-3444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: Other nucleic acid US-07-696-793A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 252
US-07-977-694-18
; Sequence 18, Application US/07977694
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STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1042 CACACCCAACTICC 1055
SOFTWARE: Patentin version 3.0 SEQ ID NO 4138
                                                                                                                                                                                                                                                                                                                                              1015 GAAGCATCATCATA 1028
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA
CORGANISM: Homo sapiens
US-09-685-6648-4138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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; Sequence 4138, Application US/09685664B
; Sequence 4138, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: Bacobedo, Jaime
; APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Becobedo, Jaime
; APPLICANT: Becobedo, Jaime
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recptor
; TITLE OF INVENTION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 1995-10-26
; PRIOR PILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WESULT 249
US-09-371-772B-4138
US-09-371-772B-4138
Sequence 4138, Application US/09371772B
Sequence 4138, Application US/09371772B
Sequence 4138, Application US/09371772B
Sequence 4138, Application
Sequence 105-107
Sequen
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                                                                                                                                                                                                        Query Match 1.1%; Score 12.4; DB 1; Length 15; Best Local Similarity 92.9%; Pred. No. 2.1e+02; Matches 13; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1015 GAAGCATCATA 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    455 GAGCAGTGGTAGCA 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 78.6%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            15 GAGCAGTGGCAGCA 2
                          ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-433-123-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-4138
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US-09-685-664B-4138
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ORGANISM: Homo sapiens
US-09-410-416-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-410-416-19/c
US-09-479-005A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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Sequence 12, Application US/09479005A

Patent No. 6656731

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

TITE OF INVENTION: Nucleac Acid Catalysts with Endonuclease Activity

FILE REFERENCE: MBHB00-884-C

CURRENT APPLICATION NUMBER: US/09/479,005A

CURRENT FILING DATE: 1090-01-07

PRIOR FILING DATE: 1999-11-19

PRIOR PILING DATE: 1999-11-19

PRIOR APPLICATION NUMBER: US 60/059,473

PRIOR PILING DATE: 1997-09-22

NUMBER OF SEQ ID NOS: 1208

SOFTWARE: PatentIn version 3.0

SEQ ID NO 12

LENGTH: 16
       PAPLICANT: Saiki, Randall K.
APPLICANT: Saiki, Randall K.
APPLICANT: Saiki, Randall K.
APPLICANT: Nagarabaddi, Shanavaz L.
TITLE OP INVENTION: Typing
TITLE OP INVENTION: Typing
NUMBER OF INVENTION: Typing
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingeland Street
CITY: Nutley
STREET: 340 Kingeland Street
CITY: Nutley
COUNTY: U.S.A.
ZIP: 07110-1139
COMPUTER: New Jersey
COUNTY: U.S.A.
ZIP: 07110-1139
COMPUTER: Nacintosh
COUNTY: U.S.A.
ZIP: 07110-1139
COMPUTER: Macintosh
COUNTY: WordPerfet
COUNTY: WordPerfet
COUNTY: WordPerfet
SOFTWARE: WordPerfet
COURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,694
FILING DATE: 19921117
CLASSIFICATION NUMBER: 32,630
REPERENCE/DOCKET NUMBER: 32,630
REPERENCE/DOCKET NUMBER: 8733
TELECOMMUNICATION INFORMATION:
TELEPHONE: G100 814-2863
TTELEPHONE: G100 814-2877
INFORMATION FOR SEC ID NO: 18;
SEQUENCE CHARACTERISTICS:
LENGTH FOR SEC ID NO: 18;
TELEPHONE: G100 814-2877
TUNDE: MITTEL ACTION
WITHER PARENCE CHARACTERISTICS:
LENGTH FOR SEC ID NO: 18;
ELENGTH FOR SEC ID NO: 18;
TELEPHONE: GLABBERIET CATOR
TOWNER: MITTEL ACTION
WITHER PARENCE CHARACTERISTICS:
LENGTH FOR SEC ID NO: 18;
TELEPHONE: GLABBERIET CATOR
TOWNER: MITTELET ACTION
WITHER PARENCE CHARACTERISTICS:
TENEDHOUS MITTELET ACTION
WITHER PARENCE CHARACTERISTICS:
TELEPHONE: GLABBERIET CATOR
TOWNER: MITTELET ACTION
WITHER PARENCE CHARACTERISTICS:
TOWNER: WITHER PARENCE ACTION
WITHER PARENCE CHARACTERISTICS:
TOWNER: WITHER PARENCE ACTION
WITHER PARENCE CHARACTERISTICS:
TOWNER: WITHER PARENCE ACTION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-07-977-694-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 16 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1042 CACACCCAACTICC 1055
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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US-07-977-694-20
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US-07-696-793A-20
US-07-696-793A-20
Sequence 20, Application US/07696793A
Sequence 20, Application US/07696793A
Sequence 20, Application US/07696793A
Setent No. 5220004
Setent No. 5220004
Setent No. 5220004
STREAT: Negaration
TITLE OF INVENTION: Methods and Reagents for G Gamma Globin
TITLE OF INVENTION: Methods and Reagents for G Corpers
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: 58
SORRESPONDENCE ADDRESS:
ADDRESSEE: Cetus Corporation
STREAT: 1400 Fifty-Third Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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CITY: Emeryville
STATE: California
STATE: Galifornia
COUNTRY: U.S.A.
ZIP: 9460B
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COMPUTER: MordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/696,793A
FILING DATE: 19910507
CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1;
ATTORNEY/AGENT INFORMATION:

NAME: Kevin R. Kaster

REGISTRATION NUMBER: 32704

REFERENCE/DOCKET NUMBER: 2558

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 658-5239

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERICS:
LENGTH: 17 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single stranded
TYPE: MOLELIC ACID
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-07-696-793A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: Other nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Keevin R. Kaster
REGISTRATION NUMBER: 32704
REFERENCE/DOCKET NUMBER: 2598
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 658-5239
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1042 CACACCCAACTICC 1055
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SESUL 727-684-19

SESUL 77-684-19

SESUL 77-684-19

SESUL 77-684-19

SESUL 77-684-19

SERVIN 72-684-19

SERVIN 72
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 60680-0703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linea
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STATE: IL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.1%; Score 12.4; DB 1; Length 17; Best Local Similarity 92.9%; Pred. No. 2.1e+02; Matches 13; Conservative 0; Mismatches 1; Indels
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 KD storage
COMPUTER: Apple Macintosh
CORPUTER: MordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,694
FILING DATE: 19921117
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: FILING DATE:
APPLICATION NUMBER:
FILING DATE: APPLICATION: 33.630
BOTT COUNTRY APPLICATION: ASSETT TO NUMBER: STATON NUMBER: 32.630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ausich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Mukharji, Indrani
APPLICANT: Proffit, John H
APPLICANT: Yarger, James G
APPLICANT: Yen, Huei-Che B
ITILLE OF INVENTION: Beta-Carotene Biosynthesis in
ITILLE OF INVENTION: Genetically Engineered Hosts
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,726
FILING DATE: 21-UL-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: 1L
COUNTRY: USA
ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Stacey R. Sias, Ph.D.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8733
TELECOMMUNICATION INFORMATION:
TELEPAX: (510) 814-2863
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: Other nucleic acid US-07-977-694-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 46, Application US/08095726
Patent No. 5530188
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1042 CACACCCAACTICC 1055
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US-08-095-726-46/c
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Michael, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Michael, Indrani
APPLICANT: Michaelj, Indrani
APPLICANT: Yenger, James G
APPLICANT: Yen, Huei-Che B
APPLICANT: Yen, Huei-Che B
TITLE OF INVENTION: Lycopene Biosynthesis in
TITLE OF INVENTION: Genetically Engineered Hosts
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
                                                                                                                                                                                                                                                                                                                                                            Score 12.4; DB 1;
Pred. No. 2.1e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,043
FILING DATE: 22-JUL-1993
CLASSIFFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,568
FILING DATE: 30-OCT-1991
ATTORNEY/AGRNT INFORMATION:
NAME: Galloway, NO. 5530189val B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Galloway, No. 5530189val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180
FILING DATE: 30-OCT-1991
TATCRNEY FAGENT INFORMATION:
NAME: Galloway, No. 5530188val
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-096-043-43/c
; Sequence 43, Application US/08096043
Patent No. 5530189
; GENERAL INFORMATION:
                                                                                       TELEPHONE: 3128567180
TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
COSCULE TYPE: DNA (genomic)
US-08-095-726-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: DNA (genomic)
US-08-096-043-43
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 92.9%;
Matches 13; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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US-08-390-850-601
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                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Proffitt, John H
APPLICANT: Proffitt, John H
APPLICANT: Yarger, James G
APPLICANT: Anoto Corp., Patents and Licensing Dept
CITT: Chicago
STATE: T.
    1; Indels
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTY: USA
ZIP: GEOGO-0703
ZIP: GOGO-0703
ZIP: GOGO-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IDM DATA:
APPLICATION NUMBER: US 07/785,569
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
TELEBCOMMUNICATION INFORMATION:
TELEBCOMMUNICATION INFORMATION:
TELEBCOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-390-850-601/c
; Sequence 601, Application US/08390850
; Patent No. 5612215;
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofeon, John
; APPLICANT: Stinchcomb, Dan T.
                                                                                                                                                                     RESULT 261
US-08-093-577-39/C
'Sequence 39, Application US/08093577
', Patent No. 5545816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.1%;
Best Local Similarity 92.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 CCCGGGCCGTGGCA 33
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                                                     20 CCCGGGCCGTGGCA 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: single
           13; Conservative
                                                                                                 17 cccedeccarecca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 262
                  Matches
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TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
NUMBER OF REQUENCES: 1151
CORRESPONDERS 1151
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CORRESPONDERS 1151
CORRESPONDERS 1151
CORPERS 1151
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MEDIUM TIRE: BLOIAGUE
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
PILING DATE: Annuary 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: Pebruary 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: AUGUST 2, 1992
APPLICATION NUMBER: 07/936,422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 CTGGAATTGTTGTT 307
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2 CUGGAAUUGUUGCU 15
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Best Local Similarity 50.00
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: 1.
US-08-373-124A-1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
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50.0%; Pred. No. 2.1e+02;
tive 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 264
US-08-373-124A-1611
Sequence 1611, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: Drayer, Kenneth
APPLICANT: MSWiggen, James
APPLICANT: MSWIGSEN, James
APPLICANT: MSSWIGSEN, James
APPLICANT: MSSWIGSEN, James
APPLICANT: MSSWIGSEN, ABRESS:
AUWHER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
STREET: Suite 4700
STREET: California
COUNTRY: U.S.A.
                                                  MEDIUM TYPE: storage
COMPUTER: ISM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION NUMBER: 08/195,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/195,943
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/936,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: Pebruary 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: Pebruary 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
RELECOMUNICATION NUMBER: 32,327
RELECOMUNICATION NUMBER: 32,327
RELEEPAR: (213) 955-0440
INFORMATION FOR SEQ ID NO: 572:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
INFORMATION FOR SEQ ID NO: 572:
LENGTH: 17 base pairs
INFORMATION FOR SEQ ID STRANDEDNESS: single
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: GLORAGE
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: January 13, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 CTGGAATTGTTGTT 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.04
Matches 7; Conservative
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Gaps
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i Sequence 1917, Application US/08373124A

i Patent No. 5646042

i GENERAL INFORMATION:

APPLICANT: Braper, Kenneth

APPLICANT: Braper, James

APPLICANT: Jarvis, Thale

ITILE OF INVENTION:

TITLE OF I
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50.0%; Pred. No. 2.1e+02;
trive 6; Mismatches 1;
PRIOR APPLICATION TOWNER: 08/245,400
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: Pebruary 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/986,422
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/986,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
RAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATI
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STREET: 120 S.
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: IL
                                                                                                                                                                                                                                                      US-08-434-411-55
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1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONTEST ON TEACURENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US /08/434,411
FILING DATE: 03-MAY-1995
CLIASSIFICATION: 435
PRIOR APPLICATION NUMBER: UP 306799/86
FILING DATE: 23-DEC-1986
PRIOR APPLICATION NUMBER: UP 51357/88
FILING DATE: 31-DEC-1988
PRIOR APPLICATION NUMBER: UP 51357/88
FILING DATE: 31-MAR-1988
PRIOR APPLICATION NUMBER: UP 51357/88
FILING DATE: 31-MR-1988
ATTORNEY ADSTRUCTION NUMBER: 25327
REGISTRATION NUMBER: 25327
REGISTRATION NUMBER: 25327
REGISTRATION NUMBER: 25327
REFERENCE/DOCKET NUMBER: 249-73
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MIYAJI, HIROMASA
APPLICANT: SATO, MORIVUKI
APPLICANT: OKABA, MASAMI
APPLICANT: OKABA, MASAMI
APPLICANT: TOH, SEIGA
APPLICANT: YAMASAKI, MOTOO
APPLICANT: YAMASKI, MOTOO
APPLICANT: YOKOO, YOSHIHARU
APPLICANT: YOSHIDA, HAJIME
APPLICANT: YOSHIDA, HAJIME
APPLICANT: YOSHINORI, KAZUO
APPLICANT: YOSHINORI, KAZUO
APPLICANT: YOSHINORI, KAZUO
APPLICANT: YOSHINORI, KAZUO
APPLICANT: YOSHINORI, KOMATSU
TITLE OF INVENTION: NOVEL POLYPEPTIDES
NUMBER OF SEQUENCES: 61
                                                                              209/035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 55, Application US/0843411
Patent No. 5681720
GENERAL INFORMATION:
APPLICANT: KUGA, TETSURO
ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard
REGISTRATION NUMBER: 32.327
REFERENCE/DOCKET NUMBER: 209/03
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELER: 67-3510
INFORMATION FOR SEQ ID NO: 1917:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
US-08-373-124A-1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KUGA, TETSURO
MIYAJI, HIROMASA
SATO, MORIYUKI
OKABE, MASAMI
MORIMOTO, MAKOTO
ITOH, SEIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 ACTGGCATATTTCT 287
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US-08-434-411-55/c
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TELERONE: (701) 816-4100
TELERONE: 20179 116-4100
TELERON: 20179 116-4100
TELERON: 20179 116-4100
TELERON: 20179 116-4100
TYPE: macker for sex pt to 10 in the pair of the rucleic acid
reporter: 17 base pairs
TYPE: macker asid
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Gaps

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Indels

Length 17;

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1.1%; Score 12.4; DB 1; Length 17;
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; Sequence 601, Application US/08435634
; Patent No. 5731283
; Patent No. 5731283;
; Patent INFORMATION:
APPLICANT: Draper, Kenneth G.
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Gustofson, John
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                       Query Match
1.1%; Score 12.4; DB 1;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: SULLE 4''O'
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATIOS SYSTEM: IBM P.C. DOS 5.0
SOFTWARNT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,634
FILING DATE: 05-MAY-1995
CLASSIFICATION NUMBER: 08/354,920
FILING DATE: PEDELUATION DATA:
APPLICATION NUMBER: 08/354,920
FILING DATE: 06-MAY-1995
APPLICATION NUMBER: 08/352,487
FILING DATE: December 13, 1994
APPLICATION NUMBER: 07/989,848
FILING DATE: December 13, 1994
APPLICATION NUMBER: 07/989,848
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
RESTERRENCE/DOCKET NUMBER: 211/084
TELERAK: (213) 955-0440
TELERAK: (213) 955-0440
TELERAK: (213) 955-0440
TELERAK: (213) 955-0440
TELERAK: (7-3510
INFORMATION FOR END IN DO: 601:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                    STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-08-434-402-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                              835 CAGGAAGGCCGGGG 848
                                                                                                                                                                                                                                                                                       17 CAGGCAGGCCGGGG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
      nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-435-634-601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MORIMOTO, MAKOTO
APPLICANT: ITOH, SEIGA
APPLICANT: YAMASAKI, MOTOO
APPLICANT: YAMAGUCHI, KAZUO
APPLICANT: YAMAGUCHI, KAZUO
APPLICANT: YOSHIDA, HAJIME
APPLICANT: YOSHIDA, HAJIME
APPLICANT: YOSHIDA, HAJIME
APPLICANT: YOSHINORI, KOWATSU
TITLE OF INVENTION: NOVEL POLYPEPTIDES
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 306799/86
FILING DATE: 23-DEC-1986
PRIOR APPLICATION NUMBER: JP 51357/88
FILING DATE: 04-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 51357/88
PRIOR APPLICATION NUMBER: JP 80088/88
PILING DATE: 31-MAR-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 55, Application US/08434402
Patent No. 5714581
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: CRAMPORD, ARTHUR
REGISTRATION NUMBER: 25327
REFERENCE/DOCKET NUMBER: 249-
TELECOMMUNICATION INFORMATION:
TELEPAX: (703)816-4100
TELEX: 200797 NIXN UR
INPORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KUGA, TETSURO
MIYAJI, HIROMASA
SATO, MORIYUKI
OKABE, MASAMI
                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-096-623A-51
                                                                                                                                                                                                                                                                                                              20 CCCGGGCCGTGGCA 33
TELEFAX: (312) 655-1501
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 17 base pairs
                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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US-08-434-402-55/c
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Gaps

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1; Indels

Mismatches

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2 CUGGAAUUGUUGCU 15
                                                          835 CAGGAAGGCCGGGG 848
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Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 17 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
Matches 13; Conservative
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                                              1; Indels
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Pred. No. 2.1e+02;
               Best Local Similarity 92.9%; Pred. No. 2.1e+02; Matches 13; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "SYHTHETIC DNA"
US-08-783-288-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: YOSHIDA, HAJIME
APPLICANT: YOSHINORI, KOMATSU
TITLE OF INVENTION: NOVEL POLYPEPTIDES
NUMBER OF SEQUENCES: 61
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 25327
REGISTRATION NUMBER: 249-73
REFERENCE/DOCKET NUMBER: 249-73
TELECOMMUNICATION INFORMATION:
TELECHONE: (703)816-4000
                                                                                                                                                                                                                                                                                                                 TELEFAX: (703)816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.1%;
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YOKOO, YOSHIHARU
YAMAGUCHI, KAZUO
                                                                                                                  925 CCTTATTAGAAATG 938
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17 CCTTATCAGAAATG 4
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EDNESS: single
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Best Local Similarity
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                  US-08-783-288-55/c
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PRESULT 271

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BURGOLT 273

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US-08-313-185-35/c
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Sequence 1611, Application US/08435628
Fatent No. 5817396
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSviggen, James
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: TREATMENT OF RESTENOSIS
ITILE OF INVENTION: TREATMENT OF RESTENOSIS
ANDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STREET: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: 35" Diskette, 1.44 Mb MEDIUM TYPE: 35" Diskette, 1.44 Mb MEDIUM TYPE: 35" Diskette, 1.44 Mb MEDIUM TYPE: 50" O'DEALTING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/435,628 FILING DATE: 05-MAY-1995
CLASSIFICATION NUMBER: 08/33,124 FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466 FILING DATE: Bebruary 7, 1994
APPLICATION NUMBER: 08/292,943
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 20, 1992
APPLICATION NUMBER: 32,327
REFERENCE/POCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1917, Application US/08435628
Patent No. 5817796
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 67-3510
INFORMATION POR ESC 1D NO: 1611:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
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US-08-435-628-1611
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**PRICANT: NESHIGAM: Damesh **
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RESULT 276
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APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
TITLE OF INVENTION: in Mycobacterium Tuberculosis
TITLE OF INVENTION: in Mycobacterium Tuberculosis
TUBECSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
STATE: D.C.
COMPUTER: D.C.
COMPUTER: D.C.
COMPUTER: IBM PC compatible
COMPUTER: INFORMATION INFORMATION:
TELEPHONE: (202) 408-4000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEPHONE: CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SECUENCE CHARACTERISTICS:
SECUENCE CHARACTERISTICS:
SECUENCE COMPATION SECUENCE CHARACTERISTICS:
SECUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: YOSHIDA, HAJIME
APPLICANT: YOSHINORI, KOMATSU
TITLE OF INVENTION: NOVEL POLYPEPTIDES
NUMBER OF SEQUENCES: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 275
US-08-890-640-55/C
US-08-890-640-55/C
Sequence 55, Application US/08890640
Patent No. 5994518
GENERAL INFORMATION:
APPLICANT: KUGA, TETSURO
APPLICANT: SATO, MORIYUKI
APPLICANT: GARAE, MASAMI
APPLICANT: MOKABE, MASAMI
APPLICANT: TOWAR, MASAMI
APPLICANT: TOWAR, NOTOO
APPLICANT: YAMASAKI, MOTOO
APPLICANT: YAMAGUCHI, KAZUO
APPLICANT: YAMAGUCHI, KAZUO
APPLICANT: YAMAGUCHI, KAZUO
APPLICANT: YAMAGUCHI, MAJIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) US-08-313-185-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1021 TCATCATAGAGAAG 1034
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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COMPATION: THEN PC COMPATION:

OFFERENTIAGE SYSTEM: PC-DOS/NS-DOS

GOFFWAND: Parentin Release #1.0, version #1.30

CURRENT APPLICATION DAY:

APPLICATION NUMBER: US /00/930,640

FILING DAYE: 31-90.73

FILING DAYE: 0.3-90.73

FILING APPLICATION NUMBER: US /00/930/66

FILING APPLICATION NUMBER: US /00/930/66

FILING APPLICATION NUMBER: US /00/930/66

FILING APPLICATION NUMBER: 19 8008/88

FILING APPLICATION NUMBER: 20 90/93/66

FILING APPLICATION NUMBER: 90/93/6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.1%; Score 12.4; DB 1; Length 17; Best Local Similarity 92.9%; Pred. No. 2.1e+02; Matches 13; Conservative 0; Mismatches 1; Indels
                                   PILING DATE:
CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
FILECOMMUNICATION INFORMATION:
FILECHOMEN: (202) 408-4400
FILECHEX: (202) 408-4400
FILECHEX: (202) 408-4400
FILECHEX: (202) 408-4400
FILECHEX: (202) 408-4300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 277
US-09-306-595C-27
Sequence 27, Application US/09306595C
Patent No. 6284506
GENERAL INFORMATION:
APPLICANT: HOSHINO, Tateuo
APPLICANT: HOSHINO, Tateuo
TITLE OF INVENTION: ISOPRENOID PRODUCTION
TITLE OF INVENTION: ISOPRENOID PRODUCTION
CURRENT PELLIGATION NUMBER: US/09/306,595C
CURRENT FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: 98108210
PRIOR APPLICATION NUMBER: 98108210
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 43
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2568, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1021 TCATCATAGAGAAG 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             863 TGTTGTAGTCCATG 876
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US-08-584-040-2568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-082-614A-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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LENGTH: 17
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Gaps
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APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STREET: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pavco, Pamela
APPLICANT: Pavco, Pamela
APPLICANT: Bacobodo, Jaime
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Becobedo, Jaime
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH PACTOR
TITLE OF INVENTION: GROWTH PACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.1%; Score 12.4; DB 1;
42.9%; Pred. No. 2.1e+02;
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Best Local Similarity 42.9%; Pred. No. 4.1.2
Matches 6; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: 1BM Compatible
OPERATING SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 5.44
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg Richard J.
REGISTRATION NUMBER: 218/064
TELECOMMUTICATION INFORMATION:
NAME: Warburg Richard J.
REFERENCE/DOCKET NUMBER: 218/064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 3886, Application US/08584040; Patent No. 6346398
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633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               689 TTGGCTGTTCATGT 702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 67-3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suite 4700
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US-08-584-040-3886
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STREET:
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TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 78.6*
----hes 11; Conservative
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CRGANISM: Homo sapiens
US-09-474-432B-475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-474-432B-475
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US-09-634-918-1

Sequence 1, Application US/09634918

Sequence 1, Application US/09634918

PARENT NO. 6379931

APPLICANT: Swiderski, Piotr M.

APPLICANT: Swiderski, Piotr M.

TITLE OF INVENTION: Chimeric DNA/RNA Ribozymes Containing Propanediol

TITLE OF INVENTION: Chimeric DNA/RNA Ribozymes Containing Propanediol

TILE REFERENCE: 2124-302

CURRENT APPLICATION NUMBER: US/09/634,918

CURRENT APPLICATION NUMBER: 60/148,339

PRIOR FILING DATE: 1999-08-12

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

MANDER OF SEQ ID NOS: 7

MANDER OF SEQ ID NOS: 7

SEQ ID NO 1

MANDER OF SEQ ID NOS: 7

MANDER OF SEQ ID 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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78.6%; Pred. No. 2.1e+02;
tive 2; Mismatches 1;
                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" Diskette, 1.44 Mb
MEDIUM TYPE: 1 EN Compatible
COMPUTER: IBM Compatible
OPERATION SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTONIEY/AGENT INFORMATION:
NAME: WARDING, RICHARD J.
REGISTRATION NUMBER: 22,18/064
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEX: 67.3510
INFORMATION FOR SEQ ID NO: 3886:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1015 GAAGCATCATCATA 1028
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Best Local Similarity 78.61
Matches 11; Conservative
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Matches 11, Conservative
Los Angeles
California
                                                                          RY: U.S.A.
90071-2066
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                                                                              COUNTRY:
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GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Beigelman, Leo
APPLICANT: Beigelman, Alex
APPLICANT: Beaudry, Amber
APPLICANT: Beaudry, Amber
APPLICANT: Rarpelsky, Amex
APPLICANT: Sweedler, David
APPLICANT: Worlectie Highosphate and their incorporation into oligonucleo
TITLE OF INVENTION NUMBER: US (09/474,432B
CURRENT APPLICATION NUMBER: US 60/064,866
FRIOR FILING DATE: 1997-11-05
FRIOR FILING DATE: 1998-104-29
FRIOR FILING DATE: 1998-104-28
FRIOR FILING DATE: 1998-104-28
FRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1226
SEQ ID NO 475
LENGTH: 17
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                                                                                                                                          Sequence 3, Application US/09634918

| Sequence 3, Application US/09634918
| Patent No. 6379931
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Swiderski, Piotr M.
| TITLE OF INVENTION: Chimeric DNA/RNA Ribozymes Containing Propanediol
| TITLE OF INVENTION: Chimeric DNA/RNA Ribozymes Containing Propanediol
| TITLE OF INVENTION: Chimeric DNA/RNA Ribozymes Containing Propanediol
| TITLE OF INVENTION: Chimeric DNA/RNA Ribozymes Containing Propanediol
| FILE REFERENCE: 2124-302
| CURRENT APPLICATION NUMBER: 60/148,339
| PRIOR APPLICATION NUMBER: 60/148,339
| RIOR FILING DATE: 1999-08-12
| SOFTWARE: Patentin Ver. 2.1
| SOFTWARE: Patentin Ver. 2.1
| LENGTH: 17
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OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
OTHER INFORMATION: Residues 1-9 are DNA; residues 10-17 are RNA.
OTHER INFORMATION: Residue 10 is cm. Residues 11 and 14 are um.
OTHER INFORMATION: Description of Artificial Sequence: Chimeric
OTHER INFORMATION: DNA/RNA ribozyme sequence
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; Patent No. 6528640
; GENERAL INFORMATION:
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RESULT 285

US-09-371-772B-1653

Sequence 1653, Application US/09371772B

Sequence 1654, Application US/09371772B

Patent No. 6566127

GENERAL INFORMATION:

APPLICANT: Bloczyme Pharmaceuticals, Inc.

APPLICANT: Brinchcomb, Dan

APPLICANT: Brochedo, Jaime

TITLE OF INVENTION: Levels of Vacular Endothelial Growth Factor Receptor

FILE REFERENCE: MBHB00, 876-J (237/198)

CURRENT APPLICATION NUMBER: US/09/371, 772B

FRIOR APPLICATION NUMBER: US 60/005, 974

PRIOR APPLICATION NUMBER: US 08/584, 040

FRIOR APPLICATION NUMBER: US 08/584, 040

FRIOR APPLICATION NUMBER: US 08/584, 040

FRIOR PILING DATE: 1996-01-08

NUMBER OF SEQ ID NOS: 14225

SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ALCOYING FIRALMACCULICATE, THE APPLICANT: ALCOYING FIRALMACCULICATE, APPLICANT: ACSWIGGEN, Jim
APPLICANT: Baccobedo, Dan
APPLICANT: Stinchcondb, Dan
APPLICANT: SECOPEDO, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rr
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rr
FILE REFERENCE: MBHB00,876-J (237/198)
CURRENT APPLICATION NUMBER: US 60/905,974
PRIOR FILING DATE: 1995-10-26
PRIOR PELICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PALENTIN Version 3.0
SEQ ID NO 5446
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                                                                                                                        Length 17;
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                                                                                                                        Score 12.4; DB 1;
Pred. No. 2.1e+02;
7; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5446, Application US/09371772B Patent No. 6566127
                                                                                                                           1.1%;
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1 UVAGCUGUUCAUGU 14
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                                                                                                                                                                         6; Conservative
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                         TYPE: RNA
CORGANISM: Homo sapiens
US-09-371-772B-1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-371-772B-1653
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Best Local Similarity
Matches 11; Conserv
                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
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US-09-371-772B-5446
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     LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ademic, Jasenka
APPLICANT: Adamic, Jasenka
APPLICANT: Adamic, Jasenka
APPLICANT: Adamic, Jasenka
APPLICANT: Adamic, Jasenka
APPLICANT: Sweedler, David
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nuclectide triphosphate and their incorporation into oligonucleot
FILER REFERENCE: MBHB00-831-B (247/276)
CURRENT APPLICATION NUMBER: US 60/064,866
PRIOR PLILNG DATE: 1999-12-19
PRIOR APPLICATION NUMBER: US 60/084,727
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1998-11-04
PRIOR FILING DATE: 1998-11-04
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1526
SOFTWARE: Patentin version 3.0
LENGTH: 17
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Patent No. 6566127

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Resco. Pam

APPLICANT: McSwiggen, Jim

APPLICANT: Escobedo, Jaime

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Musers US/09/371,72B

CURRENT APPLICATION NUMBER: US 60/005,974

PRIOR APPLICATION NUMBER: US 60/005,974

PRIOR APPLICATION NUMBER: US 68/584,040

PRIOR PILING DATE: 1996-01-08

PRIOR PILING DATE: 1996-01-08
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Query Match 114; Score 12.4; DB 1; Length 17; Best Local Similarity 42.94; Pred. No. 2.1e+02; Matches 6; Conservative 7; Mismatches 1; Indels
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                                                                                                                                                                                                                                         18-09-474-432B-667/c
| Sequence 667, Application US/09474432B
| Patent No. 65286A|
| GENERAL INFORMATION:
| APPLICANT: Ribozyme Pharmaceuticals, Inc.
| APPLICANT: Beigelnan, Leo
| APPLICANT: Beigelnan, Leo
| APPLICANT: Beaudry, Amber
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SOFTWARE: Patentin version 3.0
SEQ ID NO 1092
                                                                                                 305 GTTTCTGCCTTTGG 318
                                                                                                                             3 GUUUUUGCCUUUGG 16
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Best Local Similarity 92.9
Matches 13; Conservative
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US-09-474-432B-667
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APPLICANT:
APPLICANT:
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APPLICANT: Blagelman, Leo
APPLICANT: Beadery, Amber
APPLICANT: Beadery, Amber
APPLICANT: Beadery, Amber
APPLICANT: Rarpeisky, Alex
APPLICANT: Rarpeisky, Alex
APPLICANT: Karpeisky, Alex
APPLICANT: Sweedler, Dave
APPLICANT: Sunen, Shawn
APPLICANT: Sunen, Shawn
APPLICANT: Sweedler, Dave
APPLICANT: Sunen, Shawn
APPLICANTION NUMBER: US/09/476,387
CURRENT APPLICATION NUMBER: 09/474,432
PRIOR FILING DATE: 1999-04-28
PRIOR FILING DATE: 1999-04-28
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1997-11-04
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                                                                                                                                 Gaps
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                                                                  Query Match
1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                  US-09-925-388-27

US-09-925-388-27

Sequence 27, Application US/09925388

Sequence 27, Application US/09925388

Patent No. 6586202

GENERAL INFORMATION:

APPLICANT: HOSHINO, Tatsuo

APPLICANT: GOIMA, Kazuyuki

APPLICANT: GOIMA, Kazuyuki

APPLICANT: SETOGUCHI'N Yutaka

TITLE OF INVENTION: ISOPRENOID PRODUCTION

FILE REFERENCE: ISOPRENOID PRODUCTION

CURRENT APPLICATION NUMBER: US/09/925,388

CURRENT FILING DATE: 1999-06-06

PRIOR FILING DATE: 1999-06-06

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTIN VOY: 2.1

SEQ ID NO 27
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Patent No. 6617438
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                    1015 GAAGCATCATA 1028
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US-09-371-772B-6260
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; Sequence 6260 Application US/09371772B
; Patent No. 6566127
; Patent No. Fatent No. Fatent No. Management of Diseases or Conditions Repticant: Stinchcomb, Dan
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Stinchcomb, Dan
; PAPLICANT: Stochedo, Jaime
; PALICA PAPLICANTON NUMBER: US/09/371, 772B
; CURRENT APLICATION NUMBER: US 60/005, 974
; PRIOR APPLICATION NUMBER: US 60/005, 974
; PRIOR PILING DATE: 1995-10-26
; PRIOR FILING DATE: 1995-10-26
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 6260
; LENGTH: 17
; TYPE: RNA
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US-09-371-772B-6259

Sequence 6259, Application US/09371772B

Sequence 6259, Application US/09371772B

Sequence 6256, Application US/09371772B

Sequence 6256, Application

Patent No. 6566127

GENERAL INFORMATION:

APPLICANT: Ribozywa Pharmaceuticals, Inc.

APPLICANT: Scinchcomb, Dan

APPLICANT: Scinchcomb, Dan

APPLICANT: Recobedo, Jaime

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF ILING DATE: 1995-08-10

PRIOR APPLICATION NUMBER: US 60/005,974

PRIOR APPLICATION NUMBER: US 60/005,974

PRIOR APPLICATION NUMBER: US 08/584,040

PRIOR PILING DATE: 1995-01-08

NUMBER OF SEQ ID NOS: 14225

SOFTWARE: Patentin version 3.0
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                                                                                                                                    Query Match 1.1%; Score 12.4; DB 1; Length 17; Best Local Similarity 42.9%; Pred. No. 2.1e+02; Matches 6; Conservative 7; Mismatches 1; Indels
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1.1%; Score 12.4; DB 1;
1. Similarity 78.6%; Pred. No. 2.1e+02;
11; Conservative 2; Mismatches 1;
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4 UUAGCUGUUCAUGU 17
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CORGANISM: Homo sapiens
US-09-371-772B-6259
                                  ; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5446
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Matches 11; Conserva
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US-09-371-772B-6260
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Sequence 514, Application US/09827998

Fatent No. 6656700

GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
APPLICANT: Gu, Yizhong
APPLICANT: Ghannon, Mark
TITLE OF INVENTION: MOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REFERENCE: MDHWORP 8
CURRENT APPLICATION NUMBER: US/09/827,998
CURRENT PILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELLING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 544
ILENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INCRMATION:
APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: FENN, Sharron G.
APPLICANT: FENN, David K.
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David R.
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: Wonsheng
APPLICANT: SHANNON, Mark
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-46
PRIOR FILING DATE: 2000-06-46
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
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  PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6656700
SEQ ID No. 513
LENGTH: 17
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; Sequence 1694, Application US/09866108A
; Patent No. 6686188
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Best Local Similarity 92.9
Matches 13, Conservative
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CORGANISM: Homo sapiens
US-09-827-998-514
                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-827-998-513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-827-998-514/c
                                                                                                                                                                      TYPE: DNA
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beagelman, Leo
APPLICANT: Beagelman, Leo
APPLICANT: Beagelman, Leo
APPLICANT: Beadelwy, Alex
APPLICANT: Adamic, Jasenka Matulic
APPLICANT: Sweedler, Dave
APPLICANT: Sweedler, Dave
APPLICANT: Sweedler, Dave
APPLICANT: Sweedler, Dave
CURRENT Elmen, Shawn
FILE OF INVENTION: NUMBER: US/09/476,387
CURRENT PLILING DATE: 1999-10-04
PRIOR PILING DATE: 1999-04-28
PRIOR PLILING DATE: 1999-04-28
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-10-4
PRIOR FILING DATE: 1999-10-4
PRIOR PLILING DATE: 1999-10-4
PRIOR PLILING DATE: 1999-10-4
PRIOR FILING DATE: 1999-10-6
PRIOR FILING DATE: 1999-11-05
SOFTWARE: PROMER: 60/064,866
PRIOR FILING DATE: 1999-11-05
SOFTWARE: PROMER: 60/064,866
PRIOR FILING DATE: 1999-11-05
SOFTWARE: PROMER: 60/064,866
PRIOR FILING DATE: 1999-11-05
SOFTWARE: PROMER: 1997-11-05
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Batent No. 6656700

GENERAL INFORMATION:

APPLICANT: Gu, Yizhong

APPLICANT: Shannon, Mark

TITLE OF INFURITION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REPERRORE: MDHAORF: US/09/827,998

CURRENT APPLICATION NUMBER: US/09/827,998

PRIOR PRILING DATE: US 60/207,456

PRIOR PILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/236,359
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                                                                                                                                                                                                Length 17;
                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                          Query Match
1.1%; Score 12.4; DB 1;
Best Local Similarity 42.9%; Pred. No. 2.1e+02;
Matches 6; Conservative 7; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 666, Application US/09476387
Patent No. 6617438
GENERAL INFORMATION:
SOFTWARE: PatentIn version 3.0 SEQ ID NO 474 LENGTH: 17 TYPE: RNA
                                                                                                                                                                                                                                                                                                        305 GTTTCTGCCTTTGG 318
                                                                                                                                                                                                                                                                                                                                     3 GUTUUUGCCUUUGG 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-666
                                                                                                          ; ORGANISM: Homo sapiens
US-09-476-387-474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-476-387-666/c
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Patent No. 6686188
SEQ ID NO 1695
LENGTH: 17
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                                                                                                                                                    TYPE: DNA
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APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, WASN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE OF INVENTION' NUMBER: US/09/866,108A
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PELICR DATE: 2000-05-27
PRIOR APPLICATION NUMBER: GS 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PELICR DATE: 2000-09-27
PRIOR PLICATION NUMBER: PCT/US01/00666
PRIOR PLICATION NUMBER: PCT/US01/00666
PRIOR PLICATION NUMBER: PCT/US01/00666
PRIOR PLICATION NUMBER: PCT/US01/00669
PRIOR PLILNG DATE: 2001-01-30
PRIOR PRILNG DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR PRILNG DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
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                                                                  PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00668
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KESOLI 253

Sequence 1695, Application US/09866108A

; Patent No. 6686188

; GENERAL INFORMATION:

APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             505 CICATACTATCIGT 518
                                   FILING DATE: 2000-09-27
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Best Local Similarity 92.99
Matches 13; Conservative
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Pred. No. 2.18+02;
0; Mismatches 1; Indel8
              Score 12.4; DB 1; Length 17; Pred. No. 2.18+02; 0; Mismatches 1; Indels
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                Query Match 1.1%;
Best Local Similarity 92.9%;
Matches 13; Conservative
                                           505 CICATACTATCIGT 518
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Best Local Similarity 92.9
Matches 13; Conservative
                                                     CTCATACCATCTGT 3
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ORGANISM: Homo sapiens
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US-09-866-108A-1697/c
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     US-09-866-108A-1695
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APPLICATION NUMBER: US 60/236,359
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APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYSOIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PLICATION NUMBER: GB 24263.6
PRIOR PLICATION NUMBER: GB 24263.6
PRIOR PLICATION DATE: 2000-10-04
                                                                                                                                                                                                                                                                         PPLICANT: RANK, David R.
PPLICANT: GRANN WONDHOOD
PPLICANT: SHANNON, MARK
ITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
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Pred. No. 2.1e+02;
0; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT PILING DATE: 2001-05-25

RICOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-06-36

PRIOR PILING DATE: 2000-06-37

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30
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; Sequence 2568 Application US/09866108A
; Patent No. 6666188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David K.
; APPLICANT: RANK, David K.
; APPLICANT: CHEN, Wensheng
Sequence 1697, Application US/09866108A
Patent No. 6686188
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Best Local Similarity 92.9%;
Matches 13; Conservative
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ORGANISM: Homo sapiens
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APPLICANT:
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GENERAL INFORMATION:
APPLICANT: 01, Yachong
APPLICANT: 01, Yachong
APPLICANT: 01, Yachong
APPLICANT: PENN, Sharron G.
APPLICANT: PENN, David K.
APPLICANT: RANK, David K.
APPLICANT: APPLICANTON: WIGHER: 2001-05-25
FILE REFRENCE: AEDMICA: 2001-05-25
FILE REFRENCE: AEDMICA: 2001-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-00-04
FRIOR FILING DATE: 2000-00-04
FRIOR FILING DATE: 2000-10-04
FRIOR FILING DATE: 2001-01-30
FRIOR FIL
PRIOR PILING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00667
PRIOR PLING DATE: 2001-01-30
PRIOR PRIOR DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR DATE: 2001-01-
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NUMBER OF SEQ ID NOS: 15755
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Pred. No. 2.1e+02;
); Mismatches 1; Indels
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Best Local Similarity 92.99
Matches 13; Conservative
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US-09-866-108A-2568
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j Sequence 6290, Application US/09866108A

patent No. 668618B

j Ratent No. 668618B

j GENERAL INFORMATION:

APPLICANT: GI, Yizhong

APPLICANT: BANK, Bharron G.

APPLICANT: HANZEL, David K.

APPLICANT: HANZEL, David K.

APPLICANT: HANZEL, David K.

APPLICANT: GHAN, Wensheng

APPLICANT: GHAN, Wensheng

PROFICANT: GHAN, WENSHENG

ITLE OF INVENTION: MYOSIR: 2001-05-25

PRIOR PELIANG DARE: 2001-05-26

PRIOR PELIANG DARE: 2001-05-26

PRIOR PELIANG DARE: 2000-10-30

PRIOR PELIANG DARE: 2000-09-27

PRIOR PELIANG DARE: 2000-09-27

PRIOR PELIANG DARE: 2001-01-30

PRIOR PELIANG DARE: 2001
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                                                                                                                                                                                                                                                     Score 12.4; DB 1; Length 17; Pred. No. 2.1e+02; 0; Mismatches 1; Indels
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 6286
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 92.9%;
Matches 13; Conservative
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Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-6286
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                                                                                                         LENGTH
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RESULT 301

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US-09-866-108A-6311/C
US-09-866-108A-6311/C
US-09-866-108A-6311/Application US/09866108A

Patent No. 6686188

GENERAL INFORMATION:
APPLICANT: GI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: PENN, Sharron G.
APPLICANT: RANKE, David R.
APPLICANT: RANKE, David R.
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYCSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE OF INVENTION: MYCSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263.6
US-09-66-108A

Sequence 6110. Application US/09866108A

Sequence 6110. Application US/09866108A

Sequence 6110. Application US/09866108A

Sequence 6110. Application US/09866108A

Septicant: Gut, Yizhong

APPLICANT: GUT, Yizhong

APPLICANT: CHEN, Wensheron

APPLICANT: ERRNAR, David K.

APPLICANT: RANK, David K.

APPLICANT: SHANKON, MARK

TITLE OF INVENTION: WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFRENCE: AEOMICA-7

CURRENT PLILIAG DATE: 2001-05-25

FRIOR PILIAG DATE: 2000-05-26

FRIOR PLILING DATE: 2000-05-26

FRIOR PLILING DATE: 2000-05-26

FRIOR PLILING DATE: 2001-01-04

FRIOR PLILING DATE: 2001-01-06

FRIOR FILING DATE: 2001-01-06

FRIOR FILI
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Best Local Similarity 92.9
Matches 13; Conservative
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US-09-866-108A-6310
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US-09-866-108A-7016/c
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; ORGANISM: Homo E
US-09-866-108A-7016
                                                                                                                                                                                        LENGTH: 17
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APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2000-10-04
PRIOR PLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00667
PRIOR PILING DATE: 2001-01-30
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CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
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US-09-866-108A-7015/C
US-09-866-108A-7015/C
; Sequence 7015, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: GI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
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Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108A-6311
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APPLICANT: GT, Yizhong
APPLICANT: GT, Yizhong
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MATK
TITLE ON INVENTIONS: MOSTK
FILE REPERENCE: ABOMICA-7
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Remaining Prior Application data removed - See File Wrapper or PALM.
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Pred. No. 2.1e+02;
0; Mismatches 1;
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1.1%; Score 12.4; DB 1;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1;
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FILE REFERENCE.

CURRENT PELICATION NUMBER: US/09/866,108A

CURRENT PELING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PELING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR PELING DATE: 2000-10-04

PRIOR PILING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 7015
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Best Local Similarity 92.9
Matches* 13; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108A-7015
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APPLICANT: NO. 1095109
APPLICANT: PERN, Sharron G.
APPLICANT: PERN, Sharron G.
APPLICANT: PERN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: SHANNON, MALK
TITLE OF INVENTION: WANDSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE OF INVENTION: WASSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILLS REFERENCE: AEOMICA-7
CURRENT FILLING DATE: 2000-05-26
PRIOR PELLOATION NUMBER: US 60/207,456
PRIOR PELLOATION NUMBER: US 60/236,359
PRIOR PELLOATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PELLOATION NUMBER: PCT/US01/00666
PRIOR PELLOATION NUMBER: PCT/US01/00666
PRIOR PLILNG DATE: 2001-01-30
PRIOR PRIOR PRIOR PRIOR SQUENCE: 2001-01-30
PRIOR PRIOR PRIOR SQUENCE: 2001-01-30
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PRIOR PLING DATE: 20
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: SHANNON, Wark
TITLE OF INVENTION: WOSSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
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Pred. No. 2.10+02;
0; Mismatches 1; Indels
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; Sequence 7020, Application US/09866108A
; Patent No. 6686188
RESULT 305
US-09-866-108A-7019/c
; Sequence 7019, Application US/09866108A
; Patent No. 6686188
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Best Local Similarity 92.9%;
Matches 13; Conservative (
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US-09-866-108A-7019
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APPLICANT: JI, Yonggang
APPLICANT: BENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: GENN, WENSHANG
APPLICANT: GENN, WENSHANG
APPLICANT: GIRN, WENSHANG
APPLICANT: GIRN, WENSHANG
APPLICANT: GIRN, WENSHANG
TITLE OF INVENTION: WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE OF INVENTION: WORDER: US/09/866,108A
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PILING DATE: 2000-10-04.56
PRIOR PILING DATE: 2000-10-04.70
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
                     Gaps
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Pred. No. 2.1e+02;
0; Mismatches 1; Indels
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APPLICATION NUMBER: PCT/USO1/00663
FILING DATE: 2001-01-30
FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
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2.09-86-108A-7789/C
; Sequence 7789, Application US/09866108A
; Patent No. 6686188
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Best Local Similarity 92.9
Matches 13; Conservative
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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| FRACE NO. 6666188
| GENERAL INOCRAWATON:
| APPLICANT: GU, Yiahong
| APPLICANT: GU, Yiahong
| APPLICANT: GU, Yiahong
| APPLICANT: GU, Yiahong
| APPLICANT: GU, Yahong
| APPLICANT: GU, Yahong
| APPLICANT: GU, David R.
| APPLICANT: GUEN, Wencheng
| APPLICANT: GUEN, WENCHENG
| APPLICANT: SHANNON, MARK
| TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
| FILE PEPERAGES. AEGOING. | CURRENT APPLICANTON NUMBER: US 60/207, 456
| PRIOR APPLICANTON NUMBER: US 60/207, 456
| PRIOR APPLICANTON NUMBER: US 60/207, 456
| PRIOR FILING DATE: 2000-10-5-26
| PRIOR FILING DATE: 2001-01-30
| PRIOR FILING DAT
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 7889
LENGTH: 17
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Pred. No. 2.1e+02;
0; Mismatches 1; Indels
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Pred. No. 2.1e+02;
0; Mismatches 1;
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; Sequence 7790, Application US/09866108A
; Patent No. 6686188
                                                                                                                                                                                                                                                                                                                                Query Match
1.1%;
Best Local Similarity 92.9%;
Matches 13; Conservative
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1.1%;
Best Local Similarity 92.9%;
Matches 13; Conservative
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CORGANISM: Homo sapiens
US-09-866-108A-7789
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GENERAL INPORMATION:
APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: PENN, SHATON G.
APPLICANT: PENN, SHATON G.
APPLICANT: PENN, SHATON G.
APPLICANT: HANZEL, David R.
APPLICANT: GTEN, Wensheng
APPLICANT: GTEN, Wensheng
CURRENT: GTEN, Wensheng
FILE OF INVENTION: WOSSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: ADOMICA-7
CURRENT APPLICATION NUMBER: US 60/207, 456
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2001-01-30
PRIOR PLIN
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APPLICANT: GU, Yizhong

APPLICANT: GI, Yonggang

APPLICANT: FIN, Sharron G.

APPLICANT: RANK, David K.

APPLICANT: RANK, David R.

APPLICANT: GINW Wensheng

APPLICANT: GINNENNON, Mark

TITLE OF INVENTION: MARY

FILE REFERENCE: AEOMICA-7
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Pred. No. 2.1e+02;
); Mismatches 1;
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                          Sequence 7791, Application US/09866108A Patent No. 6686188 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-866-108A-7792/c
; Sequence 7792, Application US/09866108A
; Patent No. 6686188
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US-09-866-108A-7791
JS-09-866-108A-7791/c
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FILE REFERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2001-09-27

PRIOR PILING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
PILE REFERENCE: ABOMICA-7
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PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 9275
LENGTH: 17
TYPE: DNA
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1.1%; Score 12.4; DB 1;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1;
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; Sequence 9276, Application US/09866108A
; Patent No. 6686188
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: PANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||| ||||||
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US-09-866-108A-9275
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RESULT 311

RESULT 311

RESULT 311

Sequence 9275, Application US/09866108A

Fatent No. 6686418

GENERAL INFORMATION:

APPLICANT: GU, Yalxong

APPLICANT: Hand, Yalxong

APPLICANT: PENN, Sharron G.

APPLICANT: APRICAL INVEST. David K.

APPLICANT: SHANNON MARK

TITLE OF INTENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

TITLE OF INTENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

TITLE OF INTENTION: WHOMER: US/09/666,108A

CURRENT FILING DATE: 2001-05-25

PRIOR FILING DATE: 2000-06-27

PRIOR FILING DATE: 2000-10-49

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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                           PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR PELLING DATE: 2000-10-04

PRIOR PELLING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR PLILING DATE: 2000-09-27

PRIOR PELLING DATE: 2001-01-30

PRIOR PELLING DATE: 2001-01-30
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US-09-866-108A-7792
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Query Match
Best Local Similarity
Matches 13; Conserv
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US-09-866-108A-9278
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LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                   APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYSOIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
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APPLICANT: GU, Yizhong

APPLICANT: JI, Yonggang

APPLICANT: HANZEL, David R.

APPLICANT: RANK, David R.

APPLICANT: RANK, David R.

APPLICANT: HANZEL, David R.

APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE PIER REFERREE AROMGATA

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THERE OF INVENTION: MYOSIN-LIKE GENE FARRESSED IN HUMAN HEART AND MUSCLE PIER REFERREE AROMGATA

THERE OF INVENTION: MYOSIN-LIKE GENE FARRESSED IN HUMAN HEART AND MUSCLE PIER REFERREE AROMGATA

THERE OF INVENTION: MYOSIN-LIKE GENE FARRESSED IN HUMAN HEART AND MUSCLE PIER REFERREE AROMGATA

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SOFTWARE: Acomica Sequence Listing Engine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PILING DATE: 2000-10-04
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/866,108A CURRENT FILING DATE: 2001-05-25
Sequence 9277, Application US/09866108A Patent No. 6686188 GENERAL INFORMATION: APPLICANT: GU, Yizhong APPLICANT: T, Yonggang APPLICANT: PENN, Sharron G. APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 314
US-09-866-108A-9278/c
Sequence 9278, Application US/09866108A
; Patent No. 6686188
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Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108A-9277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 15755
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APPLICANT: John Landers
APPLICANT: John Landers
APPLICANT: David Houseman
APPLICANT: Barbara Jordan
APPLICANT: Alain Charest
ITLLE OF INVENTION: Methods and Products Related to
ITLE OF INVENTION: Methods and DNA Analysis
FILE REPERENCE: M0656/7045 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/404,912
CURRENT FILING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: US 60/101,757
PRIOR PILING DATE: 1999-09-25
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 691
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 12.4; DB 1;
Pred. No. 2.1e+02;
0; Mismatches 1;
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Pred. No. 2.1e+02;
0; Mismatches 1;
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PLICATION NUMBER: GB 24263.6
PRIOR PLILNG DATE: 2000-10-04
PRIOR PLILNG DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PLILNG DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 9278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-404-912-589
; Sequence 589, Application US/09404912
; Patent No. 6703228
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Best Local Similarity 92.9%;
Matches 13; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              505 CTCATACTATCTGT 518
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; ORGANISM: Homo Sapiens
US-09-404-912-589
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US-09-685-6648-1092
; Sequence 1092, Application US/0968564B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Racoingen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relat:
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recptor
; TITLE OF INVENTION: 1950-10-10
; FILE REPERENCE: MBHB00-876-K (400/0021)
; TILE REPERENCE: MBHB00-876-K (400/0021)
; FILE REPERENCE: MBHB00-876-K (400/0021)
; FILE REPERENCE: MBHB00-876-K (400/0021)
; PRIOR PILING DATE: 1995-01-08
; PRIOR FILING DATE: 1995-01-08
; PRIOR FILING DATE: 1995-01-08
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SEQ ID NOS: 8231
; SEQ ID NOS: 8231
; SEQ ID NO 1092
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ORGANISM: Homo sapiens
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                                                                               APPLICANT: STUTYER, LIEVEN
ROSEAU, RUDI
ROSEAU, RUDI
ROSEAU, RUDI
ROSEAU, RUDI
ROSEAU, RUDI
ADDRESSE: NIXON EVANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STRY: U.S.A.
COMPUTER: URGINIA
COMPUTER: LIBM PC compatible
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 21-ARR-1997
APPLICATION NUMBER: S6,663
RATORNICATION NUMBER: 2551-5
FELERPAX: (703) 816-4100
INFORMATION FOR SED ID NO: 14-4
CUERTHER TYPE: DNA (GENOMIC)
HYPOTHETICAL: NO
CUERTHER TYPE: DNA (GENOMIC)
HYPOTHETICAL: NO
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SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-155-885A-14
                                 Sequence 14, Application US/09155885A Patent No. 6709812 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGGTGGATCCCTC 858
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RESULT 316
US-09-155-885A-14
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CUTIT: AUGINALYN
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC COMPATIBLE
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
CLASSIFICATION NUMBER: PCT/EP97/02002
PILING DATE: 21-APR-1996
APPLICATION NUMBER: EP 96870053.4
APPLICATION NUMBER: EP 96870053.4
APPLICATION NUMBER: BP 96870053.4
APPLICATION NUMBER: BP 96870053.4
APPLICATION NUMBER: BP 96870053.4
APPLICATION NUMBER: BP 96870053.4
APPLICATION NUMBER: PC 96870053.4
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1.1%; Score 12.4; DB 1;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 2551-5
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ); ATTI-SENSE: NO SEQUENCE DESCRIPTION: SEQ ID NO: 33: US-09-155-885A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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STRANDEDNESS: single
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                                                                                                                                                               Length 17;
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                                                                     ; FEATURE:
; OTHER INFORMATION: PCR primer for S. cerevisiae PRC1 gene
US-09-993-192A-5
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 322
519452-80/c
; Patent No. 5194592
; APLICANT: YOSHIDA, HAJIME
; POLYPEPTIDES DENIVITIVES OF HUMAN GRANULOCYTE COLONY
; STIMULATING FACTOR
; UNMBER OF SEQUENCES: 83
; CURRENT APPLICATION DATA:
; FILING DATE: 3-MAR-1989
; PROFIN APPLICATION DATA:
; FILING DATE: 22-DEC-1987
; FILING DATE: 22-DEC-1987
                                                                                                                                                                                                                                                                                                                                                                                          SIGNATION OF STATE APPLICATION ON STATE OF TITLE OF INVERTION ON STATE OF INVENTION ON STATE OF INVENTION ON STATE OF INVENTION ON STATE OF INVENTION ON STATE OF STATE OF STATE OF STATE OF STATE OF SEQUENCES: 83

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/318,527

FILING DATE: 3-MAR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 136,647

FILING DATE: 22-DEC-1987

SEQ ID NO:80:

LENGTH: 17
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                                                                                                                                                          Score 12.4; DB 1;
Pred. No. 2.1e+02;
0; Mismatches 1;
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Pred. No. 2.1e+02;
0; Mismatches 1;
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US-08-390-850-479/c
; Sequence 479, Application US/08390850
                                                                                                                                                               Query Match
Best Local Similarity 92.9%;
Matches 13; Conservative (
                                                                                                                                                                                                                                                             414 GGTTTTTCCTTATA 427
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                                                                                                                                                                                                                                                                                                   15 GGTTTCTCCTTATA 2
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Matches 13; Conservative
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Best Local Similarity 92.9
Matches 13; Conservative
                     TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Fatent No. 6818447

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Recomment of Diseases or Conditions Relate

TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate

TITLE OF INVENTION: Method and Reagent for Treatment of Conditions Relate

TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate

TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate

TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate

TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate

TITLE OF INVENTION NUMBER: US 00/065,974

FILE REPRENCE: MHBBO0-876-K (400/021)

CURRENT FILING DATE: 1995-10-26

FRIOR FILING DATE: 1995-01-08

FRIOR FILING DATE: 1995-01-08

FRIOR PILING DATE: 1995-01-08

FRIOR PILING DATE: 1995-01-08

NUMBER OF SEQ ID NOS: 8231

SOFTWARE: PatentIn version 3.0

SEQ ID NOS: 8231

SEQ ID NO 1653
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APPLICANT: Sohn, Junghoon
APPLICANT: Sohn, Junghoon
APPLICANT: Sohn, Junghoon
APPLICANT: Ma, Moowoong
APPLICANT: Rim, Moowoong
APPLICANT: Agaphonov, Michasel
TITLE OF INVENTION: Hansenula polymorpha mutants and process for the preparation of
TITLE OF INVENTION: Hansenula polymorpha mutants and process for the preparation of
TITLE OF INVENTION: Hansenula polymorpha mutants and process for the preparation of
TITLE OF INVENTION: 108/09/993,192A
CURRENT APPLICATION NUMBER: US/09/993,192A
FRIOR APPLICATION NUMBER: US/09/674,617
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                                                                                              ö
                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dong Kook Pharmaceutical Co. APPLICANT: Rhee, Sangki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.1%; Score 12.4; DB 1; Length 17; Best Local Similarity 78.6%; Pred. No. 2.1e+02; Matches 11; Conservative 2; Mismatches 1; Indels
                                             Score 12.4; DB 1; Length 17; Pred. No. 2.1e+02;
                                                                                              1; Indels
                            1.1%; Scc. No. 2...
42.9%; Pred. No. 2...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09993192A
Patent No. 6838555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1015 GAAGCATCATA 1028
                                                                                                                                       689 TTGGCTGTTCATGT 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GAAGCAUCAGCAUA 15
                                                                                                                                                                 1: ||:|:||:|
1 UUAGCUGUUCAUGU 14
                                             Query Match
Best Local Similarity 42.9%
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euisung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
CORGANISM: Homo sapiens
US-09-685-664B-1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
US-09-685-664B-1092
                                                                                                                                                                                                                                                        RESULT 319
US-09-685-664B-1653
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US-09-993-192A-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
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Query Match
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels
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Sequence 456, Application US/08373124A
Sequence 456, Application US/08373124A
Sequence 456, Application US/08373124A
Setcome No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: McSwig
                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 9007I

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM COMPUTED: 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
RIUNG DATE: Pebruary 17, 1995
FILING DATE: Pebruary 17, 1995
FILING DATE: December 13, 1994
APPLICATION NUMBER: 08/152,487
APPLICATION NUMBER: 08/152,487
APPLICATION NUMBER: 07/989,848
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/989,848
FILING DATE: December 7, 1992
ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 211/084
TELEPPANE: (213) 489-1600
TELEPPANE: (213) 489-1600
TELEPPANE: (213) 955-0440
TELEPPANE: (213) 955-0440
TELEPPANE: G135 BOSIGE
TELEPHONE: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEGUENCE CHARACTERISTICS:

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STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              901 CAAGAGCCTCAACATTT 917
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                                                                                                                                                                             CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
US-08-390-850-480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
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Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NESCUL: 243
US-08-390-850-480/C

1/S-08-390-850-480/C

1/S-08-390-850-480/C

1/S-08-390-850-480/C

1/S-08-390-850-80/C

1/S-08-390-850-80/C

1/S-08-390-80/C

1
                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Deaper, Kenneth G.
APPLICANT: Deaper, James
APPLICANT: Braveo, Pamela
APPLICANT: Generoforn, John
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: METHON, DAN T.
TITLE OF INVENTION: METHON AND REAGENT FOR TREATMENT
TITLE OF INVENTION: METHON E. Lyon
STREET: 633 West Fifth Street
STREET: 634 West Fifth Street
STREET: Galte 4700
CITY: Los Angeles
STREET: Galter 4700
CITY: Los Angeles
STR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        902 AAGAGCCTCAACATTTC 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 ATGAGCCAAAACATTTC 1
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US-08-390-850-479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
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1.1%; Score 12.2; DB 1; Length 17; 82.4%; Pred. No. 2.3e+02; tive 0; Mismatches 3; Indels
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Patent No. 5646042

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: TREATMENT OF RESTENCISIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Saite 4700
STREET: Saite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage COMPUTER: 1EW Compatible OPERATING SYSTEM: IEW COMPATIBLE OF SOFTWARE: WORD PERFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/373,124A PTLING DATE: January 13, 1995 APPLICATION NUMBER: 08/192,943 APPLICATION NUMBER: 08/192,943 FILING DATE: FEBRUARY 7, 1994 APPLICATION NUMBER: 07/987,132 FILING DATE: December 7, 1992 APPLICATION NUMBER: 07/987,132 FILING DATE: December 7, 1992 APPLICATION NUMBER: 07/987,132 FILING DATE: December 7, 1992 APPLICATION NUMBER: 07/987,132 FILING DATE: AUGUST 26, 1992 ATPLING DATE: December 7, 1994 APPLICATION NUMBER: 07/987,132 APPLICATION NUMBER: 07/987
                              FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: AUGUST 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WATAURY RICHARD
REFERENCE/DOCKET NUMBER: 209/035
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELEPAX: 67-3510
TELEX: 67-3510
TELEX: 67-3510
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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        597 TTAAGAAAGACTTCATA 613
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-08-373-124A-458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 327
US-08-373-124A-504
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1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 326

US-08-373-124A-458/C

Sequence 458, Application US/08373124A

PERENT No. 5646042

REPLICANT: Stinchcomb, Dan T.

APPLICANT: Branchcomb, Dan T.

APPLICANT: Draper, Kenneth

APPLICANT: Draper, Kenneth

APPLICANT: Jarvis, Thale

TITLE OF INVENTION: METHODS AND COMPOSITIONS POR

TITLE OF INVENTION: TREATMENT OF RESTENCES

NUMBER OF SEQUENCES: 2627

CORRESPONDENCES: 2627

CORRESPONDENCES: 2627

CORRESPONDENCES: 2627

CORRESPONDENCES: 2627

CORRESPONDENCES: 2627

CORRESPONDENCES: 2627

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: SILLE 4700

CITY: Los Angeles

STATE: COLUTRY: U.S.A.

ZIP: OCCUPIENT: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.

ZIP: 90071
ZIP: 90071
ZIP: 90071
ZIP: BOOTO
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Brorage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/73,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION NUMBER: 08/245,466
FILING DATE: PROFERS: 08/25,466
FILING DATE: PEDRUARY 7, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: PEDRUARY 7, 1994
APPLICATION NUMBER: 07/981,132
FILING DATE: DECEMBER 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: AUGUST 26, 1992
ATTORNEY, AGENT INFORMATION:
NAME: WAPDLICATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECEX: 67-3510
INFORMATION FOR SEQ ID NO: 456:
SEQUENCE CHARACTERS: ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      598 TAAGAAAGACTTCATAA 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-08-373-124A-456
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Gaps
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                                                  Score 12.2; DB 1; Length 17;
Pred. No. 2.38+02;
9; Mismatches 3; Indel8
                                                                                                                                                                                                                                                                              US-08-373-124A-1341/C

US-08-373-124A-1341/C

Sequence 1341, Application US/08373124A

Patent No. 5646042

GENERAL INFORMATION:
APPLICANT: Stinchoomb, Dan T.
APPLICANT: Braper, Kenneth
APPLICANT: Jarvis, Thale
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF SEQUENCES: 2627

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: S13 West Fifth Street
STREET: S11te 4770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDLUM TYPE: 3.5" Diskette, 1.44 Mb
MEDLUM TYPE: 5.5" DISKETTE, 1.00 S.0.
SOFWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/122,943
FILING DATE: Pebruary 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: AUGUST 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: AUGUST 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: AUGUST 7, 1992
APPLICATION NUMBER: 30,327
REFERENCE/DOCKET NUMBER: 32,327
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 67-310
INFORMATION FOR ESO ID NO: 1341:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 TGGCTTGGGCAGGCTGC 20
                                                                                                                                                  855 CCTCTTTGTGTTGTAGT 871
                                                                                                                                                                               Query Match 1.1%;
Best Local Similarity 29.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
TOPOLOGY: linear
           ;
US-08-373-124A-716
                                                                                                                                                                                                                                                                          RESULT 329
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Best Local Similarity 58.8%; Pred. No. 2.3e+02; Antches 10; Conservative 4; Mismatches 3; Indels
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US-08-37-124-716

US-08-37-124-716

Sequence 716, Application US/08373124A

Patent No. 564642

CENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.

APPLICANT: McSwiggen, James

APPLICANT: McSwiggen, James

APPLICANT: McSwiggen, James

APPLICANT: McSwiggen, James

APPLICANT: McSwiggen, Thale

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

TITLE OF INVENTION: TREATMENT OF RESTENCISS

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: US.A.

ZIP: 900.1

ZONPUTER: IBM Compatible

COMPUTER: IBM Compatible

OMPUTER: Word Perfect 5.1

CUMPUTER: Word Perfect 5.1

CUMPUTER: Word Perfect 5.1

CUMPUTER: Wand Perfect 5.1

CUMPUTER: Wand Perfect 5.1

CUMPUTER: Wand Perfect 5.1

CUMPUTER: May 18, 1995

PILING DATE: December 7, 1994

APPLICATION NUMBER: 08/192, 943

FILING DATE: PEDLUARY 07/997,132

FILING DATE: PEDLUARY 07/997,132

FILING DATE: AUGUST 26, 1992

ATPONDENT NUMBER: 07/996,222

FILING DATE: AUGUST 26, 1992

APPLICATION NUMBER: 07/996,222

FILING DATE: AUGUST 26, 1992

ATPONDENT NOWNER: 07/996,222

FILING DATE: AUGUST 26, 1992

ATDONEY MANNER: 07/996,222

FILING DATE: AUGUST 26, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209/035
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TELEPHONE: (213) 489-1600
TELERX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 504:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYRE: nucleic acid
STRANDENNES: single
                                                                                                                                                                                                                                                                                                                                                                              910 CAACATTTCCTAGAGCC 926
                                                                                                                                                                                                                                                                                                                                                                                                                1 CACCAUTUCAUAGAGAC 17
                                                                                                                                                                                                                       ; TOPOLOGY: linear
US-08-373-124A-504
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1.1%; Score 12.2; DB 1; Length 17; 58.8%; Pred. No. 2.3e+02; ive 4; Mismatches 3; Indels
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Patent No. 5646042

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: McSwiggen, Vames
APPLICANT: Marvies, James
APPLICANT: Marvies, Thale
ITTLE OF INVENTION: TREATMENT OF RESTENOSIS AND
ITTLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
                           APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: acrosque COMPUTER: 1EM COMPALIALE OPERATING SYSTEM: IEM COMPALIALE OPERATING SYSTEM: IEM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 08/195, 94 APPLICATION NUMBER: 08/195, 94 APPLICATION NUMBER: 07/991, 132 FILING DATE: Rebruary 7, 1994 APPLICATION NUMBER: 07/991, 132 FILING DATE: AUGUST 07/991, 132 APPLICATION NUMBER: 07/991, 132 ATTORNEY/AGENT INPORMATION: NAME: Warburg, Richard RESERENCE/DOCKET NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 30,9035 TELECOMMUTER 1001 NUMBER: 30,9035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2393:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 910 CAACATTTCCTAGAGCC 926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
       APPLICANT: Draper, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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US-08-373-124A-2437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 52.9%; Pred. No. 2.38+02;
Matches 9; Conservative 5; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: POST 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: PEDLUARY 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: PEDCEMBER 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: AUGUBER 7, 1992
APPLICATION NUMBER: 26,1992
ATTORNEY/AGENT INFORMATION:
NAME: WAFDLICATION NUMBER: 209/035
TELESEMONICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 1559:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                     RESULT 330
82-08-37-124A-1559
Sequence 1559, Application US/08373124A
Patent No. 5646042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-373-124A-2393
; Sequence 2393, Application US/08373124A
; Patent No. 5646042
; Patent No. 5646042
; APPLICANT: Stinchcomb, Dan T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  499 TTAGAACTCATACTATC 515
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  17 TGGCTTTGGAAGGCTTC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-08-373-124A-1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 331
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; Sequence 5, Application US/08200232
; Patent No. 5721349
; Patent No. 5721349
; GENERAL INFORMATION:
    APPLICANT: COVET, Timothy L. APPLICANT: Blaser, Martin J. TITLE OF INVENTION: WACUCLATING TOXIN-DEFICIENT H. PYLORI TITLE OF INVENTION: WACUCLATING TOXIN-DEFICIENT H. PYLORI TITLE OF INVENTION: WACUCLATING TOXIN-DEFICIENT H. PYLORI TITLE OF INVENTION: ADDRESSE: BECHESSE: RESUBERG P.C. STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta STARE: Georgia COUNTRY: USA ZIP: 30303
COMPUTER: EBOPY disk COMPUTER: IBM PC compatible COMPUTER: BEATHIR READER PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/200,232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 2.3e+02;
Matches 9; Conservative 5; Mismatches 3; Indels
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/124,943
PILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
PILING DATE: PECEMBER 7, 1994
APPLICATION NUMBER: 07/987,132
PILING DATE: DECEMBER 7, 1992
APPLICATION NUMBER: 07/987,132
PILING DATE: AUGUST 26, 1992
APPLICATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 32,327
TELECOMUNICATION INFORMATION:
TELECHOMEN (213) 955-0440
TELECHOMEN FOR SEQ ID NO: 2563:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPER: nucleic acid
TYPELOGY: 11near
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 2200.023
TELECOMUNICATION INFORMATION:
TELECHONE: 404/688-0770
TELEFRAX: 404/688-9880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        499 TTAGAACTCATACTATC 515
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1 UUAGAACUCCAGCUAUC 17
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US-08-373-124A-2563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
1.1%; Score 12.2; D.
Best Local Similarity 52.9%; Pred. No. 2.3e
Matches 9; Conservative 5; Mismatches
                                                                                                                            COUNTRY: California

COUNTRY: U.S.A.

ZIF: 90071

COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: BEACAGE
COMPUTER: BM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOGTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
PRILING DATE: January 13, 1995
PRILING DATE: PEDATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: PEDATA: 7, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: PEDECEMPER 7, 1992
APPLICATION NUMBER: 07/98/,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/986,422
FILING DATE: August 26, 1992
APPLICATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,927
REFERENCE/DOCKET NUMBER: 32,927
REFERENCE/DOCKET NUMBER: 32,937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2437:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDENBESS: single
1 TOPOLOGY: linear
US-08-373-124A-2437
                                                 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               546 ATGAAATTTAATATGCT 562
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1 AAGAAAUUAAAUAUGGU 17
                                                                                                             Los Angeles
California
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                                                                                                                                                                                                               Query Match
1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 479, Application US/08435634

Patent No. 5731295

GENERAL INFORMATION:

APPLICANT: Draper, Kenneth G.

APPLICANT: McSwiggen, James

APPLICANT: Gustofson, John T.

TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT

TITLE OF INVENTION: OF ARTHRITIC CONDITIONS

NUMBER OF SEQUENCES: 1151

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: Suite 4700

STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
COUNTRY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 30071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
MEDIUM TYPE: 0.5 Diskette, 1.44 Mb
APPLICATION NUMBER: 0.5 0.495
APPLICATION NUMBER: 0.8/354,920
FILING DATE: December 12, 1993
APPLICATION NUMBER: 0.7/989,848
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WALDLEY RICHARD
REGISTRATION NUMBER: 211/084
REFERENCE/DOCKET NUMBER: 211/084
TREFERENCE/DOCKET NUMBER: 211/084
TREFERENCE/DOCKET NUMBER: 211/084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (213) 489-1600
TELEX: (213) 955-0440
INPORMATION FOR SEQ ID NO: 479:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                               839 AAGGCCGGGGTGGATCC 855
                                                                                                                    TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-200-232-5
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 17 base pairs
                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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TOPOLOGY:
US-08-435-634-479
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    Length 17;
                                                                                        3, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Gustofson, John
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
NUMBER OF SEQUENCES: 1151
CORRESPONDENCE ADDRESS:
Query Match 1.1%; Score 12.2; DB 1;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: SCAESAGE
COMPUTER: SCAESAGE
COMPUTER: THE SCAESAGE
SUSTWARE: TRACESCO VERSION 1:5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,634
FILING DATE: 05-MAY-1995
CLASSIFICATION NUMBER: 08/390,850
FILING DATE: February 17, 1995
APPLICATION NUMBER: 08/354,920
FILING DATE: Pebruary 17, 1995
APPLICATION NUMBER: 08/152,487
FILING DATE: December 13, 1994
APPLICATION NUMBER: 07/989,848
FILING DATE: December 7, 1992
ATTORNEY AGENT INFORMATION:
NAME: WATDUER 7, 1000-1000
NAME: WATDUER 7, 10000
NAME: WATDUER 7, 1000-1000
NAME: WATDUER 7, 1000-1000
NAME: WATDUER 7, 1000-1000
NA
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 211/084 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 480, Application US/08435634
; Patent No. 5731295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                902 AAGAGCCTCAACATTTC 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     901 CAAGAGCCTCAACATTT 917
                                                                                                                                                                                                                                                                    17 Argagccaaaacarrrc 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 CATGAGCCAAAACATT
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-435-634-480
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Query Match 1.1%; Score 12.2; DB 1; Length 17; Best Local Similarity 82.4%; Pred. No. 2.3e+02; Matches 14; Conservative 0; Mismatches 3; Indels
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US-08-435-28-458/C

Sequence 458, Application US/08435628

Sequence 458, Application US/08435628

Patent No. 5817796

GENERAL INFORMATION:

SEPPLICANT: Stinchocomb, Dan T.

APPLICANT: Draper, Kenneth

APPLICANT: Draper, Kenneth

APPLICANT: Javels, Thale

TITLE OF INVENTION: TRRATMENT OF RESTENOSIS

TITLE OF INVENTION: TRRATMENT OF RESTENOSIS

NUMBER OF SEQUENCES: 2627

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: Suite 4700

STREET: Suite 4700

STREET: California
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 610-72

COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PETFECT 5.1
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 0-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/373,124
PRIOR APPLICATION NUMBER: 08/373,124
PRIOR APPLICATION NUMBER: 08/373,124
APPLICATION NUMBER: 08/373,124
APPLICATION NUMBER: 08/373,124
APPLICATION NUMBER: 08/192,943
FILING DATE: PEDCEMBER 77, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: PEDCEMBER 77, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: AUGUST 7, 1992
APPLICATION NUMBER: 26, 1992
APPLICATION NUMBER: 26, 1992
APPLICATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER:
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       598 TAAGAAGACTTCATAA 614
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STRANDEDNESS: BILL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-435-628-456/C

Sequence 456, Application US/08435628

Sequence 456, Application US/08435628

Sequence 456, Application US/08435628

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Braper, Kenneth

APPLICANT: McSwiggen, James

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND TITLE OF INVENTION: CANCER USING RIBOZYMES

NUMBER OF SEQUENCES: 2627
                                                                                                                                                                                            Sequence 22, Application US/07936421
; Sequence 22, Application US/07936421
; Patent No. 5750390
; GENERAL INFORMATION:
    APPLICANT: James D. Thompson
    APPLICANT: James D. Thompson
    APPLICANT: Renneth G. Draper
    TITLE OF INVENTION: METHOD AND REAGENT FOR
    TITLE OF INVENTION: METHOD AND REAGENT FOR
    TITLE OF INVENTION: GENE
    NUMBER OF SEQUENCES: 2
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Lyon & Lyon
    STREET: 611 West Sixth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
COUNTRY: Los Angeles
COUNTRY: Los Angeles
COUNTRY: Los Angeles
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: Mordberfect (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/936,421
FILING DATE: 19220826
CLASSIFICATION DATA: ROST APPLICATION DATA:
PRIOR APPLICATION DATA:
RECORPLICATION DATA: Gescribed below:
APPLICATION DATA: described below:
APPLICATION NUMBER: TILING DATE:
FILING DATE:
TILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 AGCCTGCGGCCTTGTGT 377
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TELEX: 67-3510
INFORMATION FOR SEQ 1D NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear US-07-936-421-22
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Matches 14; Conserv
                                                                                                                                                                                   US-07-936-421-22/c
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Gaps

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APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 504, Application US/08435628
Fatent No. 5817796
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Jarvis, Thales
APPLICANT: Jarvis, Thales
APPLICANT: McSwiggen, James
TITLE OF INVENTION: CANCER USING RIBOZYMES
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 633 West Fifth Street
STREET: Galifornia
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: SLORAGE
MEDIUM TYPE: SLORAGE
COMPUTER: IBM Compatible
                                       COMPUTER READBLE FORM:
MEDIUM TYPE: 80.000
MEDIUM TYPE: 13.5" Diskette, 1.44 Mb
MEDIUM TYPE: 18M Compatible
OPERATING SYSTEM: 18M P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/135,628
FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/249,43
APPLICATION NUMBER: 08/192,943
APPLICATION NUMBER: 07/991,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: MAUGHE 26, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: MAUGHE 26, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: MAUGHE 26, 1992
ATTORNEY, AGENT INFORMATION:
NAME: WATDUTG, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELERA: (7-3510
TELEX: 67-3510
TENPORMATION POR SEQ ID NO: 458:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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U.S.A.
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US-08-435-628-458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-435-628-716
Sequence 716, Application US/08435628
Patent No. 5817796
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: McSwig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon STREET: 613 West Fifth Street STREET: 613 West Fifth Street STREET: 5 Suite 4700 CITY: Los Angeles STATE: California COUNTR: U.S.A.
ZIP: 90071 COMPUTER READABLE FORM: WIDJUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage CÖMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: WORT PATELICATION DATA:
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/435,628
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124
FILING DATE: May 18, 1995
APPLICATION NUMBER: 08/192,943
FILING DATE: PERTARY, 13, 1995
APPLICATION NUMBER: 07/987,132
FILING DATE: PERTARY, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/987,132
APPLICATION NUMBER: 07/987,132
APPLICATION NUMBER: 26,1992
APPLICATION NUMBER: 32,327
REGENEURS MAY 100 NUMBER: 32,327
TELECOMMUNICATION INFORMATION:
TELEFONE: (213) 955-0440
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Ouery Match
1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels
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GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Braper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Draper, Thale
TITLE OF INVENTION: TREATHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Gail West Fifth Street
STREET: Gail West Fifth Street
STREET: Suite 4700
CITY: Los Angels
COUNTY: U.S.A.
ZIP: 90071
COUNTYER READABLE FORM:
MEDIUM TYPE: Storage
COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
COMPUTER: IBM Compactible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION NUMBER: US/08/435,628
FILING DATE: Word Perfect 5.1
CURRENT APPLICATION NUMBER: 08/373,124
APPLICATION NUMBER: 08/373,124
APPLICATION NUMBER: 08/373,134
APPLICATION NUMBER: 08/373,134
APPLICATION NUMBER: 08/392,943
FILING DATE: Pebcember 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: BAUSHER 26,1992
APPLICATION NUMBER: 07/986,422
FILING DATE: AUGUST 26,1992
APPLICATION NUMBER: 07/936,422
FILING DATE: AUGUST 26,1992
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/995,422
FILING DATE: AUGUST 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1559, Application US/08435628
; Patent No. 5817796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 TGGCTTGGGCAGGCTGC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 343
US-08-435-628-1559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.1%; Score 12.2; DB 1; Length 17; Best Local Similarity 29.4%; Pred. No. 2.3e+02; Matches 5; Conservative 9; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATENT NO. 5817/308

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: Jarvis, Thale
APPLICANT: Jarvis, Thale
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATWENT OF REGTENCES:
ADDRESSE: 2627
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: 613 West Fifth Street
STREET: G13 West Fifth Street
STREET: G13 West Fifth Street
STREET: G14 FORM:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STREET: G15 FORM:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700
CITY: U.S.A.

ILE OF ONTRY: U.S.A.

ZIP: 9071
COMPUTER READABLE FORM:
MEDIUM TYPE: STOTAGE
COMPUTER: IBM Compatible
OPPERATING SYSTEM: USA PATE:
COMPUTER: WORD Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: OS-WAY-1995
CLASSIFICATION NUMBER: US/08/435,466
FILING DATE: January 13, 1995
APPLICATION NUMBER: US/245,466
FILING DATE: MAY 18, 1994
APPLICATION NUMBER: US/245,466
FILING DATE: MAY 18, 1994
                                PRIOR APPLICATION JOHNER: 08/373,124
PILING DATE: January 13, 1995
PRILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466
FILING DATE: PED 1994
APPLICATION NUMBER: 08/192,943
PILING DATE: PED 1992,943
PILING DATE: PED 1992
APPLICATION NUMBER: 07/987,132
PILING DATE: December 7, 1992
APPLICATION NUMBER: 07/986,422
APPLICATION NUMBER: 07/986,422
ATTORNEY AGENT INPORMATION:
NAME: WATDURY, RICHARD
REGISTRATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 209/035
REPERENCE/DOCKET NUMBER: 209/035
TELEN: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-435-628-1341/c ; Sequence 1341, Application US/08435628 ; Patent No. 5817796
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TOPOLOGY:
US-08-435-628-716
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STRANDEDNESS:
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US-08-435-628-2437
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                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
ITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
ITTLE OF INVENTION: TREATMENT OF RESTENOSIS AND
ITTLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                  Score 12.2; DB 1;
Pred. No. 2.3e+02;
5; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Sulte +, ...
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR PELLOCATION DATA:
APPLICATION NUMBER: 08/373,124
FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/195,466
FILING DATE: MAY 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: Pebruary 7, 1994
APPLICATION NUMBER: 07/98,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/98,132
FILING DATE: December 7, 1994
APPLICATION NUMBER: 07/98,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REPRERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
                                                    209/035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2393, Application US/08435628
Patent No. 5817796
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REPRENCE/DOCKET NUMBER: 209/C
TELECOMMUNICATION INFORMATION:
TELEPAN: (213) 955-0440
TELEXA: (7-3510
TELEXA: (7-3510
TELEX: (7-3510
INFORMATION FOR SEQ ID NO: 1559:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                             499 TTAGAACTCATACTATC 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::|||||:|
1 UUAGAACUCCAGCUAUC 17
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Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (213) 955-0440
                                                                                                                                                                                                                                                                                                      US-08-435-628-1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
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Gaps
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APPLICANT: Stinchcomb, Dan T.
APPLICANT: Braper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Drayer, Kenneth
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                Query Match
1.1%; Score 12.2; DB 1;
Best Local Similarity 58.8%; Pred. No. 2.38+02;
Matches 10; Conservative 4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CUMPUTER READBLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: a storage
COMPUTER: 18M Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FLING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124
FLING DATE: January 13, 1995
APPLICATION NUMBER: 08/195,466
FILING DATE: FEBRUARY 7, 1994
APPLICATION NUMBER: 07/997,132
FILING DATE: PEDCHUARY 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: DECEMBER 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: DECEMBER 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: AUGUST 6, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: AUGUST 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: AUGUST 26, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2437, Application US/08435628 Patent No. 5817796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                        910 CAACATTTCCTAGAGCC 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32,327
                                                                                                                                                                                                                                                                                                                                                                      1 CACCAUTUCAUAGAGAC 17
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 17 base pairs
                                                                                                                                  single
                                                                                                          TYPE: .nucleic acid
STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                        ; TOPOLOGY: linear
US-08-435-628-2393
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Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                      US-08-985-162-157/C

US-08-985-162-157/C

US-08-985-162-157/C

Sequence 157, Application US/08985162

Batent No. 6057156

GENERAL INFORMATION:
APPLICANT: Achtar's Saghir
APPLICANT: Achtar's Saghir
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
TITLE OF INVENTION: TO LEVELS OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OR EDEDERMAL GROWTH
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF TO LEVELS OF EPIDERMAL GROWTH
TITLE OF TO LEVELS OF EPIDERMAL GROWTH
TITLE OF TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
COUNTY: Los Angeles
STATE: California
COONTY: U.S.A.
ZIE: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATION TYPE: 18.5" OR 5.0
SOFTWARE: FASTESM: IBM P.C. DOS 5.0
SOFTWARE: FASTESM: IBM P.C. DOS 5.0
SOFTWARE: 04 December 1997
CLASSIFICATION NUMBER: 05/08/985,162
FILING DATE: 04 December 1997
CLASSIFICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT IRFORMATION:
NAME: WATDURG, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 33,327
TELECHMONICATION INFORMATION:
TELECHMONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 283, Application US/08985162
Patent No. 6057156
GENERAL INFORMATION:
APPLICANT: Akhtar, Saghir
APPLICANT: Fell, Patricia
APPLICANT: Rell, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            982 ATCCAAAGGAGTTGTAT 998
   499 TTAGAACTCATACTATC 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 Arccagaggagrar 1
                                          TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base; pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
;
TOPOLOGY: linear
US-08-985-162-157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 348
US-08-985-162-283
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                                                                         Query Match
1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 2.3e+02;
Matches 9; Conservative 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                         us-08-435-628-2563
j sequence 2563, Application US/08435628
j Patent No. 5817796
j GENERAL INFORMATION:
j APPLICANT: Stinnchcomb, Dan T.
APPLICANT: McSwiggen, James
j APPLICANT: McSwiggen, James
j APPLICANT: Jarvis, Thale
j TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TRATHENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCES: 2627
CORRESPONDENCES: Lyon
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,97035
TELECOMMUNICATION INFORMATION:
TELEPRACE (213) 489-1600
TELERAX: 67-3510
INFORMATION FOR SEQ ID NO: 2563:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                       546 ATGAAATTTAATATGCT 562
                                                                                                                                                                                                                                        | ||||:: ||:|: |
1 AAGAAAUUAAAUAUGGU 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 52.9
Matches 9; Conservative
, TOPOLOGY: linear
US-08-435-628-2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-435-628-2563
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Gaps

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1.1%; Score 12.2; DB 1; Length 17;
64.7%; Pred. No. 2.3e+02;
tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 631, Application US/08985162
Fatent No. 6057186
GENERAL INFORMATION:
APPLICANT: AAktar, Saghir
APPLICANT: Fall, Patricia
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, Dames
APPLICANT: Polly Patricia
APPLICANT: McSwiggen, Dames
APPLICANT: Polly Patricia
APPLICANT: McSwiggen, Dames
APPLICANT: Farror RECEPTORS
NUMBER OF INVENTION: FACTOR RECEPTORS
ADDRESSEE: Lyon & Lyon
STREET: 631 West Fifth Street
                 MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
COMPUTER: ISM COMPALIALE
OPERATING SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT PAPPLICATION DATA:
APPLICATION NUMBER: US/08/985,162
FILING DATE: 04 December 1997
CLASSIFTCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTONNEY, ADENT INFORMATION:
NAWE: WARDENEY, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1 STORAGE 1 STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
COUNTY: Los Angeles
STATE: California
COUNTY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: FASTSEQ for Windows 2.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,162
FILING DATE: 04 December 1997
CLASSIFTCATION: 514
PRIOR APPLICATION DATA:
ATTORNEY/AGBNT INFORMATION:
NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 67.3510
INFORMATION FOR SEQ ID NO: 337:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 CGCCATCTCCCCCATCC 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
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Best Local Similarity
Matches 11; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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US-08-985-162-631/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
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APPLICANT: Akhtar, Saghir
APPLICANT: Pell, Patricia
APPLICANT: Fell, Patricia
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
TITLE OF INVENTION: ENTYMATIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: FACTOR RECEPTORS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                              ENZYMATIC NUCLEIC ACID TREATMENT
OF DISEASES OR CONDITIONS RELATED
TO LEVELS OF EPIDERMAL GROWTH
FACTOR RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACII
TITLE OF INVENTION: OF DISEASES OR CONDIT.
TITLE OF INVENTION: TO LEVELS OF EPIDERMAN
TITLE OF INVENTION: FACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSEE Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 634 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STREET: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: STORAGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
CONPUTER: IBM Compatible
OPERATING SYSTEM: 184/08/985,162
FILING DATE: 04 December 1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 230/107
TELEFRONE; (213) 955-0440
TELEFRANE (213) 955-0440
TE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 349
US-08-985-162-337
Sequence 337, Application US/08985162
Patent No. 6057156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       910 CAACATTTCCTAGAGCC 926
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Matches 12; Conservative
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; Sequence 654, Application US/08985162; Patent No. 6057156; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUNESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              655 ATTTAGATTATGTTACT 671
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1 AAUUAGUUUGUGUUACU 17
                                                                                         654 AATTTAGATTATGTTAC 670
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1 AAAUUAGUUUGUGUUAC 17
Query Match 1.1%;
Best Local Similarity 41.2%;
Matches 7; Conservative
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Best Local Similarity 35.3
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (213) 955-04
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CARACACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sss: single
linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 353
US-08-988-706-45
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ARTHURY, Saghir
APPLICANT: Fell, Patricia
APPLICANT: Fell, Patricia
APPLICANT: Fell, Patricia
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF ERIDERMAL GROWTH
TITLE OF INVENTION: PACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STARET: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: 1.5" O'B S.0
COMPUTER: IBM Compatible
CLASSIFICATION NUMBER: US/08/985,162
FILING DATE: 31 January 1997
ATTORNEY, AGENT INFORMATION:
NAME: WAZDURY, Richard J.
REGISTRATION NUMBER: 32,327
REPREBRUCE/DOCKET NUMBER: 32,327
REPREBRUCE/DOCKET NUMBER: 32,327
REPREBRUCE/DOCKET NUMBER: 32,327
REPREBRUCE/DOCKET NUMBER: 32,327
RELEPAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFX: 6-3510
INPORMATION FOR SEQ ID NO: 653:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
            REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/107
TELECOMMUNICATION INFORMATION:
TELEPRAM: (213) 489-1600
TELEPRAM: (213) 489-1600
TELER: 67-3510
INFORMATION FOR SEQ ID NO: 631:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: TOPOLOGY: linear
US-08-985-162-631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 653, Application US/08985162
Patent No. 6057156
GENERAL INFORMATION:
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Best Local Similarity 82.4'
Matches 14; Conservative
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US-08-985-162-653
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US-08-985-162-653
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                                                                                                                             Gaps
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Score 12.2; DB 1; Length 17;
Pred. No. 2.38+02;
7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Aktar. Saghir
APPLICANT: Aktar. Saghir
APPLICANT: Fell, Patricia
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
TITLE OF INVENTION: FOR DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF EPIDERWAL GROWTH
TITLE OF INVENTION: FACTOR RECEPTORS
TITLE OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSES: LYON & LOOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
COUNTRY:
COUNTRY:
COUNTRY:
COUNTRY:
COUNTRY:
CONDITION:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
CONFURENT:
C
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; TYPE: DNA
; ORGANISM: Sphingomonas
US-09-192-104-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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US-09-324-867-24
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APPLICANT: OLSEN, Sheri J.
APPLICANT: ANGELLY, Tracy S.
APPLICANT: LAWRENCE, Tammy
APPLICANT: LESCALLETT, Dennifer L.
APPLICANT: ALLEN, Particia D.
APPLICANT: ALLEN, Particia B.
APPLICANT: THRUBER, Denise B.
APPLICANT: THRUBER, Denise B.
APPLICANT: SENG, Bin
APPLICANT: CENG, Bin
APPLICANT: SADZEWICZ, Lisa K.
TITLE OP INVENTION: CANCER SUSCEPTIBILITY MUTATIONS OF BRCA1
NUMBER OF SEQUENCES: 55
CORRESPONDENCES: 55
ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.1%; Score 12.2; DB 1; Length 17; Best Local Similarity 82.4%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20877
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,706
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Sequence 7, Application US/09192104B

Patent No. 6184020

GENERAL INFORMATION:
APPLICANT: Alexander Blinkovsky
APPLICANT: Tony Byun
APPLICANT: Alan V. Klotz
APPLICANT: Alan Sloma
APPLICANT: Maria Tang
APPLICANT: Maria Tang
APPLICANT: Maria Tang
APPLICANT: Maria Chiquea Marumoto
APPLICANT: Lene Venke Kofod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PA-0108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "PROBE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: TARCZA, John E.
REGISTRATION NUMBER: 33,638
REFERENCE/DOCKET NUMBER: PA-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-208-1888
TELEFRAX: 301-208-1888
TELEFRAX: 301-226-6125
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 927 TTATTAGAAATGCAGAA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Tratratradrigada 17
                                                                                                                                                                                                                                                                                                             ADDRESSEE: Oncormed, Inc.
STREET: 205 Perry Parkway
CITY: Galthersburg
STATE: MD
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
STRAIN: BRCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-192-104-7/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-988-706-45
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Sequence 7, Application US/09275680

Patent No. 6221630

GENERAL INFORMATION:

APPLICANT: Hopper, James E

TITLE OF INVENTION: A High Copy Number Recombinant Expression Construct for TITLE OF INVENTION: Yeast

TITLE OF INVENTION: Regulated High-level Production of Polypeptides in TITLE OF INVENTION: Yeast

TITLE FEFERENCE: 984.28

CURRENT APPLICATION NUMBER: US/09/275,680

CURRENT FILING DATE: 1999-03-24

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INPORMATION:
APPLICANT: Lillicrap, David
APPLICANT: Calleran
APPLICANT: Cameron, Cherie
APPLICANT: Horrocks, L. Suzanne Hoyle
APPLICANT: Horrocks, L. Suzanne Hoyle
APPLICANT: Horrocks, L. Suzanne Hoyle
TILLE OP INVENTION: Canine
FILLE CAPINGENTION: Canine
FILLE REFERENCE: 1669-0010002/JAG/BJD
CURRENT APPLICATION NUMBER: US/09/324,867A
CURRENT APPLICATION NUMBER: 09/035,141
EARLIER APPLICATION NUMBER: 109/035,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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TITLE OF INVENTION: Polypeptides Having Aminopeptidase;
FITEM OF INVENTION: Activity And Nucleic Acids Encoding Same;
FILE REFERENCE: 5379.200-US;
CURRENT APPLICATION NUMBER: US/09/192,104B;
CURRENT FILING DATE: 1998-11-13;
EARLIER APPLICATION NUMBER: 105/9719;
EARLIER APPLICATION NUMBER: 1465/97;
EARLIER FILING DATE: 1997-12-16;
EARLIER FILING DATE: 1997-12-16;
EARLIER FILING DATE: 1997-12-16;
EARLIER FILING DATE: 1997-05-15;
SARLIER FILING DATE: 1997-05-15;
SARLIER FILING DATE: 1998-05-15;
SOFTWARE: FARESOF for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.1%; Score 12.2; DB 1; Length 17; 82.4%; Pred. No. 2.3e+02; ative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.1%; Score 12.2; DB 1; Length 17; 82.4%; Pred. No. 2.3e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/09324867A Patent No. 6251632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-275-680-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  797 GGAGAGGCAGATAACGC 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 GCCTGTCGGGAACTGGC 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 14; Conservative
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LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                     STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-584-040-1689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-543-446-7/c
US-09-543-446-7/c
Sequence 7 Application US/09543446
APPLICANT: Alexander Blinkovsky
APPLICANT: Alan Sloma
APPLICANT: Maria Tang
APPLICANT: Maria Tang
APPLICANT: Maria Tang
APPLICANT: Lene Venke Kofod
TITLE OF INVENTION: Polypeptides Having Aminopeptidase
TITLE OF INVENTION: Polypeptides Having Aminopeptidase
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
STATLER APPLICATION NUMBER: US/09/543,446
CURRENT FILING DATE: 1997-12-16
SEALIER APPLICATION NUMBER: 1967/669719
SARLIER APPLICATION NUMBER: 1967/6570
SARLIER APPLICATION NUMBER: 1998-05-15
SARLIER APPLICATION NUMBER: 1998-11-13
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FRAELER FALING DATE: 1998-11-13
SOFTWARE: FRAELER FALING DATE: 1998-11-13
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                                                                                                                                                                                                                                                               Query Match
1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels
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; Sequence 1689, Application US/08584040
; Sequence 1689, Application US/08584040
; Patent No. 6346598
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Parco, Pamela
APPLICANT: Stinchoomb, Dan T.
APPLICANT: Escobedo, Jaime
; ATILE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; EARLIER APPLICATION NUMBER: 60/039,953
; EARLIER FILING DATE: 1997-03-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; TYPE: DAR
; TYPE: DAR
; ORGANISM: Synthetic oligonucleotide
US-09-324-867-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       797 GGAGAGGCAGATAACGC 813
                                                                                                                                                                                                                                                                                                                                                                                   895 ACAGACCAAGAGCCTCA 911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Sphingomonas
US-09-543-446-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-543-446-7/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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TITLE OF INVENTION: CONVITIONS SELACED TO LEVELS

NUMBERS OF SEQUENCES: 4552

NUMBERS OF SEQUENCES: 4552

NUMBERS OF SEQUENCES: 4552

ADDRESSER: 151 Worse Fitch Street

STREET: 613 Worse Fitch Street

CITY: 1008 ADDIA: 4700

CITY: 1008 ADDIA: 4700

CONFITN: 013 ADDIA: 4700

CONFITN: 014 ADDIA: 4700

CONFITN: 1810 ADD
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Gaps

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Query Match
1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.3e+02;
Matches 8; Conservative 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2167, Application US/08584040

Patent No. 6346398

GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: Bcavco, Pamela
APPLICANT: Stinchcomb, Dan T.
APPLICANT: STILE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY AGENT INFORMATION:
NAME: WATDLY, RICHARD J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,937
REGISTRATION NUMBER: 218/064
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                      PILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Watburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELERAX: (7-3510
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2165:
SEGUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1050 ACTTCCTTATCTTTCCA 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2167:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACACCUUUAUCUUUCCA 17
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                                                                                                                                                                                                                                                                                                                                                       ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY:
US-08-584-040-2165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-584-040-2167
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Pred. No. 2.3e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Parco, Pamela
APPLICANT: Parco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, James
APPLICANT: Stinchcomb, James
APPLICANT: Stinchcomb, James
APPLICANT: Stinchcomb, Jame
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: SIJ West Fifth Street
STREET: SILLe 4700
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/005,974
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INPORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/POCKET NUMBER: 218/064
TELEFRONE: (213) 489-1600
TELEFRA: 67-3510
INPORMATION FOR SEQ ID NO: 1739:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-584-040-2165; Sequence 2165, Application US/08584040; Patent No. 6346398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 TTTCCTGTTATTCTTGC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 rrrccrrcrarrac 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 82.4%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-584-040-1739
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RESULT 364
US-08-584-040-5710/c
                                        RESULT 363
US-08-584-040-5664/c
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                                                                                                                                     Query Match
1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.3e+02;
Matches 8; Conservative 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-564-040-4021
US-08-564-040-4021
Sequence 4021, Application US/08584040
Fatent No. 6346398
GENERAL INFORMATION:
APPLICANT: PavCo, Pamela
APPLICANT: PavCo, Pamela
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: SECONDEOUS, Danier
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: GROWTH FACTOR
TITLE OF INVENTION: GROWTH FACTOR
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 35" Diskette, 1.44 Mb
MEDIUM TYPE: 35" Diskette, 1.44 Mb
MEDIUM TYPE: 35" DISKETE, 1144 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: SCORED COMPUTER: IBM COMPUTER: IBM COMPATION SYSTEM: IBM P.C. DOS 5.0 SOFTMARE: Word Perfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/584,040 FILING DATE: January 11, 1996 CLASSIFICATION NUMBER: 60/05,974 APPLICATION NUMBER: 60/05,974 FILING DATE: OCCOBER 26, 1995 ATTORNEY/AGENT INFORMATION: NAME: WATDLES: WATDLES: WATDLES: WATDLES: WATDLES: WATDLES: WATDLES: WATDLES: ATTORNEY/AGENT INFORMATION: TELECOMMUNICATION INFORMATION: TELECTARY (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                881 TAAAAGTGTGGCCCACA 897
                                                                                                                                                                                                                                                                    1054 CCTTATCTTTCCAGTGG 1070
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1 CUUUAUCUUUCCAUGGG 17
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 70.6
Matches 12; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-2167
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18. Sequence 564, Application US/08584040

18. Des 248.040-564/C

Sequence 564, Application US/08584040

GENERAL INFORMATION:

APPLICANT: Revised Sequence 514, Application US/08584040

APPLICANT: Revised Sequence 514, Application US/08584040

APPLICANT: Sinder Sequence 514, Application US/08584040

TITLE OF INVERTION: OF VASCULAR ENOTHELIAL

TOTAL SAME AND APPLICATION FOR EACH ENGLY

COUNTRY: U.S.A.

TITLE OF INVERTION: OF VASCULAR ENOTHELIAL

TOTAL STATE: SAME APPLICATION FOR EACH ENGLY

TOTAL STATE: OF VARIABLE STATE: OF VASCULAR ENGLY

TOTAL STATE: OF VARIABLE STATE: OF VASCULAR ENGLY

TOTAL STATE: OF VASCULAR ENGLY
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Length 17;
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Sequence 8014, Application US/08584040

Patent No. 6346396

GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: Benched, Jamela
APPLICANT: Stinchocmb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: TREATENT FOR THE
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: GROWTH FACTOR
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.1%; Score 12.2; DB 1;
Best Local Similarity 82.4%; Pred. No. 2.38+02;
Matches 14; Conservative 0; Mismatches 3;
              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER IBM Compatible
COMPATIBLE WORD PERFECT 5.1
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/584,040
FILING DATE: JANUARY 11, 1996
CLASSIFICATION NUMBER: 60/005,974
FILING DATE: COLOBER 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: WALDATON NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELEFRATION TON TREADED COMPATION:
TELEFRATION TON TREADED
TELEFRATION FOR SEQ ID NO: 7398:
SEQUENCE CHARACTERISTICS:
LENGTH 17 base pairs
TELENGTH 17 base pairs
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ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 815" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPREATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-584-040-7398
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Sequence 7398, Application US/08584040

Sequence 7398, Application US/08584040

GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: Brinchcomb, Dan T.
APPLICANT: Bri
          TREATMENT OF DISEASES OR CONDITIONS RELATED TO LEVELS OF VASCULAR ENDOTHELIAL GROWTH FACTOR
TITLE OF INVENTION: TREATMENT OF DISEASE
TITLE OF INVENTION: CONDITIONS RELATED T
TITLE OF INVENTION: OF VASCULAR ENDOTHELS
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
COUNTY: Los Angeles
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STRATE: California
COUNTY: U.S.A.
ZIE: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg Richard J.
REGISTRATION NUMBER: 218/064
FILING DATE: CALOBER 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg Richard J.
REGISTRATION NUMBER: 218/064
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5710:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 14; Conservative
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STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-584-040-5710
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1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.3e+02;
Matches 10; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-679-645-790/C
US-08-679-645-790/C
Sequence 790, Application US/08679645
Fatent No. 635034
GENERAL INFORMATION:
APPLICANT: Zwick, Michael G.
APPLICANT: McSwiggen, James A.
APPLICANT: McSwiggen, James A.
APPLICANT: McSwiggen, James A.
APPLICANT: Skokut, Thomas A.
APPLICANT: Skokut, Thomas A.
APPLICANT: Skokut, Thomas A.
APPLICANT: Scokut, Thomas A.
APPLICANT: Scokut, Thomas A.
APPLICANT: Scokut, Thomas A.
APPLICANT: McIo, Donald J.
TITLE OF INVENTION: COMPOSITION OF GENE EXPRESSION
TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
TITLE OF INVENTION: NOULATION OF GENE EXPRESSION
TITLE OF INVENTION: LAYON
TITLE OF INVENTION: LAYON
STREET: ALYON & LYON
STREET: Saile 4700
CITY: Los Angeles
STREET: Saile 4700
CITY: US Angeles
STREET: SOUTHERY: U.S.A.
ZIP: POONTHEY: U.S.A.
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage COMPUTER: 1EM Compatible OPERATING SYSTEM: 1EM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/679,645 FILING DATE: UNJy 12, 1996 CLASSIFICATION NUMBER: 60/001,135 FILING DATE: UNJy 12, 1996 CLASSIFICATION NUMBER: 60/001,135 FILING DATE: UNJY 13, 1995 FILING DATE: SEPTEMBER: 08/300,726 FILING DATE: SEPTEMBER: 08/300,726 FILING DATE: SEPTEMBER: 1994 ATTORNEY/AGENT INFORMATION: NAME: WARDDUCKET NUMBER: 219/247 REFERENCE/DOCKET NUMBER: 219/247 TELECOMMATICALION: TELECOMMATICALION:
TELEPAN: (213) 489-1600
; TELERA: (213) 955-0440
; TELER: 67-3510
; INFORMATION FOR SEQ ID NO: 677: SEQUENCE CHARACTERISTICS: LENGTH: 17 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: single ; TOPOLOGY: linear US-08-679-645-677
                                                                                                                                                                                                                                                                                                                                                                                                                    719 GAAAATATATTAACGCA 735
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TELEPHONE: (213) 49.
TELERA: (213) 955-0440
TELEX: (7-3510
INFORMATION FOR SEQ ID NO: 79
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
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US-08-679-645-790/c
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41.2%; Pred. No. 2.3e+02;
trive 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Zwick, Michael G.
APPLICANT: Edington, Brent E.
APPLICANT: McMayagen, James A.
APPLICANT: McMayagen, James A.
APPLICANT: McMayagen, James A.
APPLICANT: Guo, Lining A.
APPLICANT: Young, Scott A.
APPLICANT: Werlo, Donald J.
TITLE OF INVENTION: MCDULATION OF GENE EXPRESSION
TITLE OF INVENTION: IN PLANTS
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: LYON & LYON
STREET: 633 West Fifth Street
STREET: 634 West Fifth Street
GITYT: LOS Angeles
CITYT: LOS Angeles
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
WEDIUM TYPE: 3.5" Diskette, 1.44 MD
WEDIUM TYPE: 18M Compatible
COMPUTER: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/006/79,645
FILING DATE: July 12, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/001,135
APPLICATION NUMBER: 60/001,135
APPLICATION NUMBER: 08/300,726
FILING DATE: SEPTEMBER: 2, 1994
                         APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTOREY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGIGTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELEFHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-040
TELEFAX: (213) 955-040
TELEFAX: (7-3510
TELEFAX: (7-3510
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TELEFAX: (7-3510
TELEFAX: (13) 955-040
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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-679-645-677
; Sequence 677, Application US/08679645
; Patent No. 6350934
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Best Local Similarity 41.23
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: 1
US-08-584-040-8014
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Parco, Pam
APPLICANT: Parco, Pam
APPLICANT: Parco, Pam
APPLICANT: Parco, Pam
APPLICANT: Stinchcomb, Dan
APPLICANT: McSwiggen, Jim
APPLICANT: Manual Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: McBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR PELICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 68/584,040
PRIOR PRIOR APPLICATION NUMBER: US 68/584,040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Bloozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Bacosymen, Jim

APPLICANT: Gravingen, Jim

APPLICANT: StinchComb, Dan

APPLICANT: StinchComb, Dan

APPLICANT: StinchComb, Dan

APPLICANT: Bscobedo, Jaime

ITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rr

ITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

ITLE OF INVENTION NUMBER: US/09/371,772B

CURRENT APPLICATION NUMBER: US 60/005,974

PRIOR PILING DATE: 1995-10-26

PRIOR FILING DATE: 1995-0-26

PRIOR FILING DATE: 1995-0-26

NUMBER OF SEQ ID NOS: 14225

SOFTWARE PATENTIAN VARIETY

SOFTWAR
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                                                                                                               Query Match 1.1%; Score 12.2; DB 1; Length 17; Best Local Similarity 82.4%; Pred. No. 2.3e+02; Matches 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 712, Application US/09371772B Patent No. 6566127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 710, Application US/09371772B Patent No. 6566127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1050 ACTICCITATCITICCA 1066
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 710
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           ; ORGANISM: Homo sapiens
US-09-371-772B-284
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US-09-371-772B-710
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ORGANISM: Homo sapiens
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LENGTH: 17
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US-09-371-772B-284/C

Sequence 284, Application US/09371772B

Sequence 284, Application US/09371772B

Sequence 284, Application US/09371772B

Setent No. 6566127

GENERAL INFORMATION:

APPLICANT: Ribozywe Pharmaceuticals, Inc.

APPLICANT: Bacobedo, Jaim

APPLICANT: Stinchromb, Dan

APPLICANT: Bacobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION NUMBER: US/09/371,772B

CURRENT FILING DATE: 1995-10-26

FRIOR FILING DATE: 1995-10-26

FRIOR APPLICATION NUMBER: US 60/005,974

FRIOR FILING DATE: 1995-01-08

NUMBER OF SEQ ID NOS: 14225

SEQ ID NO 284

LENGTH: 17

LENGTH: 17
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US-371-772B-234/C

Sequence 234, Application US/09371772B

Sequence 234, Application US/09371772B

Sequence 234, Application US/09371772B

Sequence 234, Application US/09371772B

Patel CANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: Pavco, Pam

APPLICANT: Pavco, Pam

APPLICANT: Pavco, Pam

APPLICANT: Bicobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: WORBER: US/09/371,772B

CURRENT FILING DATE: 1995-08-10

PRIOR PILING DATE: 1995-10-26

PRIOR PILING DATE: 1995-01-08

NUMBER OF SEQ ID NOS: 14225

SOFTWARE PAPELICATION VUMBER: DE VOS: 14225
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                                                                                                                                                      Length 17;
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                                                                                                                                                                                                                               3; Indels
                                                                                                                                                  Score 12.2; DB 1;
Pred. No. 2.3e+02;
0; Mismatches 3;
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Best Local Similarity 82.4%;
Matches 14; Conservative
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       single
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CORGANISM: Homo sapiens
US-09-371-7728-234
                                          linear
; STRANDEDNESS:
; TOPOLOGY: lir
US-08-679-645-790
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LENGTH: 17
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APPLICANT: Stinchcomb, Dan APPLICANT: Stinchcomb, Dan APPLICANT: Stinchcomb, Dan APPLICANT: Stinchcomb, Dan APPLICANT: Escobedo, Jaime and Reagent for the Treatment of Diseases or Conditions R TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor; CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
SEQ ID NO 2594
LENGTH: 17
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US-09-371-772B-3206/C
US-09-371-772B-3206/C
Sequence 3206, Application US/09371772B
Sequence 3206, Application US/09371772B
Sequence 3206, Application US/09371772B
Sequence 3206, Application US/09371772B
Sequence 3206, Application Sequence 3206, Applicant No. 6566127
Septicant Stinchcomb, Dam
APPLICANT: Bichocomb, Dam
APPLICANT: Bichocomb, Dam
APPLICANT: Estinchcomb, Dam
APPLICANT: Estinchcomb, Dam
APPLICANT: Estonedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
TITLE OF INVENTION: Levels of Vaccular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00, 876-3 (237/198)
FILE REFERENCE: MBHB00, 876-3 (237/198)
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
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Score 12.2; DB 1; Length 17;
Pred. No. 2.38+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                          NSC-09-371-772B-2594/c
; Sequence 2594, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 TCATTGCCAAAAGAGTC 235
                                                                                                                           421 CCTTATATTTGGAAGAG 437
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              Query Match 1.1%;
Best Local Similarity 82.4%;
Matches 14; Conservative (
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; ORGANISM: MUB 8P.
US-09-371-772B-3206
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; ORGANISM: Mus sp.
US-09-371-772B-2594
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| Sequence 2553, Application US/09371772B
| Patent No. 6566127 |
| Patent Ribozyme Pharmaceuticals, Inc. |
| APPLICANT Ribozyme Pharmaceuticals, Inc. |
| APPLICANT Stinchomb, Dan APPLICANT Stinchomb, Dan APPLICANT Stinchomb, Dan APPLICANT: Stoched, Jaime |
| TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor FILE REFERENCE: MBHB00,876-J (237/198) |
| CURRENT APPLICATION NUMBER: US 09/9311,772B |
| CURRENT APPLICATION NUMBER: US 08/584,040 |
| PRIOR FILING DATE: 1995-10-26 |
| PRIOR FILING DATE: 1995-01-08 |
| NUMBER OF SEQ ID NOS: 14225 |
| SEQ ID NO 2553 |
| LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                           GENEKAL INFURMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: Action Dana
APPLICANT: Stinchoub, Dan
APPLICANT: Stinchoub, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00, 876-J (2377,18)
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-08
NUMBER OF SEQ ID NOS: 14225
SEQ ID NO 1788
ELENGTH: 178
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                                                         Score 12.2; DB 1; Length 17;
Pred. No. 2.3e+02;
6; Mismatches 3; Indels
                                                               Query Match
1.1%; Score 12.2; L
Best Local Similarity 47.1%; Pred. No. 2.3e
Matches 8; Conservative 6; Mismatches
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; Sequence 178B, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
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Best Local Similarity 70.6*
warches 12; Conservative
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US-09-371-772B-1788
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CRGANISM: Mus sp.
US-09-371-772B-2553
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                       US-09-371-772B-712
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Sequence 4854, Application US/09371772B

j Sequence 4854, Application US/09371772B

j Rener No. 6566127

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: RosSwiggen, Jim

APPLICANT: Stinchcomb, Dam

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REPERENCE: MBHB00, 876-J (237/198)

CURRENT APPLICATION NUMBER: US/09/371,72B

CURRENT APPLICATION NUMBER: US 60/005,974

PRIOR FILING DATE: 1996-101-08

PRIOR FILING DATE: 1996-01-08

NUMBER OF SEQ ID NOS: 14225

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4854
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Sequence 6139, Application US/09371772B

Patent No. 6566127

GENERAL INFORMATION:
APPLICANT: Bavco, Pam
APPLICANT: Bavco, Pam
APPLICANT: Bascobedo, Jaim
APPLICANT: Stinchcomb, Dan
APPLICANT: Bascobedo, Jaime
CURRENT FILING DATE: 1999-08-10
FRION APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-01-0-26
PRIOR FILING DATE: 1996-01-08
NUMBER: US 08/584,040
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     Best Local Similarity 82.4%; Pred. No. 2.3e+02; Matches 14; Conservative 0; Mismatches 3;
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82.4%; Pred. No. 2.3e+02;
cive 0; Mismatches 3;
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Pred. No. 2.3e+02;
                                                                                 1033 AGTAAACATCACACCCA 1049
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SOFTWARE: Patentin version 3.0
SEQ ID NO 6139
LENGTH: 17
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82.4%;
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                                                                                                                 17 AGTTAACATGAAACCCA
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US-09-371-772B-4854
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US-09-371-772B-6139
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Best Local Similarity
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                             RESULT 379
US-09-371-772B-4854/c
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Sequence 3797, Application:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Bacobodo, Dan

APPLICANT: Bacobodo, Jaime

APPLICANT: Bacobodo, Jaime

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION UNMER: US 60/005,974

PRIOR PLICATION NUMBER: US 60/005,974

PRIOR PELICATION NUMBER: US 60/005,974

PRIOR PELICATION NUMBER: US 60/005,974

PRIOR FILING DATE: 1995-01-08

NUMBER OF SEQ ID NOS: 14225

SEQ ID NO 3797

LENGTH: 177

LENGTH: 177
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APPLICANT: Pacco, Pam
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,72B
CURRENT PILING DATE: 1999-08-10
PRIOR FILING DATE: 1995-10-26
PRIOR PILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                      ö
Query Match 1.1%; Score 12.2; DB 1; Length 17; Best Local Similarity 82.4%; Pred. No. 2.3e+02; Matches 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 12.2; DB 1; Length 17;
Pred. No. 2.3e+02;
7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.1%; Score 12.2; DB 1; Length 17;
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; Sequence 4538, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
                                                                                                         580
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                                                                                                                                                    17 GGTTTTTAAATAGCCTT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.1%;
Best Local Similarity 41.2%;
Matches 7; Conservative
                                                                                                         564 GGTTTTTTAATACCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: RNA
; ORGANISM: MUB BP.
US-09-371-772B-3797
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
TOPOLOGY:
US-09-401-063-283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-401-063-337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 383
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  Gaps
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                                                                                                                                                                                                                              Sequence 157, Application US/09401063
; Sequence 157, Application US/09401063
; Patent No. 6623952
; GENERAL INFORMATION:
    APPLICANT: Akhtar, saghir
    APPLICANT: ARTOR RECEPTORS
    NUMBER OF SEQUENCES: 1877
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Lyon & Lyon

     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 634 West Fifth Street
STREET: Los Angeles
CITY: Los Angeles
COUNTY: U.S.A.
ZIP: 90071-2066
COMPTER: BOO71-2066
COMPTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 15" DISKETE, 1.44 Mb
MAME: 10" DATE: 11" DIAMER: 1397
MEDIENATION NUMBER: 32,327
MEDIENATION: TELEPHONE: (213) 489-1600
MEDIUM TYPE: 230,107
MEDIENATION: MEDIUM TYPE: 230,107
MEDIENATION: MEDIUM TYPE: 230,107
MEDIENATION: MEDIUM TYPE: 231) 955-0440
        Mismatches
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US-09-401-063-283
; Sequence 283, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  982 ATCCAAAGGAGTTGTAT 998
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INFORMATION FOR SEQ ID NO: 157:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
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                                                                123 TGACTTTTCTTATGCTG 139
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Similarity 82.48;
                                                                                                                    17 rererrrrrerarecre 1
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Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
           14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                         US-09-401-063-157/c
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                    Matches
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Gaps
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; Sequence 337, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
APPLICANT: Rell, Patricia
APPLICANT: Rell, Patricia
APPLICANT: Rell, Patricia
APPLICANT: Pell, Patricia
APPLICANT: Polly. Patricia
APPLICANT: Polly. Patricia
APPLICANT: Polly. Patricia
APPLICANT: Polly. Patricia
APPLICANT: Akhtar, Saghir
APPLICANT: Fell, Patricia
APPLICANT: Fell, Patricia
APPLICANT: McSwiggen, James
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: TO LEVELS OF EDIDERMAL GROWTH
TITLE OF INVENTION: FATTOR RECEPTORS
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 631 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.1%; Score 12.2; DB 1;
70.6%; Pred. No. 2.3e+02;
tive 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM COMPATISH:
COMPUTER: IBM P.C. DOS 5.0
SOFTWARE: FASTERN: IBM P.C. DOS 5.0
CURRENT APPLICATION DATA:
APPLICATION UNMERR: US/09/401,063
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,162
FILING DATE: 04 December 1997
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPAN: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   910 CAACATTTCCTAGAGCC 926
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
DEDNESS: single
OGY: linear
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,162
FILING DATE: 04 December 1997
APPLICATION NUMBER: 60/036,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 31 January 1997 attorner/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               613 AAGTAGGAGATGAGTTT 629
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US-09-401-063-631
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| Patent No. 6623962
| GENERAL INFORMATION:
| APPLICANT: Fell, Patricia |
| TITLE OF INVENTION: ENZYMENE |
| TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED |
| TITLE OF INVENTION: PATOR RECEPTORS |
| NUMBER OF SEQUENCES: 1877 |
| CORRESPONDENCE ADDRESS: ADDRESSEE: Lyon & Lyon |
| STREET: 633 West Fifth Street |
| STREET: 631404700 |
| STREET: 63140470
CITY: Los Angeles
STATE: California
COUNTY: U.S.A.
ZIP: 90071-2066
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/401,063
FILING DATE: 04 December 1997
APPLICATION NUMBER: 08/985,162
FILING DATE: 31 January 1997
APPLICATION NUMBER: 08/985,162
FILING DATE: 31 January 1997
APPLICATION NUMBER: 08/32,327
REGESTRATION NUMBER: 32,327
REGESTRATION NUMBER: 32,327
TELECOMMUTICATION INPORMATION:
TELECOMMUTICATION NUMBER: 32,327
TELECOMMUTICATION INPORMATION:
TELECOMMUTICATION INPORMATION:
TELECOMMUTICATION INPORMATION:
TELECOMMUTICATION INPORMATION:
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ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IEM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSEQ for Windows 2.0

CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (213) 489-1600
TELERA: (213) 955-0440
TELEX: 67-3510
INPORMATION FOR SEQ ID NO: 337:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 CGCCATCTCCCCCATCC 212
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STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
US-09-401-063-337
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1.1%; Score 12.2; DB 1;
Best Local Similarity 82.4%; Pred. No. 2.38+02;
Matches 14; Conservative 0; Mismatches 3;
CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,162
FILING DATE: 04 December 1997
APPLICATION NUMBER: 60/005,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (7-3510
TELEFX: (7-3510
TELEFY: (7-351
                                                                                                                                                                                                                                                                                                                                                                                  230/107
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RESULT 387
US-09-827-998-333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 654 Application US/09401063
; Sequence 662 Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
    APPLICANT: Akhtar, Saghir
    TITLE OF INVENTION: DAISHARSES OR CONDITIONS RELATED
    TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
    TITLE OF INVENTION: PACTOR RECEPTORS
    NUMBER OF SEQUENCES: 1877
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Lyon & Lyon
    ADDRESSEE: Lyon & Lyon
    ADDRESSEE: Lyon & Lyon
    ADDRESSEE: Lyon & Lyon

                                                                                                                                                                                                                                                              Length 17;
                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 41.2%; Pred. No. 2.38+02;
Matches 7; Conservative 7; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE AUGUSTO.

ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STREET: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READBALE FORM:
MEDIUM TYPE: Storage
COMPUTER: IEM COMPATIBLE
COMPUTER: IEM COMPATIBLE
COMPUTER: Exerage
COMPUTER: BASISEQ for Windows 2.0
SOFTWARES: FastSEQ for Windows 2.0
SOFTWARES: FastSEQ for Windows 2.0
CURRENT APPLICATION NUMBER: US/09/401,063
FILING DATE:
CLASSIFICATION NUMBER: 08/985,162
FILING DATE: 04 December 1997
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
APPLICATION NUMBER: 60/036,476
FILING DATE: 04 December 1997
APPLICATION NUMBER: 230/107
FELECOMMUNICATION INFORMATION:
TELEPAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELERY: 67-3510
INFORMATION FOR SEQ ID NO: 654:
SEQUENCE CHARACTERISTICS:
| TELEPHONE: (213) 489-1600
| TELEFAX: (213) 955-0440
| TELEX: 67-3510
| INFORMATION FOR SEQ ID NO: 653:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 17 base pairs
| TYPE: nucleic acid
| STRANDEDNESS: single
| TOPOLOGY: linear
| US-09-401-063-653
                                                                                                                                                                                                                                                                                                                                                          654 AATTTAGATTATGTTAC 670
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1 AAAUUAGUUUGUGUUAC 17
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TYPE: nucleic acid
STRANDEDNESS: single
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US-09-401-063-654
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Sequence 1795, Application US/09827998

Sequence 1795, Application US/09827998

Patent No. 6656700

GENERAL INFORMATION:
APPLICANT: Shannon, Mark
TILE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
TILE REFERENCE: MDHWORE-8
CURRENT APPLICATION NUMBER: US/09/827,998
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-05-26
PRIOR PAPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Acomica Sequence Listing Engine
PATENT NO 6656700
SEQ ID NO 1795
LENGRIH: 17
                                                                                                                                                                         Sequence 333, Application US/09827998

Sequence 333, Application US/09827998

Benefat No. 6656700

GENERAL INFORMATION:
APPLICANT: Ghannon, Mark
APPLICANT: Shannon, Mark
TILE OF INVENTY DATE.
FILE REFERENCE: MDhWORF-8

CURRENT FILING DATE: 2001-04-06

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-27

NUMBER OF SEQ ID NOS: 1881

SOFTWARE Acomica Sequence Listing Engine

SEQ ID NO 333
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                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 12.2; DB 1; Length 17;
Pred. No. 2.3e+02;
0; Mismatches 3; Indels
Best Local Similarity 35.3%; Pred. No. 2.3e+02;
Matches 6; Conservative 8; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               789 ATGTGCTTGGAGAGGCA 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1001 ACATGAAAGTTTGAGAA 1017
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Best Local Similarity 82.4
Matches 14; Conservative
                                                              655 ATTTAGATTATGTTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
US-09-827-998-1795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA; ORGANISM: Homo sapiens
US-09-827-998-333
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Patent No. 66
SEQ ID NO 401
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Best Local S
Matches 14
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                                                                                                                                                                                                                                                                          APPLICANT: CLOURS MATUMOTO
APPLICANT: CLOUR MATUMOTO
APPLICANT: Lene Venke Kofod
TITLE OF INVENTION: Polypepides Having Aminopeptidase
TITLE OF INVENTION: Polypepides Having Aminopeptidase
TITLE OF INVENTION: Activity And Nucleic Acids Encoding Same
TITLE OF INVENTION: ACTIVITY And Nucleic Acids Encoding Same
FILE REPERENCE: 5379-200-US
CURRENT PILLING DATE: 0001-09-19
FRIOR PILLING DATE: EARLIER APPLICATION NUMBER: 09/192,104
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PA 1998 00670
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PA 1998
PRIOR PILLING DATE: EARLIER FILING DATE: 1998-05-15
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: JI, Yonggang

APPLICANT: HANZEL, David K.

APPLICANT: HANZEL, David R.

APPLICANT: RANK, David R.

APPLICANT: RANK, David R.

APPLICANT: SHANNON, WAREH

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: ABOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT PEDILCATION NUMBER: US/09/866,108A
CURRENT PILING DATE: 2001-05-25
PRIOR PEDILCATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR PEDILCATION NUMBER: PCT/USO1/00666
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR PILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 390
2.09-866-108A-400/c
; Sequence 400, Application US/09866108A
; Patent No. 6686188
                           Sequence 7, Application US/09957189
Patent No. 6673571
GENERAL INFORMATION:
APPLICANT: Alexander Blinkovsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    797 GGAGAGGCAGATAACGC 813
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                                                                                                                                                                                                                                      Maria Tang
Mikio Fujii
Chigusa Marumoto
Lene Venke Kofod
                                                                                                                                        Tony Byun
Alan V. Klotz
Alan Sloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Sphingomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 14; Conserv
US-09-957-189-7/c
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APPLICANT:
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APPLICANT: SHANNOW, MARK

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR PAPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
PATENT NO. 6686188
SEQ ID NO 400
LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12.2; DB 1;
Pred. No. 2.3e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-866-108A-401/c; Sequence 401, Application US/09866108A; Patent No. 6686188
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 82.4 14; Conservative
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Best Local Similarity 82.4
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapiens
US-09-866-108A-400
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US-09-866-108A-401
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RESULT 394

Na.-09-66-108A-733/c

Squence 733, Application US/09866108A

Patent No. 6686188

Saneshai INOCHAMION:

APPLICANT: GI, Yizhong

APPLICANT: DAVId R.

APPLICANT: HANZE, DAVId R.

APPLICANT: HANZE, DAVId R.

APPLICANT: SHANNON, MARK

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

TITLE OF INVENTION: WOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

TITLE OF INVENTION: WOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

TITLE OF INVENTION: WOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: ABOMICA-7

CURRENT FILING DATE: 200-05-26

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/USO1/00664

PRIOR APPLICATION NUMBER: PCT/USO1/00669

PRIOR APPLICATION NUMBER: PCT/USO1/00669

PRIOR APPLICATION NUMBER: PCT/USO1/00669

PRIOR APPLICATION NUMBER: PCT/USO1/00669
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APPLICANT: HO. 6681484
APPLICANT: U. Y VIADORS
APPLICANT: U. Y VIADORS
APPLICANT: U. Y VIADORS
APPLICANT: U. Y VIADORS
APPLICANT: TO J. YONGGONG
APPLICANT: PENN, DAVIG R.
APPLICANT: RANK, DAVIG R.
APPLICANT: RANK, DAVIG R.
APPLICANT: SHANKON, MARK
TITLE OF INVENTION WOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE FILE OF INVENTION NUMBER: US/09/866,108A
CURRENT PELLING DAVIE: 2001-05-25
RRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DAVIE: 2000-10-26
PRIOR PRILING DAVIE: 2000-10-36
PRIOR PRILING DAVIE: 2001-01-30
PRIOR PLILING DAVIE: 2
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82.4%; Pred. No. 2.3e+02;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 437, Application US/09866108A
Sequence 437, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: FINY YONGGANG
APPLICANT: PENN, Sharron G.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: SHANNON, Mark
                                                                                                                                                                                             .09-866-108A-402/c
Sequence 402, Application US/09866108A
Patent No. 6686188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 CACTACTGGAATTGTTG 305
290 ACTACTGGAATTGTTGT 306
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Best Local Similarity 82.4<sup>§</sup>
Matches 14; Conservative
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CORGANISM: Homo sapiens
US-09-866-108A-402
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US-09-866-108A-437
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FILE REFERENCE: AEOMICA-7
CURRENT PLILION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-00-05-26
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
TILE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; Score 12.2; DB 1;
82.4%; Pred. No. 2.3e+02;
tive 0; Mismatches 3;
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Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-437
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Page 137

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14; Conservative
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             Matches
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APPLICANT: CHEN, Wensheng
APPLICANT: SHAMNON, Mark
TITLE OF INVENTION: MYSOIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/99/866,108A

CURRENT PILING DATE: 2001-05-25

PRIOR PAPLICATION NUMBER: US 60/207,456

PRIOR PAPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6866188
SEQ ID NO 733
LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
1.1%; Score 12.2; DB 1;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3;
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US-09-866-108A-1071/c
; Sequence 1071, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1052 TTCCTTATCTTTCCAGT 1068
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CRGANISM: Homo sapiens
US-09-866-108A-733
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; ORGANISM: Homo sapiens
US-09-866-108A-1071
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Best Local Similarity
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
PILE REPERENCE: AEOMICA-7
Gaps
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NUMBER OF SEQ ID NOS: 15755
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  3,
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82.4%; Pred. No. 2.3e+02;
cive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT PEPLICATION NUMBER: US/09/866,108A CURRENT PEPLICATION NUMBER: US 60/207,456 PRIOR PEPLICATION NUMBER: US 60/207,456 PRIOR PELING DATE: 2000-05-25 PRIOR PELING DATE: 2000-05-26 PRIOR PILING DATE: 2000-10-04 PRIOR PELING DATE: 2000-10-04 PRIOR PELING DATE: 2000-10-03 PRIOR PELING DATE: 2000-09-27 PRIOR PELING DATE: 2000-09-27 PRIOR APPLICATION NUMBER: PCT/USO1/00667 PRIOR APPLICATION NUMBER: PCT/USO1/00667 PRIOR PELING DATE: 2001-01-30 PRIOR PELING DATE: 2001-01-30
0; Mismatches
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Patent No. 6686188
SEQ ID NO 1072
                                                                                                                                                                                             RESULT 396
2.09-86-108A-1072/c
; Sequence 1072, Application US/09865108A
; Patent No. 6686188
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                                                     1042 CACACCCAACTTCCTTA 1058
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APPLICANT: GV. Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: RANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: CHEN, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 rcacrcccracercrr
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Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
US-09-866-108A-1072
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Query Match
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US-09-866-108A-6438/C
is Sequence 6438, Application US/09866108A
is Patent No. 6686188
is Patent No. 6686188
is Application:
APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: PRANK, David R.
APPLICANT: RANK, Wensheng
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: RANK, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: COURT RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: COUNTING R.
APPLICANT: SADNON, Mark
ITLIE OF INVENTY PLIL REPERENCE: AEONICA-7
CURRENT PILING DATE: 2000-05-25
PRIOR PLILOR DATE: 2000-09-27
PRIOR PLILING DATE: 2000-09-27
PRIOR PPLICATION NUMBER: US 60/236,359
PRIOR PPLICATION NUMBER: DET/US01/00666
PRIOR PPLICATION NUMBER: PET/US01/00666
PRIOR PLILING DATE: 2001-01-30
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APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEGM/LCA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT PILING DATE: 2001-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLILNG DATE: 2001-01-30
PRIOR PLING PAPEL CATION NUMBER: PCT/US01/00668
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1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Acomica Sequence Listing Engine Patent No. 6686188
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US-09-866-108A-1487
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PRIOR FILING DATE: 2011-01-30
PRIOR FILING DATE: 2011-01-30
PRIOR FILING DATE: 2010-01-30
PRIOR PRIOR PRINCE DATE: 2010-01-30
PRIOR PRIOR PRINCE DATE: 2010-01-30
PRIOR PRIOR PRINCE DATE: 2010-01-30
PRIOR PRINCE DATE: 2010-01-30
PRIOR PRILING DATE: 2010-01-30
PRIOR PRINCE DATE
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Length 17;

DB 1;

1.1%; Score 12.2;

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CHEN, Wensheng
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APPLICANT: RANK, David R.

APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SIANNON, MAT.

ITILE OF INVENTION MASSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT PELLING DATE: 2001-05-25
PRIOR PELLING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-05
PRIOR PELLING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILI
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                                        Gaps
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Pred. No. 2.3e+02;
0; Mismatches 3; Indels
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                                 Indels
Best Local Similarity 82.4%; Pred. No. 2.38+02;
Matches 14; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                      US-09-866-108A-6618/c
; Sequence 6618, Application US/09866108A
; Patent No. 6686188
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JS-09-866-108A-v.
j Sequence 6751, Ap.
j Patent No. 6686188
j GENERAL INFORMATION:
TAPPLICANT: GU, Yizhong
TPLICANT: JI, Yonggang
TCANT: PENN, Sharron G.
TCANT: PENN, Sharron G.
TYANTER, David K.
                                                                                             962 ACCCAGGACATTTTGAT 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          896 CAGACCAAGAGCCTCAA 912
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Best Local Similarity 82.4%;
Matches 14; Conservative
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                                                                                                                                                      17 AGCCGGGACCTTTGAT
                                                                                                                                                                                                                                                                                                                                                                                GENERAL INPORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-866-108A-6618
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APPLICANT: CHEN, WEBERERY
APPLICANT: CHEN, WEBERERY
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUWAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: RE 24263.6
PRIOR APPLICATION NUMBER: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PELING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR P
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ASOMICA-7
CURRENT APPLICATION NUMBER: 105/09/866,108A
CURRENT FILING DATE: 2001-05-25
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Pred. No. 2.3e+02;
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PRIOR PILLING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-10-04
PRIOR PILLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR PILLING DATE: 2001-01-30
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; Sequence 7102, Application US/09866108A
; Patent No. 668618
; GENERAL INFORMATION:
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
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Best Local Similarity
Matches 14; Conserv
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PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2010-01-30
PRIOR FILING DATE: 2010-01-30
PRIOR FILING BATE: 2010-01-30
PRIOR FILING APPLICATION REPORTED TO SEQ. 10 NOS: 15755
PACENT NO. 6686188
PRIOR FILING BATE: 1102
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; Sequence 7368, Application US/09866108A
; Patent No. 6686188
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
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CORGANISM: Homo sapiens
US-09-866-108A-7368
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APPLICANT:
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PREMERAL INCOMMATION:
APPLICANT: No. 905 LOB
APPLICANT: DAVIG M. Yikhong
APPLICANT: JI, Yonggang
APPLICANT: DAVIG M.
APPLICANT: PERN, Sharron G.
APPLICANT: RANK, David M.
TITLE OF INVENTION: WYCSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPRENANT FILING DATE: 2001-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PRIOR APPLICATION NUMBER: US 60/207,666
PRIOR PRIOR PLILING DATE: 2000-05-26
PRIOR PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-0
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1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels
       Length 17;
                                                                          3; Indels
Score 12.2; DB 1;
Pred. No. 2.3e+02;
0; Mismatches 3;
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US-09-866-108A-7964/C
Sequence 7964, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7438, Application US/09866108A
Patent No. 6686188
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              Query Match 1.1%;
Best Local Similarity 82.4%;
Matches 14; Conservative
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US-09-866-108A-7438
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US-09-866-108A-7970
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CURRENT APPLICATION: MUNBER: US/09/866,108A
CURRENT TELING DATE: 2001-05-25
FRIOR APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-26
FRIOR PELING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-27
FRIOR PELING DATE: 2000-09-27
FRIOR PELING DATE: 2001-01-03
FRIOR PELIN
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: DI, Yonggang
APPLICANT: BANK, David K.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AROMGA-7
APPLICANT: RANK, David R.
APPLICANT: CHEW, Wenebeng
APPLICANT: SHANNON, MAIK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
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Pred. No. 2.3e+02;
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CURRENT PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
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Patent No. 6686188
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1.1%;
Best Local Similarity 82.4%;
Matches 14; Conservative (
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US-09-866-108A-7964
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GENERAL INFORMATION:

APPLICANT: GU, YIZADON
APPLICANT: GU, YIZADON
APPLICANT: HANZEL, DAVIG K.
APPLICANT: HANZEL, DAVIG K.
APPLICANT: HANZEL, DAVIG K.
APPLICANT: HANZEL, DAVIG R.
APPLICANT: GENERAL MOSIN LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE TITLE OF INVENTION: WOOSIN LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE TITLE OF INVENTION: WOOSIN LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE CURRENT FILING DATE: 2001-05-25
PRIOR PAPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2000-10-04-26
PRIOR FILING DATE: 2000-10-04-27
PRIOR APPLICATION NUMBER: DET/USO1/00666
PRIOR FILING DATE: 2001-01-30
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                  PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR PILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER: OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6666188
SEQ ID NO 7969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 12.2; DB 1; Length 17;
Pred. No. 2.3e+02;
0; Mismatches 3; Indels
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SOFTWARE: Acomica Sequence Listing Engine
Parent No. 6686188
LENYAM.
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; Sequence 7970, Application US/09866108A
; Patent No. 6686188
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FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-09-866-108A-7969
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                                                                                                                                                                                                                                                                                                                                                           RESULT 408

US-09-666-108A-7971/C

Sequence 7971, Application US/09866108A

Patent No. 6686188

GENERAL INFORMATION:

APPLICANT: GT YIZANON

APPLICANT: BANK, David R.

APPLICANT: HANZEL, David R.

TITLE OF INVENTION: WOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE FILE REPRENCE: ABOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT FILING DATE: 2000-65-26

PRIOR PELING DATE: 2000-65-26

PRIOR PELING DATE: 2000-10-04-30

PRIOR PELING DATE: 2000-10-04-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION APPLICATION NUMBER: PCT/US01/00666
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                                                                           Gaps
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NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 7971
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Pred. No. 2.3e+02;
0; Mismatches 3; Indels
Query Match
1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels
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US-09-866-108A-9279/C
US-09-866-108A-9279/C
Sequence 9279, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GV Xizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
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                                                                                                                                                          310 TGCCTTTGGATTTCCTG 326
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Best Local Similarity 82.4%;
Matches 14; Conservative (
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ORGANISM: Homo sapiens
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| APPLICANT: RANK ABRADES
| APPLICANT: GIRN, Weanhers
| CURRENT FORT | CORO - 05-25 |
| CORON SINT | CORO - 05-25 |
| CORON SINT | CORO - 05-25 |
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TYPE: RNA
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PRIOR APPLICATION NUMBER: PCT/USO1/00664

PRIOR PILING DATE: 2001-01-30

PRIOR PLEING DATE: 2001-01-30

PRIOR PLICATION NUMBER: PCT/USO1/00669

PRIOR PILING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/USO1/00663

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/USO1/00663

PRIOR DATE: 2001-01-30

PRIOR DATE:
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82.4%; Pred. No. 2.3e+02;
tive 0; Mismatches 3; Indels
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Fatent No. 670328
GENERAL INPORMATION:
APPLICANT: John Landers
APPLICANT: John Landers
APPLICANT: Barbara Jordan
APPLICANT: Barbara Jordan
APPLICANT: Alain Charest
APPLICANT: Alain Charest
TITLE OF INVENTION: Methods and Products Related to
TITLE OF INVENTION: Genctyping and DNA Analysis
FILE REPERRNCE: M0656/7045(HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/404,912
CURRENT APPLICATION NUMBER: US 60/101,757
FRIOR PELING DATE: 1999-09-24
FRIOR APPLICATION NUMBER: PCT/US99/22283
FRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 691
SEQ ID NO 319
LENGTH: 17
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US-09-685-664B-234/c
; Sequence 234, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           672 CAAATTATGTTACTTGT 688
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McSwiggen, Jim
Stinchcomb, Dan
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Matches 14, Conservative
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Conditions Relat:
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APPLICANT: Pavco, Pam

APPLICANT: Backiggen, Jim

APPLICANT: Bachedon, Dan

APPLICANT: Bachedon, Dan

APPLICANT: Bachedon, Jame

APPLICANT: Bachedon, Jame

APPLICANT: Bachedon, Jame

APPLICANT: Bachedon, Jame

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recptor

TITLE OF INVENTION: WHABR: US/09/685,664B

CURRENT APPLICATION NUMBER: US/09/685,664B

CURRENT PILING DATE: 1995-10-26

PRIOR APPLICATION NUMBER: US 08/584,040

PRIOR APPLICATION NUMBER: US 08/584,040
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TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or ConditITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recptor FILE REFERENCE: MBHB00-876-K (400/021)
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR PAPLICATION NUMBER: US 60/005,974
PRIOR PLING DATE: 1995-10-26
PRIOR PLING DATE: 1995-10-26
PRIOR PLING DATE: 1995-10-26
PRIOR FLING DATE: 1995-10-80
PRIOR FLING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 8231
SOFTWARE: Patentin version 3.0
SEQ ID NO 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1%; Score 12.2; DB 1; 82.4%; Pred. No. 2.3e+02;
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1.1%; Score 12.2; DB 1;
Best Local Similarity 82.4%; Pred. No. 2.38+02;
Matches 14; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 284, Application US/09685664B Patent No. 681847
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-685-664B-710
; Sequence 710, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 564 GGTTTTTAATACCTTT 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 TITCCIGITATICITGC 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-234
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US-09-685-664B-284
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Best Local Similarity
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US-09-685-664B-284/c
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APPLICANT: Pavco, Pam
APPLICANT: McSaviggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recptor
TITLE OF INVENTION: MUMBER: US/09/685,664B
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR APPLICATION NUMBER: US 08/371,772
PRIOR PELING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 8231
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Pavco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Strinchcomb, Dan
APPLICANT: Strinchcomb, Dan
APPLICANT: Eschedo, Jame
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recptor
FILE REFERENCE: MBHB00-876-K (400/021)
CURRENT APPLICATION NUMBER: US 09/005, 974
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1995-01-08
PRIOR FILING DATE: 1995-08-10
PRIOR FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 8231
SEQ ID NOS: E33
SEQ ID NO 2553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.1%; Score 12.2; DB 1; Length 17; 70.6%; Pred. No. 2.3e+02; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 417
US-09-685-664B-2553/c
; Sequence 2553, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
            APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 CCTTATATTTGGAAGAG 437
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Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
US-09-685-664B-1788
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US-09-685-664B-2553
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
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TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recptor
FILE REFERENCE: MEHBOO-876-K (400/021)
FILE REFERENCE: MEHBOO-876-K (400/021)
CURRENT PELING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 09/584,040
PRIOR APPLICATION NUMBER: US 09/371,772
PRIOR FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 8231
SEQ ID NOS: 8231
SEQ ID NO SEQ ID NOS: 8231
ENGTH: 17
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1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.3e+02;
Matches 8; Conservative 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.3e+02;
Matches 8; Conservative 6; Mismatches 3; Indels
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US-09-685-664B-1788
; Sequence 1788, Application US/09685664B
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Stinchcomb, Dan
Escobedo, Jaime
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CORGANISM: Homo sapiens
US-09-685-6648-712
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
CORGANISM: Homo sapiens
US-09-685-6648-710
Pavco, Pam
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US-09-685-664B-712
                     APPLICANT
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Sequence 3797, Application US/0968564B

Sequence 3797, Application US/0968564B

Sequence 3797, Application US/0968564B

SEQUENCE INCORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Bacocomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Pactor Recptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Pactor Recptor

FILE REFERENCE: MBHB00-876-K (400/021)

CURRENT APPLICATION NUMBER: US/09/685,648

FILOR APPLICATION NUMBER: US 08/584,040

PRIOR FILING DATE: 1995-10-26

PRIOR FILING DATE: 1996-01-08

PRIOR FILING DATE: 1996-01-08

PRIOR FILING DATE: 1996-01-08

PRIOR FILING DATE: US 09/371,772
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GENERAL INFORMATION:
APPLICANT: Cover, Timothy L.
APPLICANT: Blaser, Martin J.
TITLE OF INVENTION: VACUCLATING TOXIN-DEFICIENT H. PYLORI
TITLE OF INVENTION: AND RELATED METHODS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG P.C.
STREET: 127 Peachtree Street, Suite 1200
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ZIP: 30303
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2200.023
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ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFRENCE/DOCKET NUMBER: 2200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/68-0770
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SOFTWARE: PatentIn version 3.0
17 GGTTTTTAAATAGCCTT 1
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US-09-685-664B-3797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Atlanta
STATE: Georgia
COUNTRY: USA
                                                                                RESULT 420
US-09-685-664B-3797
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        US-09-685-648-2594/c

Sequence 2594 Application US/0968564B

Sequence 2594 Application US/0968564B

Sequence 2594 Application US/0968564B

Sequence 2594 Application US/0968564B

Sequence 2594 Application

APPLICANT: Raiozyme Pharmaceuticals, Inc.

APPLICANT: Raiozyme Pharmaceuticals, Inc.

APPLICANT: Bacobedo, Jaime

TITLE OF INVENTION: Mewels of Vascular Endothelial Growth Factor Recptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recptor

TITLE OF INVENTION: Mewels: US/09/685,664B

CURRENT APPLICATION NUMBER: US 60/005,974

PRIOR APPLICATION NUMBER: US 08/584,040

PRIOR PILING DATE: 1995-01-08

SPRIOR PLING DATE: 1995-01-08

NUMBER OF SEQ IN NOS: 8231

SOFTWARE: PatentIn version 3.0

SEQ IN 0. 2594

LENGTH. 17
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ravoc, Pam
APPLICANT: Ravoc, Pam
APPLICANT: Bavoc, Pam
APPLICANT: Bavoc, Pam
TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recptor
FILE REPRENCE: MBHBOO-876-K (400/021)
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
PRIOR FILING DATE: 1996-01-08
PRIOR PILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 8231
SOFTWARE: Patentin version 3.0
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Pred. No. 2.3e+02;
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; Sequence 3206, Application US/09685664B
; Patent No. 6818447
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Best Local Similarity 82.49
Matches 14, Conservative
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US-09-685-664B-2594
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US-09-685-664B-3206
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Sequence 372, Application US/09338907
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Sequence 5, Application PC/TUS9502219A

GENERAL INFORMATION:
APPLICANT: Cover, Timothy L.
APPLICANT: Tummuru, Murali KR
APPLICANT: Tummuru, Murali KR
APPLICANT: Thompson, Stuart A.
APPLICANT: Thompson, Stuart
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Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Length 17;
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COMPUTER READABLE FORM:
COMPUTER: Floppy disk
APPLICATION NUMBER: FCT/US95/02219A
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
1.1%; Score 12.2; DB 1;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3;
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NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REPERENCE/DOCKET NUMBER: 2200.023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
TELEFAX: 404/688-9880
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                                       INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
HODECULE TYPE: DNA (genomic)
PCT-US95-02219-5
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TELEFAX: 404/688-2000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
FRNGTH: 17 base pairs
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Atlanta
STATE: Georgia
COUNTRY: USA
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CLASSIFICATION:
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| COGNATION: 1..19 | NAME/KEY: DOCATION: 1..19 |
| COGNATION: Upstream amplification primer for SEQ 251, SEQ 328 |
| US-09-218-207-372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1..19
OTHER INFORMATION: upstream amplification primer for SEQ 251, SEQ 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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1.0%; Score 11.6; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 4; Indels
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Pred. No. 3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 372, Application US/09218207
; Sequence 372, Application US/09218207
; Patent No. 6346381
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
; TITLE OF INVENION: Prostate cancer gene
; FILE REFERENCE: GENSET.018CP1
; CURRENT APPLICATION NUMBER: US/09/218,207
; CURRENT FILING DATE: 1998-12-22
; CARALIER APPLICATION NUMBER: 08/996,306
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER APPLICATION NUMBER: 60/099,658
; RARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: PATENT.PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Chen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Bugueleret, Lydie
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: PROSTATE CANCER GENE
FILE REPERENCE: GENEST: 18CPLCP
CURRENT APPLICATION NUMBER: 08/996,306
EARLIER PILING DATE: 1999-06-22
EARLIER PILING DATE: 1999-09-09
EARLIER PILING DATE: 1997-12-22
EARLIER PILING DATE: 1998-12-22
EARLIER PILING DATE: 1998-12-22
NUMBER: OF SEQ ID NOS: 578
SOFTWARE: PATENTE OF SEQ ID NOS: 578
SEQ ID NO 372
LANGTH: 19
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Best Local Similarity 77.8%;
Matches 14; Conservative 0
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo Sapiens
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LENGTH: 19
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RESULT 423 US-09-338-907-372

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APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: GU, Yonggang
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David K.
APPLICANT: CHEN, Wenaheng
APPLICANT: RANK, David R.
APPLICANT: SHANNON, Mark
ITTLE OF INVENTION: WOOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ABOMICA-7
CURRENT APPLICATION NUMBER: US 60/207, 456
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR APPLICATION NUMBER: US 60/205-26
PRIOR APPLICATION NUMBER: US 60/236
PRIOR APPLICATION NUMBER: US 60/236
PRIOR APPLICATION NUMBER: US 60/236
PRIOR APPLICATION NUMBER: US 60/236, 359
                                                                                 APPLICANT: Ji, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
THE REPERBRUCE: ABOMICAT
CURRENT APPLICATION UNMER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
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Pred. No. 3.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Aeomica Sequence Listing Engine
SEG ID NO 2565
LENGTH: 17
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Best Local Similarity 81.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CORGANISM: Homo sapiens
US-09-866-108A-2565
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APPLICANT: Cohen, Daniel

APPLICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REPERENCE: GENSET.020CP1

CURRENT APPLICATION NUMBER: US 09/298,850

EARLIER PILING DATE: 1999-04-21

EARLIER PLING DATE: 1999-04-21

EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER PLING DATE: 1998-04-21

MUMBER OF SEQ ID NOS: 11796

SEQ ID NO 4387
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LOCATION: 1..19
COTHER INFORMATION: upstream amplification primer 99-1481 for SEQ 453, US-09-422-978-4387
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Patent No. 6436706
BATELL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Donna T. Watc
APPLICANT: Andrew T. Watc
APPLICANT: Andrew T. Watc
APPLICANT: ANDREW T. Watc
APPLICANT: NUMBER: NS-020
CURRENT APPLICATION NUMBER: 2001-02-23
NUMBER OF SEQ ID NOS: 89 . .
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 11.6; DB 1; Length 19;
Pred. No. 3e+02;
0; Mismatches 4; Indels
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Pred. No. 3.2e+02;
0; Mismatches 1; Indels
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US-09-792-594-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 427
US-09-866-108A-2565
; Sequence 2565, Application US/09866108A
                                                                                                                                Sequence 4387, Application US/09422978 Patent No. 6537751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GGCTCCCTTTTGAGTTG 19
GGCTCCCCTTTTGAGTTG 19
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.0%;
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Best Local Similarity 77.84
Matches 14; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo Sapiens
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US-09-792-594-57/c
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Length 17; Indels

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1.0%; Score 11.2; DB 1;
81.2%; Pred. No. 3.4e+02;
tive 0; Mismatches 3;
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1.0%; Score 11.2; DB 1;
Best Local Similarity 81.2%; Pred. No. 3.4e+02;
Matches 13; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 24, Application US/09324867A
; Patent No. 6251632
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CRGANISM: Homo sapiens
US-09-827-998-514
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Best Local Similarity
Matches 13; Conserva
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US-09-324-867-24/c
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US-09-392-580-12
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US-09-827-998-515

Sequence 515, Application US/09827998

Sequence 515, Application US/09827998

Sequence 515, Application US/09827998

Sequence 515, Application US/09827998

APPLICANT: Gu, Yizhong

APPLICANT: Gu, Yizhong

APPLICANT: Ghannon, Mark

ITILE OF INVENTION: WOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

ITILE OF INVENTION: WOVEL: US/09/827,998

CURRENT FILING DATE: 2001-04-06

PRIOR PAPLICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-27

NUMBER OF SEQ ID NOS: 1881

SOFTWARE: Acomica Sequence Listing Engine

Patent No. 6656700

SEQ ID NO 515

LENGTH: 17
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81.2%; Pred. No. 3.4e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.0%; Score 11.2; DB 1; Length 17; Best Local Similarity 81.2%; Pred. No. 3.4e+02; Matches 13; Conservative 0; Mismatches 3; Indels
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLILOATION NUMBER: PCT/USO1/00665
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION SUMBER: PCT/USO1/00663
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CORGANISM: Homo sapiens
US-09-827-998-515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 13; Conserv
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Parent No. 6087173
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Lex M. Cowsert
APPLICANT: Lex M. Cowsert
APPLICANT: Lex M. TINTERNSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSIV
FILE REPERRNCE: RTS-0072
CURRENT APPLICATION NUMBER: US/09/392,580
APPLICANT: Shannon, Mark
TILLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REPERENCE: MDIMORF-8
CURRENT APPLICATION NUMBER: US/09/827,998
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 514
LEMENT: THE SECOND S
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GENERAL INFORMATION:

APPLICANT: Lillicrap, David

APPLICANT: Cameron, Cherie

APPLICANT: Cameron, Cherie

APPLICANT: Cameron, Cherie

APPLICANT: Hough, Christine

TITLE OF INVENTION Canine Factor VIII Gene, Protein and Methods of Use

TITLE OF INVENTION Canine Factor VIII Gene, Protein and Methods of Use

TITLE OF INVENTION CANINE RACE, 1999-046-03

CURRENT APPLICATION NUMBER: US/09/324,867A

CURRENT FILING DATE: 1999-03-06-03

EARLIER PILING DATE: 1998-03-059

EARLIER PLING DATE: 1998-03-059

EARLIER FILING DATE: 1997-03-06

SEALIER FILING DATE: 1997-03-06

SEALIER PLING DATE: 1997-03-06

SEALIER PLING DATE: 1998-03-059

SEALIER PLING DATE: 1997-03-06

SEQUING APPLICATION NUMBER: 06/039,953

SEQUING APPLICATION OF CANING APPLICATION OF C
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APPLICANT: GL Yizhong
APPLICANT: GL Yizhong
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: SHALON, Wensheng
APPLICANT: SHANNON, MARK
TITLE OF INVENTIONS: MOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT FILING DATE: 2001-05-25

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30
                                                                                                                                       Gaps
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                                                                     Length 20;
                                                                                                                                       Indels
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                                                              Query Match
1.0%; Score 10.8; DB 1;
Best Local Similarity 85.7%; Pred. No. 3.9e+02;
Matches 12; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.0%; Score 10.6; DB 1; 76.5%; Pred. No. 4.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Aeomica Sequence Listing Engine atent No. 6686188
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 7015, Application US/09866108A ; Patent No. 6686188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4732, Application US/09422978; Patent No. 6537751; GENERAL INFORMATION: APPLICANT: Cohen, Daniel; APPLICANT: Blumenfeld, Marta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                         391 AGTCATTTTCCTTA 404
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Best Local Similarity 76.5
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         RESULT 435
US-09-866-108A-7015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-422-978-4732
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SEQ ID NO 7015
LENGTH: 17
          US-09-433-699-36
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Sequence 4538, Application US/09371772B

Sequence 4538, Application US/09371772B

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Bacobedo, Jam
APPLICANT: Stinnformb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00,876-J (237/198)
CURRENT FILING DATE: 1999-08-10
PRIOR PLILING DATE: 1995-10-26
PRIOR PILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-26
SPRIOR FILING DATE: 1995-10-26
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Parent No. 6165786
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. COWSETT
TITLE OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION
CURRENT APPLICATION NUMBER: US/09/433,699B
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 89
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                                                                                                                                                                                                                                                                                                                                      Query Match 1.0%; Score 11; DB 1; Length 20; Best Local Similarity 73.7%; Pred. No. 3.7e+02; Matches 14; Conservative 0; Mismatches 5; Indels
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1.0%; Score 10.8; DB 1;
Best Local Similarity 35.7%; Pred. No. 3.9e+02;
Matches 5; Conservative 7; Mismatches 2;
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                                                                                                                                                                                                                                  ; OTHER INFORMATION: Antisense Oligonucleotide US-09-392-580-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          586 TCATGTTCACTTTAAGAAA 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 rcarcrrcrcrrcaaaara 20
CURRENT FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 12
LENGTH: 20
                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-371-772B-4538
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LENGTH: 20
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TYPE: DNA
ORGANISM: Homo Sapiens
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US-09-198-452A-5159/c
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APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
TTLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE CONRENT PILING ENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT PILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 60/109,732
APPLICANT: Chumakov, 11ya
TITLE OF INVENTIVON: Biallelic markers for use in constructing a high density...
FILE OF INVENTIVON: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422, 978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-04-21
EARLIER FILING DATE: 1998-04-21
EARLIER FILING DATE: 1998-04-21
EARLIER FILING DATE: 1998-04-21
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-21
EARLIER FILING DATE: 1998-11-21
EARLIER FILING DATE: 1998-11-21
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; OTHER INFORMATION: upstream amplification primer 99-8576 for SEQ 2107,
US-09-422-978-6041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: primer_bind

LOCATION: 1..18

COTATION: Upstream amplification primer 99-1739 for SEQ 798,

US-09-472-978-4732
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1.0%; Score 10.6; DB 1; Length 18;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.0%; Score 10.6; DB 1; Length 18;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 438
US-09-422-978-7460
; Sequence 7460, Application US/09422978
; Patent No. 6537751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6041, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             614 AGTAGGAGATGAGTTT 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 ATCANATGGGGAGCCTG 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 Arganiccrcancers 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: primer_bind LOCATION: 1..18
                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-422-978-6041/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 6041
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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Sequence 5159, Application US/09198452A

; Sequence 5159, Application US/09198452A

; Patent No. 655294

; GENERAL INFORMATION:

APPLICANT: Griffais, R.

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preverting of INVENTION: and treatment of infection

TITLE OF INVENTION: and treatmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 440

US-09-198-452A-5166/c

Sequence 5166, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: GFIffals, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment;

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev.

TITLE OF INVENTION: and treatment of infection

TITLE REPRESENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A
APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, 11ya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
TITLE REFERENCE: GENNET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT APPLICATION NUMBER: US/09/298,850
EARLIER PPLICATION NUMBER: US 60/109,732
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER PLING DATE: 1999-11-23
EARLIER PLING DATE: 1998-11-23
EARLIER PLING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 7460
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: 1..18 -
; OTHER INFORMATION: upstream amplification primer 99-49 for SEQ 3526,
US-09-422-978-7460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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1.0%; Score 10.6; DB 1; Length 20;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 18;
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1.0%; Score 10.6; DB 1;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 4;
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CRGANISM: Chlamydia pneumoniae
US-09-198-452A-5159
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California : U.S.A.

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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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APPLICANT: Lander, Eric S.
APPLICANT: Lander, Eric S.
APPLICANT: Treland, James S.
APPLICANT: Treland, James S.
APPLICANT: Bolk, Stacey
APPLICANT: Bolk, George Q.
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
TITLE OF INVENTION: 2855.1027-001
CURRENT FALING DATE: 2805-09-07
FRIOR APPLICATION NUMBER: US 60/153,357
PRIOR FILING DATE: 1999-09-10
PRIOR PILING DATE: 2000-09-07
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-08-16
PRIOR FILING DATE: 2000-08-16
SPRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2551
SOFTWARE FREESEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 21;
                                                                                                                                                                                                                                           4; Indels
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Sequence 2437, Application US/08373124A

Patent No. 5646010:
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: S13 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.0%; Score 10.6; DB 1;
Best Local Similarity 68.4%; Pred. No. 4.1e+02;
Matches 13; Conservative 1; Mismatches 5;
                                                                                                                                                                                         Query Match
1.0%; Score 10.6; DB 1;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 441
US-09-657-472-1733
; Sequence 1733, Application US/09657472
; Patent No. 6727063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 TGGGCAGGCTGCCCGGGCC 27
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CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 5166
LENGTH: 20
                                                                                                                                                                                                                                                                                         599 AAGAAAGACTTCATAAG 615
                                                                                          TYPE: DNA; Chlamydia pneumoniae; ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                      18 AACAACGACTCCAGAAG 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-1733
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APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Jarvis, James
APPLICANT: Jarvis, Thale
ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.9%; Score 10.4; DB 1; Best Local Similarity 91.7%; Pred. No. 4.5e+02; Matches 11; Conservative 0; Mismatches 1;
COMPUTER: IBM COMPACTURE
COMPUTER: WORD PERFOCE 5.1

SOFTWARE: WORD PERFOCE 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: MAY 18, 1995
APPLICATION NUMBER: 08/245,466
APPLICATION NUMBER: 08/29,2943
FILING DATE: PEDCHARY 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: DECEMBER 7, 1992
APPLICATION NUMBER: 07/936,422
APPLICATION NUMBER: 07/936,422
APPLICATION NUMBER: 32,327
REFREENCY AGENT INFORMATION:
NAWE: WARCHING NUMBER: 32,327
REFREENCY POSCAT NUMBER: 209/035
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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US-08-435-628-2437/c
; Sequence 2437, Application US/08435628
; Patent No. 5817796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YSTEM: IBM P.C.
Word Perfect 5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             489 ATTGAATTTCTT 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 ATTTAATTTCTT 1
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STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
US-08-373-124A-2437
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psequence 4185, Application US/09422978

patent No. 6537751

patent No. 6537751

grammar No. 6537751

grammar No. 6537751

patent No. 6537751

patent No. 6537751

patent Cohen, Daniel

APPLICANT: Cohen, Daniel

APPLICANT: Chumakcov, Ilya

prile REFERRENCOV, Ilya

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERRENCE: GRANEST.020COV

CURRENT FILING DATE: 1999-10-20

GRALIER PILING DATE: 1999-04-21

BARLIER PILING DATE: 1999-04-21

BARLIER PILING DATE: 1998-04-21

SRALIER PILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 4185

SEQ ID NO 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAMEKEY: primer_bind
LOCATION: 1..20
CHER INFORMATION: upstream amplification primer 99-13853 for SEQ 251,
US-09-422-978-4185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.9%; Score 10.4; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 4.4e+02; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                       GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Carull, John P.

APPLICANT: Carull.

APPLICANT: Little, Randall D.

APPLICANT: Recker, Robert R.

APPLICANT: Recker, Robert R.

TILLE OF INVENTION: High bone mass gene of 11q13.3

FILE REFREENCE: 032796-014

CURRENT APPLICATION NUMBER: US/09/543,71B

CURRENT FILING DATE: 1999-01-13

PRIOR APPLICATION NUMBER: US 60/071,449

PRIOR FILING DATE: 1998-01-13

PRIOR FILING DATE: 1998-01-13

PRIOR FILING DATE: 1998-01-13

PRIOR FILING DATE: 1998-10-23

NUMBER OF SEQ ID NOS: 641

SOFTWARE: FASELSEQ for Windows Version 4.0

SEQ ID NO 310
                                                                                                                                             US-09-543-771B-310
; Sequence 310, Application US/09543771B
; Patent No. 6780609
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-543-771B-310
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0.9%; Score 10.4; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.9%; Score 10.4; DB 1; Length 17; Best Local Similarity 91.7%; Pred. No. 4.5e+02; Matches 11; Conservative 0; Mismatches 1; Indels
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Sequence 310, Application US/09544398B

Patent No. 6770461

GENERAL INFORMATION:

APPLICANT: Carulli, John P.

APPLICANT: Carulli, John P.

APPLICANT: Recker, Robert R.

APPLICANT: Johnson, Mark L.

TITLE OF INVENTION: High bone mass gene of 11q13.3

FILE REFERENCE: 032796-013

CURRENT APPLICATION VUMBER: US/09/544,398B

CURRENT FILING DATE: 1299-01-13

PRIOR APPLICATION NUMBER: US 60/71,449

PRIOR FILING DATE: 1998-01-13

PRIOR FILING DATE: 1998-01-13

PRIOR FILING DATE: 1998-01-13

NUMBER OF SEQ ID NOS: 641

SOFTWARER: FREEEN FARLENT 
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/33,124
FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/192,943
FILING DATE: MAY 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: AUGUST 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
RELEPONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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US-09-544-398B-310
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ADOMICA-7
CURRENT APPLICATION UMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
                                                                                                                                                         Sequence 526, Application US/09081646
| Patent No. 6333152|
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Kinzler, Kenneth
| APPLICANT: Vogelstein, Bert
| APPLICANT: Zahang, Lin
| APPLICANT: Wei
| TITLE OF INVENTION: Geneer Cells
| TITLE OF INVENTION: Cancer Cells
| FILE REFERENCE: 01107,74646
| CURRENT APPLICATION NUMBER: US/09/081,646
| CURRENT FILING DATE: 1998-05-20
| EARLIER APPLICATION NUMBER: 60/047,352
| BARLIER PILING DATE: 1997-05-21
| NUMBER OF SEQ ID NOS: 871
| SOFTWARE: FastSEQ for Windows Version 3.0
| SEQ ID NO 526
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0.9%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 4.9e+02;
Matches 12; Conservative 0; Mismatches 3; Indels
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PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2566, Application US/09866108A Patent No. 6686188
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RANK, David R. CHEN, Wensheng
3 CCTTATTAAAA 14
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; ORGANISM: Homo sapiens
US-09-081-646-526
                                                                                                                    RESULT 447
US-09-081-646-526/C
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APPLICANT: SHANNOW, MARK

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT PELLORION NUMBER: US/09/866,108A
CURRENT PELLORION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELLORION NUMBER: US 60/2036,359
PRIOR PELLOR DATE: 2000-10-20
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PELLORION NUMBER: PCT/US01/00667
PRIOR PELLORION NUMBER: PCT/US01/00667
PRIOR PELLORION NUMBER: PCT/US01/00667
PRIOR PELLORION NUMBER: PCT/US01/00669
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 2566
LENGTH: 17
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Pred. No. 4.8e+02;
0; Mismatches 3;
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0.9%; Score 10.2; DB 1;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 12; Conservative 0; Mismatches 3;
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Best Local Similarity 80.0%;
Matches 12; Conservative (
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: RANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wenbheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 galagecegecaecrec 17
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                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-866-108A-2566
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; ORGANISM: Homo
US-09-866-108A-2563
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976 GATGAGATCCAAAGG 990
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Best Local Similarity 80.03
Matches 12; Conservative
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                                                                                                                ORGANISM: Homo sapiens
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Best Local Similarity
Matches 12; Conserv
Patent No. 6686188
SEQ ID NO 7017
LENGTH: 17
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CRGANISM: HOM
US-09-827-998-513
                                                                                      TYPE: DNA
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                                                                             GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: GU, Yizhong

TITLE OF INVENTION: Mark

TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PRECNANCY-ASSOCIATED PROTEIN E

FILE REFERENCE: MDHAMPER: US/09/827,998

CURRENT APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-27

NUMBER OF SEQ ID NOS: 1881

SOFTWARE: Acomica Sequence Listing Engine

SEQ ID NO 5:6

LENGTH: 17
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APPLICANT: CHEN, WARSHENGER
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: ADMICA-7
CURRENT PILING DATE: 2001-05-25
CURRENT FILING DATE: 2001-05-26
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-04
PRIOR PILING DATE: 2001-01-07
PRIOR PILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.9%; Score 10.2; DB 1; Length 17; 80.0%; Pred. No. 4.8e+02; tive 0; Mismatches 3; Indels
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Patent No. 6686188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            977 ATGAGATCCAAAGGA 991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0°
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRGANISM: Homo sapiens
US-09-827-998-516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 451
US-09-866-108A-7017
                                                   RESULT 450
US-09-827-998-516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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| SEGNATION | 1971
| 1988 | 1989 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 19
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OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium OTHER INFORMATION: diernhoferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 459
US-08-785-750-2
; Sequence 2, Application US/08785750
; Patent No. S8465710;
GENERAL INFORMATION:
APPLICANT: PODSAKOFF, GREGORY M.
APPLICANT: MUTZMAN, GARY J.
TITLE OF INVENTION: METCHODS OF TREATING ANEMIA USING
TITLE OF INVENTION: METCHODS OF TREATING ANEMIA USING
TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRLONS
NUMBER OF SEQUENCES:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITYS: MAILO PARK
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80.0%; Pred. No. 4.7e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUMTRY: USA

ZIP: 94025

COUNTRY: USA

ZIP: 94025

COMPUTER READABLE FORM:
MEDTIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,750
FILING DATE: 16-JAN-1997

CLASSIFICATION NUMBER: US 08/588,355
FILING DATE: 18-JAN-1996

ATTORNEY/AGENT INFORMATION:
NAMME: MCCASACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548

REFERENCE/OCKET NUMBER: 38,548

REFERENCE/OCKET NUMBER: 38,548

REFERENCE/OCKET NUMBER: 38,548
PRIOR APPLICATION NUMBER: KK LULLOSON PRIOR FILING DATE: 1999-05-29
PRIOR PELLING DATE: 1999-05-29
PRIOR FILING DATE: 1999-05-29
PRIOR FILING DATE: 1999-05-29
PRIOR APPLICATION NUMBER: KR 10-1999-0019635
PRIOR APPLICATION NUMBER: KR 10-2000-018189
PRIOR APPLICATION NUMBER: KR 10-2000-018189
PRIOR APPLICATION NUMBER: KR 10-2000-018189
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ 1D NOS: 243
SOFTWARE: Kopatentin 1.71
SEQ ID NO 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 325-7812
TELEFAX: (415)325-7823
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       668 TACTCAAATTATGTT 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 rrcrcaaagrrrcrr 6
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Best Local Similarity 80.03
Matches 12; Conservative
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EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-980-052-219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-785-750-2
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US-09-980-052-219/c
US-09-980-052-219/c
; Sequence 219, Application US/09980052
; Patent No. 6670130
; GENERAL INFORMATION:
APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
APPLICANT: KIM, Cheol Min
APPLICANT: KIM, Cheol Min
TILLE OF INVENTION: Oligonuclectide for detection and identification of Mycobacteria
TILLE REFERENCE: PP05020/PCT
CURRENT APPLICATION NUMBER: US/09/980,052
CURRENT FILING DATE: 2001-11-28
FRIOR APPLICATION NUMBER: KR 10-1999-0019631
PRIOR PLING DATE: 1999-05-29
PRIOR FILING DATE: 1999-05-29
PRIOR FILING DATE: 1999-05-29
                                                                                                                                                                                                                                                                   APPLICANT: GIESENDORF, BELINDA
APPLICANT: GIESENDORF, BELINDA
APPLICANT: QUINT, WILHELMUS
APPLICANT: VAN DOORN, LERDBERT-JAN
TITLE OF INVENTION: NEW POLYNUCLEIC ACID SEQUENCES FOR USE IN THE
TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF PROKARYOTIC ORGANISMS
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: 1 LAALS
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICTOSOFE WORD 6.0 / ASCII text output
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,261A
FILING DATE: 25 Apr 1997
FILING DATE: 25 Apr 1997
FILING DATE: 20 Ct 1995
FILING DATE: 20 Ct 1995
FILING DATE: 20 Ct 1995
FILING DATE: 20 Ct 1994
ATTORNEY/AGET INVABER: PATRICIA A.
REGISTRATION NUMBER: 29,775
REGISTRATION NUMBER: 29,775
INFORMATION FOR SEQ ID NO: 72:
CONTENT OF THE FREENCE FOR THIS SECONO CONTENT OF THE FREENCE FOR THE FOR TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXA
                                                                                                                                               US-08-836-261A-72/c
; Sequence 72, Application US/08836261A
Patent No. 622158;
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               526 TGCACATGCGGCATT 540
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LENGTH: 20 base pairs
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              16 AGACACAACAATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 12; Conserva
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APPLICANT: Botestein, David A.
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Levine, Arnold J.
APPLICANT: Levine, Arnold J.
APPLICANT: Levine, Arnold J.
APPLICANT: Wood, William I.
ARLIER REFERENCE: P1176R2
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/091,695
EARLIER PELLING DATE: 1998-02-04
NUMBER OF SEQ ID NOS: 156
SEALLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
PRIOR APPLICATION NUMBER: PCT/USO1/00667

PRIOR FILING DATE: 2001-01-30

PRIOR PELICATION NUMBER: PCT/USO1/00668

PRIOR PELING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

SRING PILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILI
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0.9%; Score 10.2; DB 1; Length 18;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

0.9%; Score 10.2; DB 1;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 12; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1-18
OTHER INFORMATION: Sequence is synthesized.
Patent No. 6387657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 131, Application US/09182145B Patent No. 6387657 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                738 CTTGTAGGCAGCTGC 752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-866-108A-7016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-182-145-131/c
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US-09-182-145-131
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US-09-543-771B-588/C

Sequence 588, Application US/09543771B

Patent No. 6780609

Patent No. 6780609

APPLICANT: Carulli, John P.

APPLICANT: Little, Randall D.

APPLICANT: Little, Randall D.

APPLICANT: Johnson, Mark L.

TITLE OF INVENTION: High bone mass gene of 11q13.3

FILE REFERENCE: 032796-014

CURRENT APPLICATION NUMBER: US/09/543,771B

CURRENT PILING DATE: 2000-04-05

PRIOR PILING DATE: 1999-01-13

PRIOR FILING DATE: 1999-01-13

PRIOR FILING DATE: 1998-01-13

PRIOR FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 641

SOFFWARE: FastSEQ for Windows Version 4.0

LENGTH: 19

TENDY PATENTION NUMBER: US 60/105,511

PRIOR FILING DATE: 1998-10-23

NUMBER OF SEQ ID NOS: 641

SEQ ID NO 588

LENGTH: 19

TENDY PATENTION NUMBER: US 60/105,511
US-09-544-39BB-58B/C

Sequence 58B, Application US/0954439BB
Patent No. 6770461
GENERAL INFORMATION:
APPLICANT: Carulli, John P.
APPLICANT: Little, Randall D.
APPLICANT: Inittle, Randall D.
APPLICANT: Johnson, Mark L.
TITLE OF INVENTION: High bone mass gene of 11q13.3
FILE REFERENCE: 032796-013
CURRENT APPLICATION NUMBER: US/09/544,39BB
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US 60/071,449
PRIOR FILING DATE: 1999-01-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 641
SOFTWARE: FastSEQ for Windows Version 4.0
ILENCTH' 10 808
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Best Local Similarity 80.0
Matches 12; Conservative
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CRGANISM: Homo sapiens
US-09-543-771B-588
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US-09-544-398B-588
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US-08-812-102-1
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APPLICANT: KESSLER, PAUL D.
APPLICANT: KESSLER, PAUL D.
APPLICANT: BYRNE, BARX J.
TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
TITLE OF INVENTION: CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
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Patent No. 5945335
GENERAL INFORMATION:
APPLICANT: COLOSI) Peter
TITLE OF INVENTION: Adenovirus Helper-Free Systems for Producing
TITLE OF INVENTION: Recombinant AAV Virions Lacking Oncogenic Sequences
                                             Gaps
  0.9%; Score 10; DB 1; Length 14; 100.0%; Pred. No. 5.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.9%; Score 10; DB 1; Length 14;
100.0%; Pred. No. 5.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,355
             100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/588,355
FILING DATE: 18-JAN-1996
CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94025
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             Sequence 1, Application US/08588355
Patent No. 5858351
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE DOCKET NUMBER: 080
TELECOMMUNICATION INFORMATION:
TELEPAK: (650) 325-7812
TELEPAK: (650) 325-7823
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
Query Match 0.5
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
                                                                                    744 GGCAGCTGCC 753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: MENLO PARK
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 10; Conserv
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USA
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US-09-116-780-5
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GENERAL INFORMATION:

APPLICANT: KURTZMAN, GARY J.

APPLICANT: KURTZMAN, GARY J.

APPLICANT: COLOSI, PETER C.

APPLICANT: YOSHIDA, JUN

APPLICANT: MIZUNO, MASAAKI

APPLICANT: MIZUNO, MASAAKI

APPLICANT: OKADA, HIDEHO

TITLE OF INVENTION: GENE THERAPY FOR THE TREATMENT OF SOLID

TITLE OF INVENTION: TUMORS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide US-09-116-780-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                      Score 10; DB 1; Length 14;
Pred. No. 5.2e+02;
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CONFURE: Patentin Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,102
FILING DATE: 05-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/013,209
FILING DATE: 06-MAR-1996
ATTORNEY/AGENT INPORMATION:
NAME: MCCRACKEN, THOMAS.
REFERENCE/DOCKET NUMBER: 0800-0008
TELECOMMUNICATION NUMBER: 0800-0008
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.9%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 5.2 Matches 10; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/116,780
CURRENT FILING DATE: 1998-07-16
EARLIER APPLICATION NUMBER: 08/745,957
EARLIER FILING DATE: 1996-11-07
EARLIER FILING DATE: 1995-11-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO S
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08812102
Patent No. 5952221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 325-7823
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        744 GGCAGCTGCC 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCCAGCTGCC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: MENLO PARK
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 462
US-08-812-102-1
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COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CAURENY APPLICATION DATA:
APPLICATION NUMBER: US/09/309,042
FILING DATE:
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: 12
ADDRESSE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECTLE TYPE: DNA (genomic)
US-08-745-957-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    744 GGCAGCTGCC 753
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USA
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COUNTRY: USI
ZIP: 94025
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US-09-309-042-1
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                                                                                                                               Sequence 1, Application US/08784757
; Sequence 1, Application US/08784757
; Sequence 1, Application US/08784757
; Patent No. 5962313
; Patent No. 5962313
; APPLICANT: PODEARCPF, GREGORY M. APPLICANT: PARE, BARRY J. APPLICANT: KIRTZMAN, GARY J. TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE TITLE OF INVENTION: CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRIONS NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS: ASSOCIATES STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                 Gaps
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            Length 14;
                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
COMFUTER: IBM PC compatible
COMFUTER: IBM PC compatible
COMFUTER: IBM PC compatible
SUFFWARE: PatentIn Release #1.0, Version #1.30
SUFFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/784,757
FILING DATE: 16-JAN-1997
CLASSIFICATION NUMBER: US 08/588,355
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN THOWAS P.
REGISTRATION NUMBER: 0800-0009.20
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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19.08-08-79-57-1

1 Sequence 1, Application US/08745957

2 Patent No. 6004797

3 GENERAL INFORMATION:

3 APPLICANT: COLOSI, PETER C.

1 TITLE OF INVENTION: ACCESSORY FUNCTIONS FOR USE IN
          DB 1; Le
5.2e+02;
          Query Match 0.9%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 5.2 Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               744 GGCAGCTGCC 753
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                                                                                             744 GGCAGCTGCC 753
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USA
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                                                                                                                                                                                                    RESULT 463
US-08-784-757-1
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Sequence 1, Application US/09309042

Sequence 1, Application US/09309042

Patent No. 6211163

GENERAL INFORMATION:
APPLICANT: PODSAKOFF, GREGORY M.
APPLICANT: KESSLER, PAUL D.
APPLICANT: KESSLER, PAUL D.
APPLICANT: WINTEMAN, GARY J.
APPLICANT: WINTEMAN, GELS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
TITLE OF INVENTION: CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200

CHIY: MENLO PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.2e+02;
0; Indels
TILE OF INVENTION: RECOMBINANT AAV VIRION PRODUCTION
                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Flopped disk

MEDIUM TYPE: Flopped disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: APERICATION DATA:

APPLICATION NUMBER: US/08/745,957

FILING DATE: 07-NOV-1996

CLASSIFICATION NUMBER: US 60/006,402

RADICATION NUMBER: US 60/006,402

APPLICATION NUMBER: US 60/006,402

APPLICATION NUMBER: US 60/006,402

ATTORNEY/AGENT INFORMATION:

NAME: MCCRACKEN, THOMAS P.

REGISTRATION NUMBER: 38,548

REGISTRATION NUMBER: 38,548

REFERENCE/DOCKET NUMBER: 0800-0007

TELERENCE/DOCKET NUMBER: 0800-0007
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GENERAL INFORMATION:
             US-09-205-337-2
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US-09-406-362-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PODSAKOFF, GREGORY M.
KURTZMAN, GARY J.
TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING
RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                           0.9%; Score 10; DB 1; Length 14;
100.0%; Pred. No. 5.2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/205,337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 04-Dec. 1998
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/785,750
FILING DATE: «Unknown-
ATTORNEY/AGENT INFORMATION:
NAME: WCCRACKEN, THOWAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009.21
TELEPHONE: (415) 325-7812
TELEPHONE: (415) 325-7812
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/588,355
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOWAS P.
REGISTRATION NUMBER: 0800-0009
TELEPONMUNICATION INFORMATION:
TELEPONES: 6509 325-7812
TELEPAX: (650) 325-7813
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09205337
Patent No. 6325998
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-309-042-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              744 GGCAGCTGCC 753
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US-09-205-337-2
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KURTZMAN, GARY J.
KURTZMAN, GARY J.
TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
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                                             Gape
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Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/406,362
FILING DATE: 28-Sep-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/784,757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: "CUNCHONDANDATONEY/AGENT INFORMATION:
NAME: MCKRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009.20
TELECOMUNICATION INFORMATION:
TELEFRANCE (415) 325-7812
TELEFAX: (415) 325-7823
0.9%; Score 10; DB 1; Lo
100.0%; Pred. No. 5.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
Query Match 0.9%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 5.2 Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                    APPLICANT: PODSAKOFF, GREGORY M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                               Sequence 1, Application US/09406362
Patent No. 6335011
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 468
US-09-755-734-1
; Sequence 1, Application US/09755734
; Patent No. 6391858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1:
                                                                                       744 GGCAGCTGCC 753
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                                                                                                                                  1 GGCAGCTGCC 10
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TITLE OF INVENTION: GENE THERAPY FOR THE TREATMENT OF SOLID TUMORS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
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COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

CORPUTER: IBM PC compatible

CORFURER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/649,890

FILING DATE: 28-Aug-2000

CLASSIFTCATION: CURNOWN>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/812,102

FILING DATE: 06-MAR-1997

APPLICATION NUMBER: US 60/013,209

FILING DATE: 06-MAR-1996

ATORNEY/AGENT INFORMATION:

NAME: MACCACKEN, THOWALS P.

REGISTRATION NUMBER: 38 548

REFERENCE/DOCKET NUMBER: 0800-0008

TELECOMMUNICATION INDMERE: 38.548

REFERENCE/DOCKET NUMBER: 0800-0008
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Pred. No. 5.2e+02;
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ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO_PARK
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/406,363
FILING DATE: 28-Sep-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/745,957
FILING DATE: 11-Jul-1996
ATTORNEY AGENT INFORMATION:
REGISTATION NUMBER: 38,548
REGISTATION NUMBER: 38,548
REGISTATION NUMBER: 38,548
TELECOMMUNICATION INFORMATION:
TELEFAX: (415)327-3400
TELEFAX: (415)327-3331
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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US-09-64-890-1
; Sequence 1, Application US/09649890
; Patent No. 6531456
; Patent No. 6531456
; GENERAL INFORMATION:
; APPLICANT: CURIZMAN, GARY J.
; COLOSI, PETER C.
; YOSHIDA, UUN
MIZUNO, MASAAKI
; MASAAKI
; OKADA, HIBBHO
OKADA, HIBBHO
                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: CALIFORNIA COUNTRY: USA
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                                                         ENTRY DESCRIPTIONS OF THE OF INVENTIONS METHODS FOR DELIVERING DNA TO MUSCLE CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/755,734
FILING DATE: 04-03m-2001
CLASSIFICATION CANAROM>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/589,355
FILING DATE: CUNKIOWN>
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09406363
Sequence 1, Application US/09406363
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: COLOSI, PETER C.
APPLICANT: COLOSI, PETER C.
TITLE OF INVENTION: ACCESSORY FUNCTIONS FOR USE IN
RECOMBINANT AAV VIRION PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.9%; Score 10; DB 1; Length 14; 100.0%; Pred. No. 5.2e+02; tive 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOODY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE
                   APPLICANT: PODSAKOFF, GREGORY M. KESSLER, PAUL D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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Best Local Similarity 100.
Matches 10, Conservative
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                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                            USA
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Gaps

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Sequence 1, Application US/0969204A
Patent No. 6610290
GENERAL INFORMATION:
APPLICANT: PODSAKOFF, GREGORY M.
BYRESELR, PAUL D.
BYRESE, BARRY J.
KURTZMAN, GARY J.
TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS
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MEDIUM TYPES Floppy disk

MEDIUM TYPES Floppy disk

COMFUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/969,204A

FILING DATE: 01-Oct-2001

CLASSIFICATION: «Unknown»

PRIOR APPLICATION NUMBER: US/09/406,362

FILING DATE: 28-Sep-1999

APPLICATION NUMBER: 08/784,757

FILING DATE: 4Unknown»

ATTORNEY/AGENT INFORMATION:

NAME: MCCRACKEN, THOMAS P.

REGISTRATION NUMBER: 38,548

REGISTRATION NUMBER: 38,548

REGISTRATION INFORMATION:

TELEPHONE: (415) 325-7813
                                                                                                                                                                                                                                                    Query Màtch 0.9%; Score 10; DB 1; Length 14; Best Local Similarity 100.0%; Pred. No. 5.2e+02; Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-649-890-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-969-204A-1
(415) 325-7823
                                                                 LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 14 base pairs
                   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: MENLO PARK
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                   744 GGCAGCTGCC 753
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TELEFAX:
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 744 GGCAGCTGCC 753

Db 1 GGCAGCTGCC 10

Search completed: August 19, 2005, 10:54:27

Job time: 9 secs
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Minimum DB Maximum DB

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Searched:

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ACCESSION: A
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ACCESSION:
ACCESSION:
AX420107
AX487296
AX667251
131384
AX665346
AX665346
AX666133
AX7389630
AX7389630
AX7389630
AX738731392
AX732713
AX73273
AX73252
AX732303
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AX467276
AX54228
BD090191
AR539512
AX539513
AX70529
AX707529
AX707520
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ACCESSION: AX189878
ACCESSION: CO8 60120
ACCESSION: CO8 60120
ACCESSION: CO8 60110
ACCESSION: CO8 60110
ACCESSION: CO8 60111
ACCESSION: CO8 60113
ACCESSION: CO8 60113
ACCESSION: CO8 60113
ACCESSION: CO8 60114
ACCESSION: CO8 60115
ACCESSION: CO8 60115
ACCESSION: CO8 60116
ACCESSION: CO8 60121
ACCESSION: AX3 02819
ACCESSION: AX3 02819
ACCESSION: AX4 12234
ACCESSION: AX4 12339
ACCESSION: AX4 12339
ACCESSION: AX4 12339
ACCESSION: AX7 38199
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                                                                                                                                                     Search time 5 Seconds (without alignments)
2.757 Million cell updates/sec
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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                                                                                                                                                          August 19, 2005, 10:52:25 ;
                                                                                                              nucleic search, using sw model
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CQ878362
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CQ860116
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CQ860122
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BD128083
CQ860126
AX378941
CQ860125
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AR302819
AR302820
AX412234
AX548339
AX738199
BD223822
B13776
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                                                                                                                                                                                                                                                                                                                                                                                                           325 seqs, 6187 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum Match 0%
Maximum Match 100%
Listing first 326 s
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seq length: 200000000
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Query
Match 1
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Perfect score:
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CQ878362.1 GI:53790915
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Patent: WO 2004072293-A 32 26-AUG-2004;
Patent: WO 200407293-A 32 26-AUG-2004;
Patent: NO 20040729-A 32 26-AUG-2004;
Patent: NO 200407-A 3
            PAT 08-AUG-2001
                                                                                                                                                                          Eukaryoja, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Nucleic acids containing single nucleotide polymorphisms and methods of use thereof.

Patent: WO 014942-A 58 05-JUL-2001;

Curagen Corporation (US)

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Sequence 58 from Patent WOO147942.
AX189879 GI:15143250
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Bailleul, B., Rouille, Y., Seron, K. and Belouzard, S. Use of the genes leprotil and ob-rgrp for the screening of active compounds for weight gain or loss or diabetes in human or animal subjects
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Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primers for synthesizing full length cDNA clones and their use Patent: EP 1396543-A 4299 10-MAR-2004; Research Association for Biotechnology (JP) Location/Qualifiers
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                                                                                              Patent: WO 2004080272-A 15 23-SEP-2004;
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Sequence 4299 from Patent
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Jockers, R., Couturier, C. and Uhlmann, E.
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                                                                                  leptin receptor 2293-A 2 26-AUG-2004; Aventis Pharms S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RACHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
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Patent: WO 2004072293-A 22 26-AUG-2004;
Patent: WO 2004072293-A 22 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSEM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
Location/Qualifiers
                Jockers, R., Couturier, C. and Uhlmann, E. Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the
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Oligonuclectides which inhibit the expression of the ob-rgrp
protein and method for detection of compounds modifying the
interaction between the proteins of the ob-rgrp family and the
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noce="ASO1"
                                                                                                                                                                                                              'organism="synthetic construct"
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Sequence 23 from Patent W02004072293.
CQ860111. GI:51981999
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1.8%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 7.6
Matches 20; Conservative 0; Mismatches
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/noTe="AS14"
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Patent: WO 2004/72293-A 23 26-AUG-2004,
Patent: WO 2004/72293-A 29 26-AUG-2004,
Patent: WO 2004/72293-A 29 26-AUG-2004,
RECHERCHE MEDICALE (INSERW) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
Location/Qualifiers
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Batch: WO 2004072293-A 24 26-AUG-2004;

Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA

RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
Scientifique (CNRS) (FR)

Location/Qualifiers
Jockers, R., Couturier, C. and Uhlmann, E. Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the
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Oligonuclectides which inhibit the expression of the ob-rgrp
protein and method for detection of compounds modifying the
interaction between the proteins of the ob-rgrp family and the
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    /note="AS02"

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100.0%; Pred. No. 7.6;
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100.0%; Pred. No. 7.6;
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Seguence 24 from Patent WO2004072293.
CQ860112
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leptin receptor
Patent: WO 2004072293-A 28 26-AUG-2004;
Patent: WO 2004072293-A 28 Z6-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
Location/Qualifiers
                                                leptin receptor
Patent: WO 2004072293-A 27 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERW) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
Location/Qualifiers
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Oligomuclectides which inhibit the expression of the ob-rgrp
protein and method for detection of compounds modifying the
interaction between the proteins of the ob-rgrp family and the
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Joligonuclectides which inhibit the expression of the ob-rgrp
protein and method for detection of compounds modifying the
protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and
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/note="AS07"
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/db xref="texon:32630"
/noTe="AS06"
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Sequence 28 from Patent WO2004072293.
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Sequence 29 from Patent WO2004072293.
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Patent: WO 2004072293-A 26 26-AUG-2004;
Patent: WO 2004072293-A INSTITUT NATIONAL DE LA SANTE ET DE LA
RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
Scientifique (CNRS) (FR)
Location/Qualifiers
                                                                                  leptin receptor
Patent: WO 2004072293-A 25 26-AUG-2004;
Patent: WO 2004072293-A INSTITUT NATIONAL DE LA SANTE ET DE LA
RAVENTIS PARAME S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
Scientifique (CNRS) (FR)
Location/Qualifiers
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             Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the
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               leptin receptor
Patent: WO 2004/02293-A 29 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
Scientifique (CNRS) (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jockers, R., Couturier, C. and Uhlmann, B.
Oligonucleotides which inhibit the expression of the ob-rgrp
protein and method for detection of compounds modifying the
interaction between the proteins of the ob-rgrp family and the
leptin receptor
Patent: WO 2004072293.A 30 26-AUG-2004;
Patent: WO 2004072293.A 30 26-AUG-2004
EXCHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
Scientifique (CNRS) (FR)
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Oligonucleotides which inhibit the expression of the ob-rgrp
protein and method for detection of compounds modifying the
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Patent: WO 2004072293-A 33 26-AUG-2004;
Patent: WO 2004072293-A 13 26-AUG-2004;
Patent: WO 20040772293-A 13 26-AUG-2004;
Patent: WO 2004072293-A 13 26-AUG-2004;
RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
Location/Qualifiers
Patent: WO 2004072293-A 31 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
Scientifique (CNRS) (FR)
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Oligonuclectides which inhibit the expression of the ob-rgrp
protein and method for detection of compounds modifying the
interaction between the proteins of the ob-rgrp family and the
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Oligonucleotides which inhibit the expression of the ob-rgrp
protein and method for detection of compounds modifying the
interaction between the proteins of the ob-rgrp family and the
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Sequence 34 from Patent WO2004072293.
CS860122 GI:51982010
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Matches 20; Conserv
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leptin receptor
Patent: WO 2004072293-A 38 26-AUG-2004;
Patent: WO 2004072293-A INSTITUT NATIONAL DE LA SANTE ET DE LA
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Scientifique (CNRS) (FR)
22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jockers, R., Couturier, C. and Uhlmann, E. Oligonuclectides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the
PD 22-JAN-2002
PP 07-UUL-2000 JP 2000253172
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHI PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHI PI ISHII,
PI YURI KAWAI,AI WAKAWATSU,TOMOYASU SUGIYAWA,KEIICHI NAGAI,SHINCHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
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100.0%; Pred. No. 7.4;
tive 0; Mismatches 0; Indels
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="Artificiel"
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Sequence 38 from Patent WO2004072293.
CQ860126
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Sequence 59 from Patent WO0210347.
AX378941
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1.8%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 7.6
Matches 20; Conservative 0; Mismatches
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/organism="unidentified"
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unclassified.
1 (bassilto 20)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Patent: WO 2004072293-A 34 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
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Primer for synthesizing full-length cDNA and use thereof.
BD128083
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Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002017375-A 3514 22-JAN-2002;
HELIX RESEARCH INSTITUTE
OS Unidentified
PN JP 2002017375-A/3514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent: WO 2004080272-A 14 23-SEP-2004;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
Location/Qualifiers
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100.0%; Pred. No. 7.6;
iive 0; Mismatches 0; Indels
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                                                                                                                  /organism="synthetic construct"
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/note="AS13"
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/db_xref="taxon:32644"
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JP 2002017375-A/3514.
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1 (bases 1 to 18)
Hess,J.W., Caskey,C.Thomas., Liu,Q. and Phillips,M.Sean.
Rat ob-receptors and nucleotides encoding them
Patent: US 6281346-A 50 28-AUG-2001;
Location/Qualifiers
               1 (bases 1 to 19)
Hess,J.W., Caskey,C.Thomas., Liu,Q. and Phillips,M.Sean.
Rat ob-receptors and nucleotides encoding them
Patent: US 6281346-A 51 28-AUG-2001;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches
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Bennett, B. and Mathews, W.
Leptin receptor having a WSX motif
Patent: US 6541604-A 30 01-APR-2003;
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Sequence 50 from patent US 6281346.
AR166700
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/organism="unknown"
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/organism≈"unknown"
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Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor
Patent: WO 2004072293-A 37 26-AUG-2004,
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
                                                                                                                             Benvenisty, N.
Directed differentiation of embryonic cells
Patent: WO 0210347-A 59 07-FBB-2002,
Yissum Research and Dev. Company of the Hebrew Univ. of Jerusalem
                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                         1. .25
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/note="3' primer of Parathyroid Hormone"
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    .21
    forganism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

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Sequence 51 from patent US 6281346.
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AR166701.1 GI:16242129
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GI:19574784
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CQ860125.1 GI:51982013
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Matches 21; Conservative
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                                                      Homo sapiens
AX378941.1
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SOURCE ORGANISM

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Length 18;

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AX738199.1 GI:30517487
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Best Local Similarity 83.3%;
Matches 20; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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BD223822/c
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AX738199
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                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                PAT 14-JUN-2002
                                                       PAT 12-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 20;
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synthetic construct
other sequences; artificial sequences.
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PROMEGA CORPORATION (US)
Location/Qualifiers
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1.6%; Score 17.6; L
Best Local Similarity 83.3%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/mol_type="taxon:9606"
/note="BAT-25 primer"
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Sequence 263 from Patent WO0240716.
AX548339
                                                                                                                                                   Unclassified.
1 (bases 1 to 18)
Bennett,B. and Matthews,W.
Leptin receptor having a WSX motif
Patent: US 6541604-A 31 01-APR-2003;
                                                                                                                                                                                                                                                                                   Query Match 1.6%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 19; Matches 18; Conservative 0; Mismatches
                                                          AR302820 18 bp 18 Sequence 31 from patent US 6541604. AR302820. GI:31691307
                                                                                                                                                                                                                                                                                                                                                                                                                                 24 bp
Sequence 60 from Patent WO0222879.
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/organism="unknown"
/mol_type="genomic DNA"
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BD223822

Novel method of regulating seed development in plants and genetic sequences therefor.

BD228822
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JP 2002526052-A/15.
synthetic construct
synthetic construct
other sequences; artificial sequences.

1 (bases 1 to 21)
Bilodeau, P., Chaudhury, A.M., Dennis, E.S., Koltunow, A.M.G., Luo, M.
and Peacock, W.J.
Novel method of regulating seed development in plants and genetic Bequences therefor Peacher: JP 2002526052-A 15 20-AUG-2002;
COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Palm,K.
Profiling tumor specific markers for the diagnosis and treatment oneoplastic disease heoplastic disease Patent: WO 0240716-A 263 23-MAY-2002; Cemines, LLC (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Telerman,A., Amson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 0302517-A 3789 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 0; Indels
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="teaxon:32630"
/noTe="Probe"
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; Pred. No. 20;
0; Mismatches
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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TGGGCAGGCTGCCCGGGCCGTG 30
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AX420107.1 GI:21524406
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ilarity 81.8%;
Conservative 1
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Candida albicans
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18; Conser
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Matches 19; Conserv
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          Query Match
Best Local S:
Matches 18
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AX487296/c
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OS Artificial Sequence
PN JP 2002526052-A/15
PD 20-AUG-2002
PP 21-SEP-1999 JP 2006573582
PR 21-SEP-1999 UP 2006573582
PR 21-SEP-1999 WS 60/101184,22-SEP-1998 AU PP 6063 PR 22-SEP-1999 AU PP 6063 PR 01-UUL-1999 AU PP 01346 PI PIERRE BILODEAU, ABDUL MUTAKABBIR CHAUDHURY, ELIZABETH SALISBURY PI DENNIS,
PI DENNIS,
PI ANNA MARIA GRAZYNA KOLTUNOW, MING LUO, WILLIAM JAMES PEACOCK PC C12N15/00, A0185/10, C12N15/00, C12N15/
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PCR primer for discriminating genotype la of HCV (Hepatitis C
virus).
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MIZOGAMI
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Ono.T., Mukaide,M., Hikichi,K. and Mizogami,M.
NEW OLIGONUCLEOTIDE, PRIMER FOR DISCRIMINATION IN GENOTYPE OF HEPATITIS C VIRUS COMPRISING THE SAME AND DISCRIMINATION IN GENOTYPE OF HEPATITIS C VIRUS BY USING THE PRIMER PATENT: JP 1997234072-A 28 09-SEP-1997;
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OC Artificial sequences.
PN JP 1997234072-A/28
PN 09-SEP-1997
PF 01-FEB-1996 JP 1996038875
PR 01-FEB-1995 JP 95P 35997, 30-DEC-1995 JP 95P
PN ONO TOMOYOSHI, MUKAIDE MASAKAZU, HIKICHI KAZUMASA, PI
PC C12N15/09,C07H21/04,C12Q1/68,C12Q1/70,(C12N15/09,C)
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.larity 90.0%; Pred. No. 30;
Conservative 0; Mismatches 2;
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    .21
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|mol_type="genomic DNA"
|db_xref="taxon:32630"

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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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topology: Linear;
hypothetical: No;
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JP 1997234072-A/28
unidentified
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CC hypotheti
CC anti-sens
FH Key
FH SOURCE
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                                    Gaps
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   DB 1;

    .24
    /organism="synthetic construct"

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Sequence 4596 from Patent WO02053728.
AX487296
                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                              synthetic construct other sequences other sequences

    .23
/organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"

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Score 16.8; DE
Pred. No. 28;
1; Mismatches
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82.6%; Pred. No. 31;
ive 0; Mismatches
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Patent: WO 0208409-A 1 31-JAN-2002;
The Secretary of Agriculture (US)
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/db_xref="taxon:32630"
/note="Primer"
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Sequence 1 from Patent WO0208409.
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Matches 18; Conserv
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CQ860133/c
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                PAT 29-SEP-1999
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Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same method of using the same Patent: Location/Qualifiers
                                                                                             Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 21)
1 (bases 1 to 21)
1 (bases 1 to 21)
Method for generation of sequence sampled maps of complex genomes Method for generation of sequence sampled maps of complex genomes Patent: US 5851760-A 600 22-DEC-1998;
Location/Qualifiers
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1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 3; Indels
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85.7%; Pred. No. 38;
ive 0; Mismatches 3;
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synthetic construct
other sequences; artificial sequences.
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Gupte, J.S.
G-protein coupled receptors
Patent: WO 0242458-A 23 30-MAY-2002;
Tularik Inc. (US)
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
                    21 bp Di
US 5851760.
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Sequence 23 from Patent WO0242458.
AX665946
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                                 Sequence 600 from patent AR067252 GI:5998474
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Unclassified.
1 (bases 1 to 21)
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Best Local Similarity 85.7
Matches 18; Conservative
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                      AR067252
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AX665946/C
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leptin receptor
Patent: WO 2004072293-A 45 26-AUG-2004;
Patent: WO 2004072293-A 45 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERW) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
Location/Qualifiers
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicamente parties, WO 0302517-A 4573 27-MAR-2003; Molecular Engines Laboratories (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jockers, R., Couturier, C. and Uhlmann, E. Oligonuclectides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the
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1. .23
//organism="synthetic construct"
/mol type="unassigned DNA"
/db xref="taxon:32650"
/note="TGR342Right PCR expression profiling primer"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="reaxon:32630"
/noTe="Artificiel"
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WO03025177.
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Sequence 45 from Patent WO2004072293.
CQ860133
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synthetic construct
other sequences; artificial sequences.
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/mol_type="unassigned DNA"
                                                                                                                                                                                                                                   117 TIGGACTGACTTTTCTTATGC 137
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AX738983
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Homo sapiens
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DEFINITION AX298650/c

ò 셤 VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL

TITLE

FEATURES

PAT 04-OCT-2003

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1. 19
/ Organism="synthetic construct"
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//db_xref="tanson:32630"
//note="Upstream primer used to detect the expression of the Lycopersicon esculentum Chy2 gene by RT-PCR"
1. 19
//note="Le -Chy2 Upstream Primer"
                                                                                                                                                                                                                                                                                                                                                Giuliano,G., Rosati,C., Dharmapuri,S., Pallara,P. and Camara,B. Recombinant plants and dna constructs Patent: Br 1323325-A 19 02-JUL-2003; ENEA ENTE PER LE NUOVE TECNOLOGIE, L'ENERGIA E L'AMBIENTE (IT); Biogen S.r.l. (IT)
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unidentified
unclassified.
Unclassified.
Glodorer I to 20)
Glosendorf, B., Quint, W. and Van, D.L.
NEW POLYNUCLEIC ACID SEQUENCES FOR USE IN THE DETECTION AND
DIPPERENTIATION OF PROKARYOTIC ORGANISMS
PAPENT: WO 961360B-A 72 09-MAY-1996;
INNOGENETICS NV (BE)
Other publication AU 3845795 960523.
Location/Qualifiers
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synthetic construct
other sequences; artificial sequences.
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89.5%; Pred. No. 47;
ative 0; Mismatches

    .20
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    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

                                                                                                                                                               19 bp
Sequence 19 from Patent EP1323825.
AX795189
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Sequence 72 from Patent WO9613608.
A50630
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Patent: WO 0183749-A 284 08-NOV-2001;
WARNER-LAMBERT COMPANY (US); The Monell Chemical Senses Center (US)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 100.0%; Pred. No. 45;
Matches 16; Conservative 0; Mismatches
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    .20
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Sequence 286 from Patent WO0183749.
AX298652

    .20
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Homo sapiens
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AX298652/c LOCUS

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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HIGHSES 1 to 20)

S Quint, W. and Doorn, L.J.V.

S Quint, W. and Doorn, L.J.V.

Probes, methods and kits for detection and typing of Helicobacter pylori nucleic acids in biological samples

INDOGRAFICS NV, DDL BV

OS Unidentified

PN JP 2001502536-A/29

PD 27-FEB-2001

PF 10-0CT-1997 JP 1998518004

PR 16-0CT-1996 EP 96870131.8

PI WILHELMUS QUINT, LEENDERT JAN VAN DOORN

PC C1201/68, CO7714/205, C12N15/11

CC

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Gene disruption methodologies for drug target discovery Patent: WO 02053728-A 4031 11-JUL-2002; Blitra Pharmaceuticals, Inc. (US) Location/Qualifiers
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                                                                                                                         /organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"
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83.3%; Pred. No. 50;
:ive 2; Mismatches
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/organism="unidentified"
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/db_xref="taxon:32644"
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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Gene disruption methodologies for drug target discovery
Patent: WO 0160975-A 382 23-AUG-2001;
Elitra Pharmaceuticals, Inc. (US)
Location/Qualifiers
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1 (bases 1 to 20)

Giesendorf, B., Quint, W. and Van Doorn, L.-J.

Giesendorf, acid sequences for use in the detection and differentiation of profarryotic organisms

Patent: 05 (221582-A 72 24-APR-2001;

Location/Qualifiers
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synthetic construct
other sequences; artificial sequences.
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Sequence 382 from Patent WO0160975.
AXZ41144
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/mol_type="unassigned DNA"
                                                                  20 bp
Sequence 72 from patent US 6221582.
AR147307
AR147307.1 GI:15111110
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AX241144/c DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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AX713192
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and Randi,A.M.
Method and reagent for the inhibition of erg
Patent: WO Q188124-A 1048 22-NOV-2001;
RIBOZYME PHARACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Pred. No. 58;
0; Mismatches 1; Indels
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 3203 from Patent WO03040369.
AX759882
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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/organism="Homo sapiens"
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Method and diagnostic kit for the molecular diagnosis of
pharmacologically relevant genes
Patent: WO 0318837-A 78 06-MAR-2003;
Adnagen AG (DE)
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Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density disequilibrium map of the human genome Patent: US 637751-A 11660 25-MAR-2003;
Location/Qualifiers
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1.4%; Score 15.4; DB 1;
Best Local Similarity 94.1%; Pred. No. 57;
Matches 16; Conservative 0; Mismatches 1;
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N Sequence 11660 from patent US 6537751.

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AR299925.1 GI:31687209
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synthetic construct
other sequences; artificial sequences.
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Best Local Similarity 94.1%; Pred. No. 58;
Matches 16; Conservative 0; Mismatches
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Best Local Similarity 94.1%; Pred. No. 57;
Matches 16; Conservative 0; Mismatches
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AX713192
AX713192.1 GI:29823781
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                                          PAT 15-MAY-2001
                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases I to 20)

Brown, S.Joel., Dattagupta, N. and Naidu, Y.M.

Brown, S.Joel., Dattagupta, N. and Naidu, Y.M.

Method for inhibiting cellular proliferation using antisense oligonucleotides to interleukin-6 receptor mENA patent: US 571686.A 14 IO-FEB-1998;

Location/Qualifiers
                                                                                                                                                                           Robbins,J.M. and Tritz,R. Ribozyme therapy for the treatment of proliferative skin and
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44.1%; Pred. No. 54;
ive 0; Mismatches 1; Indels
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Best Local Similarity 94.1%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 1; Indels
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IMMUSOL, INC. (US)
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Sequence 11 from patent US 6136604.
AR136416
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Sequence 14 from patent US 5716846.
I88036
I88036.1 GI:3407976
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Location/Qualifiers
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Matches 16; Conservative
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                          RESULT 54
AX132091/c
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AUTHORS
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1. .20 /organism="synthetic construct" /organism="synthetic construct" /mol type="unassigned DNA" /db xref="taxon:3253" /nofe="Description of Combined DNA/RNA Molecule: Synthetic oligonucleotide-Description of Artificial Sequence: Synthetic oligonucleotide"
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Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,J.D.
Chlamydia pneumoniae polymucleotides and uses thereof Patent: US 655294-A 6064 06-MAY-2003;
Location/Qualifiers
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1 (bases 1 to 20)
Monia, B.P. and Wyatt,J.
Antisense inhibition of methionine aminopeptidase 2 expression
Patent: US 6136604-A 11 24-OCT-2000;
Location/Qualifiers
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llarity 85.0%; Pred. No. 59;
Conservative 0; Mismatches 3;
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synthetic construct
other sequences; artificial sequences.
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85.0%; Pred. No. 59;
vative 0; Mismatches
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/organism="unknown"
/wol_type="unassigned DNA"
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/organism="unknown"
/mol_type="genomic DNA"
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Unclassified.
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Matches 17; Conserv
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Gaps

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PAT 24-JAN-2003

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Gaps

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PAT 03-APR-2003

LOCUS DEFINITION ACCESSION VERSION

RESULT 61

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Matches

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ACCESSION VERSION

RESULT 59 AR442611

source

TITLE JOURNAL PEATURES

REFERENCE AUTHORS

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides and polypeptides of the ifn_g(a)-21 gene Patent: WO 02079249-A 9 10-OCT-2002; Genodyssee (FR)
                                                                                                                                                                                                                                                                                                  Length 20;
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Inhibition of specific histone deacetylase isoforms
Patent: WO 03006652-A 33 23-JAN-2003;
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Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3;
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1. 20
/organism="Homo sapiens"
/mol type="unassigned DNA"
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                                                                                                            Delorme, D., Woo, S.H. and Vaisburg, A. Inhibitors of histone deacetylase Patent: WO 0170675-A 17 27-SEP-2001, Methylgene, Inc. (CA)
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85.0%; Pred. No. 59;
iive 0; Mismatches
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AX703629

    .20
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Sequence 9 from Patent WO02079249.
AX589807
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                     Homo sapiens (human)
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Matches 17; Conservative
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                                       Homo sapiens
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Unknown.
Unclassified.
I (bases 1 to 20)
Kim, C.M., Park, H.K. and Jang, H.J.
Kim, C.M., Park, H.K. and Jang, H.J.
Oligonucleotide for detection and identification of Mycobacteria
Patent: US 6670130-A 219 30-DEC-2003;
Location/Qualifiers
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1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3; Indels
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/db xref="taxon:32630"
/noTe="Hypothetical Probe Sequence"
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Sequence 219 from patent US 6670130.
 0; Mismatches
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Sequence 17 from Patent W00170675.
AX456087 GI:21715042
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                                   459 AGTGGTAGCACTTTATTCTG 478
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AR442611.1 GI:42669868
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synthetic construct
17; Conservative
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DEFINITION ACCESSION VERSION KEYWORDS

AX293011/c

RESULT 60

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SOURCE

AUTHORS

TITLE

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105 TCAGTGGGGCTATTGGACTG 124
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817 AGCAGGCCTCTCATGACCCA 836
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JP 2002112775-A/86.
unidentified
unidentified
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WO 0111951-A/10.
                synthetic construct
synthetic construct
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AUTHORS
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DEFINITION
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BD143015
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TITLE
JOURNAL
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Antisense modulation of il-1 receptor-associated kinase-1
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Pred. No. 59;
                                                                            Length 20;
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|organism="synthetic construct"
|wol_type="unassigned DNA"
|db_xref="taxon:32630"
|noce="Antisense Oligonucleotide"
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                                                                           Query Match
1.4%; Score 15.2; DB 1;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3;
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Patent: WO 03104458-A 104 18-DEC-2003;
ISIS PHARMACEUTICALS, INC. (US)
Location/Qualifiers
                                                                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                                                                              other sequences; artificial sequences.
                                                                                                                                                                                                                                                                                                                                                                                      Patent: WO 03104458-A 33 18-DEC-2003;
Patent: WO 03104458-A 33 18-DEC-2003;
ISIS PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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85.0%; Pred. No. 59;
tive 0; Mismatches
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1.4%; Score 15.2; I
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches
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Sequence 33 from Patent W003104458.
AX962777.
AX962777.1 GI:40881890
              1. .20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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                                                                                                                                   743 AGGCAGCTGCCACCTTATGC 762
                                                                                                                                                       1 AGCCAGCTGCCACTTGATGC 20
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l (bases 1 to 21)

Nishimura,M., Yaguchi,H., Naito,S. and Hiraoka,I.

Orsura, Patent: JP 200211275-A8 66 G-ARR-2002;

Orsura, Pharamaceurical Factory INC

OS human ABCB4 gene

PN JP 200211275-A/86

PD 16-ARR-2002

PR 03-OCT-2000 JP 2000303404

PR 03-OCT-2000 JP 2000303404

PR NASUHIRO NISHIMURA,HIROSHI YAGUCHI,SHINSAKU NAITO,ISAO HIRAOKA

PC C12NIS/09,C12Q1/68,C12NIS/00

CC Method of assaying human ABC transporter and probe and kit CC
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cher sequences; artificial sequences.

ther sequences; artificial sequences.

s ishida, I., Tonizuka, K., Kuroiwa, Y., Oshima, T., Suzuk, M. and Ito, K.

s ishida, I., Tonizuka, K., Kuroiwa, Y., Oshima, T., Suzuk, M. and Ito, K.

s ishida, I., Tonizuka, K., Kuroiwa, Y., Oshima, T., Suzuk, M. and Ito, K.

thuman cytcchrome P450-transgenic mouse

tririn BEBR KK, ISAO ISHIDA, KAZUMA TOMIZUKA, YOSHIMI KUROIWA, AKESHI
OSHIMA, MUTSUMI SUZUKI, KMNIO ITO
OS Artificial Sequence

NN WO 0111951-A/10

PD 22-FEB-2001

PP 11-AUG-2000 WO 2000JP005424

PR 11-AUG-2000 WO 2000JP005424

PR 11-AUG-1999 JP 99P 229094

PR ISAO ISHIDA, KAZUMA TOMIZUKA, YOSHIMI KUROIWA, TAKESHI OSHIMA, PI

MUTSUMI SUZUKI,
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     20 bp DNA
Human cytochrome P450-transgenic mouse.
BD012571
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Microsatellite markers for genetic analyses and the differentiation
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Unclassified.
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PI TANIDA EMIKO, OUE CHIHARU, YAGI SHINTARO, HASEGAWA AKIRA, PI
KIYOZAWA KENDOU,
PI YANO AKIHIKO
PC C12N15/09, C07H21/04, C07K14/705, C12N1/21, C12N5/10, C12P21/02, PC
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c GO1N33/566,GO1N33/576,(C12N1/21,C12R1:19),(C12N5/10,C12R1:91),
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Tanida,E., Oue,C., Yagi,S., Hasegawa,A., Kiyozawa,K. and Yano,A. ASIALOGLYCOPROTEIN RECEPTOR DERIVATIVE AND ITS USE
PATENT: JP 1997056580.A 2 04 "MAR-1997;
TONEN CORP, INTERNATL REAGENTS CORP, KIYOZAWA KENDOU
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                                                                                                                                            Query Match 1.4%; Score 15.2; DB 1; Length 21; Best Local Similarity 85.0%; Pred. No. 58; Matches 17; Conservative 0; Mismatches 3; Indels
                            ce 1. .21
/organism='human ABCB4 gene'.
Location/Qualifiers
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strandedness: Single;
topology: Linear;
hypochetical: No;
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Sequence 690 from patent US 6727063.

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/db_xref="taxon:3264"

    .21
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JP 1997056380-A/2
04-MAR-1997
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Rosales, Rosaceae, Rosoideae, Rosa.
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Mammalia; Butheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 21)
Lander.E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
McCarthyJ.J.'
Single nucleotide polymorphisms in genes
Patent: US 6727063-A 690 27-APR-2004;
Location/Qualifiers
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Single nucleotide polymorphisms in genes
Patent: WO 0118250-A 690 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
Pharmaceuticals, Inc. (US)
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                                                                                                                                                                                                                       1.4%; Score 15.2; DB 1;
85.0%; Pred. No. 58;
rative 0; Mismatches 3;
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Sequence 690 from Patent WO0118250.
AX095512
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85.0%; Pred. No. 58;
ive 0; Mismatches
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AX956467
AX956467.1 GI:40784976
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/organism="Homo sapiens"
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                                                                                                                                                           /organism="unknown"
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PAT 08-AUG-2001

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Losses 1 to 20)
Bennett, C.Frank., Cooke, S.T., Mancharan, M., Wyatt, J.R., Baker, B.F.,
Monia, B.P., Freier, S.M., McKay, R. and Karras, J.G.
Alteration of cellular behavior by antisense modulation of mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (Dasses 1 to 20)
Marchetti,A., Buttitta,F., Smith,G.H. and Callahan,R.
Mucleotide and deduced amino acid sequences of tumor gene Int6
Patent: US 6255105-A 9 03-UUL-2001;
Location/Qualifiers
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1 BD176269 BD176269 WO 02072815-A/69.
8ynthetic construct other seminance.
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/organism="unknown"
/wol_type="unassigned DNA"
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Patent: US 6210892-A 16 03-APR-2001;
Location/Qualifiers
1. .20
/organism="unknown"
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                                                                                     AR144288 20 bp
Seguence 16 from patent US 6210892.
AR144288
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Sequence 9 from patent US 6255105.
AR160683 GI:16225137
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ACTICCTIACCTTICCTG 19
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88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
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BD176269
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AR144288
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Dean, N.M., Karras, J.G. and McKay, R.
Antisense modulation of interleukin-5 signal transduction
Patent: US 6136603-A 152 24-OCT-2000;
Location/Qualifiers
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Pred. No. 70;
0; Mismatches 2; Indels
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Human single nucleotide polymorphisms
Patent: WO 0138776-A 213 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
Location/Qualifiers
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1.4%; Score 15.2; DB 1;
Best Local Similarity 85.0%; Pred. No. 58;
Matches 17; Conservative 0; Mismatches 3;
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Sequence 152 from patent US 6136603.
AR136349.
AR136349.1 GI:14477021
                   of roses
Patent: WO 03097869-A 17 27-NOV-2003;
Con/Cipio GmbH (DE)
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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1.3%; Score 15; DB
Best Local Similarity 88.2%; Pred. No. 63;
Matches 15; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                     21 bp 1
Sequence 235 from Patent WO0138576.
AXIS4137

    .21
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                                                                                          /organism="Rosa sp."
/mol_type="unassigned DNA"
/db_xref="taxon:36598"
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Best Local Similarity 88.9%;
Matches 16; Conservative 0
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Homo sapiens
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PAT 18-MAR-2003

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1.3%; Score 14.8; D
88.9%; Pred. No. 70;
tive 0; Mismatches
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1.3%; Score 14.8; D
Best Local Similarity 88.9%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches
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Sequence 9 from patent US 6342392.
AR183974
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                                                                                                                                                                                                                                                                                   SUMIO SUGANO, TAKAMI KOMATSU
                                20 bp
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20-FEB-2001
06-AUG-1999 JP 1999223892
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                                                                     E43993.1 GI:18629196
JP 2001046072-A/7.
                                             ACE-analogous gene.
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Best Local Similarity 88.9
Matches 16; Conservative
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PC C12
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                                E43993
  RESULT 78
E43993/C
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Antisense modulation of interleukin-5 signal transduction.
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26-MAR-1999 US 09/280799
NICHOLAS M DEAN, JAMES G KRRAS, ROBERT MCKAY
C12N15/09,A61K31/711,A61K48/00,A61P11/06,A61P29/00,A61P35/00,
                                                                                                                                                           Key
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Soeda, B.
A method of arraying genome clone
Parent: Wo 02072815-A 69 19-SEP-2002;
BICHI SOEDA, TAKESHI KUKITA
OS Artificial Sequence
PN WO 02072815-A/69
PP 19-SEP-2002
PP 17-MAY-2001 WO 2001JP0004139
PR 12-MAR-2001 JP 01P 68285
PP CILCHI SOEDA
PP CILCHI SOEDA
PP CILCHI SOEDA
PR 12-MAR-2001 JP 01P 68285
PC CILCHI SOEDA
PC CLINI5/09,CI2Q1/68
CC Description of Artificial Sequence: Synthetic DNA FH
Location/Qualifiers
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Pred. No. 70;
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/organism="synthetic construct"
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1.3%; Score 14.8; D
Best Local Similarity 88.9%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches
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Best Local Similarity 88.9%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches
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JP 2002539846-A/152.
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A61K39/395,
PC A61K39/395,A61K48/00,A61P9/12,C07K14/47,C07K16/08,C12N1/15, PC
PAT 31-JAN-2002
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C12N15/09,A61K31/00,A61K31/7088,A61K38/00,A61K38/55,A61K39/395, PC
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: Ci2N1/21,C12N5/10,C12Q1/68,G01N33/53,C12N15/00,A61K37/02, PC
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Unknown.
Unclassified.
I (bases 1 to 20)
Marchetti,A., Buttitta,F., Smith,G.H. and Callahan,R.
Marchetti,A., Buttitta,F., Smith,G.H. and Callahan,R.
Nucleotide and deduced anino acid sequences of tumor gene Int6
Patent: US 6342392-A 9 29-JAN-2002;
Location/Qualifiers
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linear
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Location/Qualifiers
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                                                                                                                                    1 (bases 1 to 20)
Sugano, S. and Komatsu, T.
ACE-analogous gene
Patent: JP 2001046072-A 7 20-FEB-2001;
OTSUKA PHARMACEUT CO LTD
OS Unidentified
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20-NOV-2001
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synthetic construct
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Best Local Similarity 88.99
Matches 16; Conservative
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                                                                         PAT 08-OCT-2004

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/db_xref="taxon:32630"
/nofe="antisense ODN directed against alphaV integrin chain"

                                                                                                                                                          Unknown.
Unclassified.
Unclassified.
1 (bases it o 20)
Archetti,A., Buttitta,F., Smith,G.H. and Callahan,R.
Marchetti,A., Butditta,F., Smith,G.H. and Callahan,R.
Nucleotide and deduced amino acid sequences of tumor gene Int6
Nucleotide and deduced amino acid sequences of tumor gene Int6
Patent: US 6737251-A 9 18-MAY-2004;
Patent: US 6737251-A 9 18-MAY-2004;
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synthetic construct
other sequences; artificial sequences.
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synthetic construct
other sequences; artificial sequences.
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1. Similarity 88.9%; Pred. No. 70;
16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                             1.3%; Score 14.8; D:
88.9%; Pred. No. 70;
ative 0; Mismatches
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                                                                            AR540678 20 bp
Sequence 9 from patent US 6737251.
AR540678
AR540678.1 GI:53931994
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Sequence 2 from Patent BP1197553.
AX417273
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             20 CTAATTAAAATGCAGAA 3
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Best Local Similarity 88.9 Matches 16; Conservative
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Best Local Similarity
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AX467276/c
LOCUS
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KEYWORDS
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DEFINITION
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AX417273/c
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AR540678/c
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PAT 27-AUG-2002
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    .20
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    /mol type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Antisense ODN directed against alphaV integrin chain"

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Patent: UP 2001321190-A 2435 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
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88.9%; Pred. No. 70;
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Kronenwett,R., Graef,T., Haas,R. and Nedbal,W. Antisense nucleic acid against alphav integrin Patent: WO 0231142-A 2 18-APR-2002; A3D GmbH, Antisense Design & Drug Development (DE) Location/Qualifiers
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88.9%; Pred. No. 70;
Live 0; Mismatches 2;
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/organism="synthetic construct"
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/noTe="Synthetic"
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JP 2001321190-A/2435.
synthetic construct
synthetic construct
cheric construct
other sequences; artificial sequences.
1 (bases 1 to 20)
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Matches 16; Conservative
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TITLE
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AX539512
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7. 12-MAR-2001 JP 2001068285

1 EIICHI SOEDA

2 CI2N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566,

C12N15/00,

3 C12N15/00
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Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unknown.
Unclassified.
1 (bases 1 to 21)
Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
McCathyl,J.J.
Single nucleotide polymorphisms in genes
Patent: US 6727063-A 1733 27-APR-2004;
                                                                         Key
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Patent: WO 0118250-A 1733 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
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                                                                      Description of Artificial Sequence:Synthetic DNA Location/Qualifiers
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                                                                                                           /organism='Artificial Sequence'
Location/Qualifiers
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Pred. No. 70;
0; Mismatches 2;
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Location/Qualifiers
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AX096555/c
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Polymorphisms in the human gene for the multidrug resistance-associated protein 1 (mrp-1) and their use in diagnostic and therapeutic applications
Patent: WO 02059142-A 299 01-AUG-2002;
Epidauros Biotechnologie AG (DE)
Location/Qualifiers
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Polymorphisms in the human gene for the multidrug
resistance-associated protein 1 (mrp-1) and their use in diagnostic
and therapeutic applications
Patent: WO 02059142-A 300 01-AUG-2002;
Epidauros Biotechnologie AG (DE)
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PAT 04-APR-2003
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                                                                                                                        Brinkmann, U., Hoffmeyer, S. and Mornhinweg, E.
Polymorphisms in the human gene for the multidrug
resistance-associated protein 1 (mrp-1) and their use in diagnostic
and therapeutic applications
Patent: WO 02059142-A 30 01-AUG-2002;
Epidauros Biotechnologie AG (DE)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="synthetic construct"
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llarity 88.9%; Pred. No. 68;
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88.9%; Pred. No. 68;
tive 0; Mismatches
Sequence 303 from Patent WO02059142.
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Best Local Similarity 88.9
Matches 16; Conservative
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Polymorphisms in the human gene for the multidrug
resistance-associated protein 1 (mrp-1) and their use in diagnostic
and therapeutic applications
Patent: WO 02059142-A 301 01-AUG-2002;
Epidauros Biotechnologie AG (DE)
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/db_xref="taxon:32630"
/noTe="k=g or t"
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/mol_type="unassigned DNA"
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Patent: WO 02059142-A 302 01-AUG-2002;
Epidauros Biotechnologie AG (DE)
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Sequence 302 from Patent WO02059142.
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Best Local Similarity 88.9%;
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Heinrich, G. and Kerb, R.
Methods for the treatment of cancer with irinotecan based on CYP3A5
Patent: WO 03013534-A 293 20-FEB-2003;
Epidauros Biotechnologie AG (DE)
Location/Qualifiers
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Methods for the treatment of cancer with irinotecan based on CYP3A5
Patent: WO 03013534-A 294 20-FEB-2003;
Epidauros Biotechnologie AG (DE)
Location/Qualifiers
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Sequence 294 from Patent W003013534.
AX706597.1 GI:29563020
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

    .21
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/db_xref="taxon:9606"

    .21
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Homo sapiens
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Heinrich, G. and Kerb, R. Methods for the treatment of cancer with irinotecan based on CYP3A5 Patent: WO 03013534-A 296 20-FEB-2003; Epidauros Biotechnologie AG (DE)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 88.9%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 2;
  DB 1;
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Sequence 293 from Patent W003013536.
AX707526.1 GI:29563699
Score 14.8; D
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/db_xref="taxon:9606"

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Best Local Similarity 88.9
Matches 16; Conservative
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Query Match
Best Local Similarity 93.8
Matches 15; Conservative
Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 88.9%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 2; Indels
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1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 2; Indels
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Sequence 295 from Patent W003013536.
AXT07528
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BD198771 Incare tor treating diseases or conditions concerning molecule participating in vasculogenic response.
BD198771 GI:33008541
JP 2002509721-A/1797.
Homo sapiens (human)
Homo sapiens (human)
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Use of intermediate-conductance potassium channels and modulators
for the diagnosis and treatment of illnesses having disturbed
keratinocyte activity
Patent: WO 0205171-A 6 11-JUL-2002;
LUDWIG MAXIMILIANS UNI (DE)
LOCATION/Qualifiers
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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CQ617826.1
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AR458889/c
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PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
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                                                         Homo sapiens (human)
JP 2002509721-A/1797
02-ARR-2002
24-MAR-1999 JP 2000541291
27-MAR-1999 US 60/079678
PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT, JAMES A MCSWIGGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAT 02-FEB-2004
Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response Patent: JP 2002509721-A 1797 02-APR-2002; RIBOZYME PHARMACEUTICALS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                         OS Homo sapiens (human)
PN UP 2002509721-A/1797
PD 02-APR-1999 JP 2000541291
PR 24-MAR-1999 US 60/079678
PI PAMBELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHO PI JAMES A MCSWIGGEN
PC C12N15/09, AG1X31/7088, AG1X31/7125, AG1X48/00, AG1P3/10, AG1P17/06,
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Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 2565 06-DEC-2001;
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larity 93.8%; Pred. No. 88;
Conservative 0; Mismatches 1; Indels
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
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Shannon,M.E.
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Patent: WO 0195224-A 2566 06-DEC-2001;
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Sequence 2565 from patent US 6686188.
AR458888
AR458888.1 GI:42693945
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Sequence 2566 from patent US 6686188.
AR458889
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Pred. No. 88;
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93.8%; Pred. No. 88;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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GI:41668044
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AX726789.1 GI:30506132
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   959 TGGACCCAGGACATTT 974
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method and 10188124-A 2054 22-NOV-2001;
Patent: WO 0188124-A 2054 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Randi,A.M.
Method and reagent for the inhibition of erg
Patent: WO 0188124-A 324 22-NOV-2001;
RIBOZYME PHARMACHALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
RIBOZYME LOCALION/Qualifiers
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Randi,A.M.
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1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels
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Sequence 2054 from Patent WO0188124.
AX423718
JOURNAL Patent: US 6686188-A 2566 03-FEB-2004;
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/db_xref="taxon:9606"
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93.8%; Pred. No. 88;
ative 0; Mismatches
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/mol_type="unassigned RNA"
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/organism="unknown"
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KEYWORDS
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PAT 27-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
Nus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
Patent: WO 03025176-A 4476 27-WAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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          linear
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                                                                                                                                                                                                                                                                                                                                                  Patent: WO 03004526-A 2498 16-JAN-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
          17 bp DNA Sequence 2498 from Patent WO03004526.
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1.3%; Score 14.4; D:
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches
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/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
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/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
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2 GCTTGGTGATGTGCTT 17
    Homo sapiens
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                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                     Telerman, A., Amson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments Patent: WO 3032177-A 2567 27-MAR-2003; Molecular Engines Laboratories (FR)
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AX762887
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Molecular Engines Laboratories (FR)
Location/Qualifiers
                AX736977 17 bp DNA Sequence 2567 from Patent W003025177. AX736977
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                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                               AX736977.1 GI:30516265
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Best Local Similarity 93.8
Matches 15; Conservative
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AX132090/c
AX736977/c
                               DEFINITION
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AX762887/c
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A61K38/00,A61K31/711,A61K39/395,A61K39/395,A61K45/00,A61K48/00, PC
A61R35/00,
PC A61K37/02,C12N15/00,CC
CC PCR Primer Location/Qualifiers
FT Source 1. Ocganism='Artificial Sequence'.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                     Robbins, J.M. and Tritz, R. Ribozyme therapy for the treatment of proliferative skin and eye diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP 2002533402-A/5.
synthetic construct
synthetic construct
other sequences, artificial sequences.
1 (bases 1 to 20)
Keting, C., Xin, H., Chan, V.W.F., Kothakota, S., Williams, L.T. and
Winner, J.A.
Methods for treating cancer and for mediating chemotaxis of
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DUADOVES for treating cancer and for mediating chemotaxis of dendritic cells.
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                                                                                                                                                                                                                                                                                                                                                     Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_trype="unassigned DNA"
/wb_xref="taxon:9666"
/noce="cyclin Bl ribozyme binding site"
                                                                                                                                                                                                                                                                                                                                                Query Match 1.3%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 84;
Matches 15; Conservative 0; Mismatches 1;
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/organism="synthetic construct"
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Patent: JP 2002533402-A 5 08-OCT-2002;
CHIRON CORP
                                                                                                                                    Patent: WO 0130362-A 3308 03-MAY-2001;
IMMUSOL, INC. (US)
Location/Qualifiers
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JP 2002533402-A/5
08-OCT-2000
28-DEC-1999 US 60/114498
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BD185951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unclassfiled.
Unclassfiled.
1 (bases 1 to 20)
Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaram,B. and Fletcher,L.D.
Chlamydia pneumoniae polynucleotides and uses thereof
Patent: US 6559294-A 1803 06-MAY-2003;
Location/Qualifiers
                                      PAT 12-JUN-2003
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1 (Dassi to 20)
Bennett, C.F. and Watt, A.T.
Antisense inhibition of vascular endothelial growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                               Unclassified.

1 (bases 1 to 20)

Cohen, D., Chumakov, I. and Blumenfeld, M.

Biallelic markers for use in constructing a high density disequilibrium map of the human genome patent: 18 537751-A 6795 25-MAR-2003;

Location/Qualifiers
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                                                                                                                                                                                                                                                                 1.3%; Score 14.4; DB 1; Length 20; 93.8%; Pred. No. 82; ative 0; Mismatches 1; Indels
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93.8%; Pred. No. 82;
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                                    Sequence 6795 from patent US 6537751.
AR295060.1 GI:31682344
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US 6559294.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
                                                                                                                                                                                                                            /organism="unknown"
/wol_type="genomic DNA"
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/organism="unknown"
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AR311266
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Best Local Similarity 93.8
Matches 15; Conservative
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Best Local Similarity
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BD189521. BD18021. T., Makai, H., Yamamoto, J., Tomono, J., Kobayashi, E., Enoki, T., Asada, K. and Kato, I. Kobayashi, E., Enoki, T., Asada, K. and Kato, I. A stabilization method and a preservation method for a reagent for mucleic acid amplification or detection reaction mucleic acid amplification or detection reaction and patent: WO 02101042-A 147 19-DEC-2002; TAKRAR BIO INC, HIROAKI SAGAWA, TAKASHI UBMORI, HIROYUKI MUKAI, JUNKO ASADA, IKUNOSHIN KATO

NAMAMOTO, JUN TOMONO, EIJI KOBAYASHI, TATSUJI ENOKI, KIYOZO ASADA, IKUNOSHIN KATO PE 12-UNN-2002 WO 2002JP005832

PR 12-UNN-2002 WO 2002JP005832

PR 12-UNN-2001 JP 01P 1777737, 20-AUG-2001 JP 01P 249689 PI HIROAKI SAGAWA, TAKASHI UBMORI, HIROYUKI MUKAI, JUNKO YAWAMOTO, PI EIJI KOBAYASHI, TATSUJI ENOKI, KIYOZO ASADA, IKUNOSHIN KATO PC PU BIJI KOBAYASHI, TATSUJI ENOKI, KIYOZO ASADA, IKUNOSHIN KATO PC
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Patent: US 6767739-A 91 27-JUL-2004;
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93.8%; Pred. No. 82;
ative 0; Mismatches
receptor-1 expression
Patent: US 6710174-A 37 23-MAR-2004;
Location/Qualifiers
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Best Local Similarity 93.83
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GOIN33/566,C12N15/09,C12Q1/68,G01N21/78,G01N33/53,G01N33/536,
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               ಗ
           Designed oligonucleotide probe as Mycol70-probe to detect DNA fragment
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llarity 84.2%; Pred. No. 91;
Conservative 0; Mismatches 3;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Matches 16; Conservative 0; Mismatches
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Sequence 9 from Patent EP0574345.
A36286.1 GI:2293718
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C12N15/09,C12Q1/68
CC Designed oligon
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Paoletti.E., Perkus.M.E., Taylor,J., Tartaglia,J., Norton,E.K.,
Riviere,M., de Taiane,C., Limbach,K.J., Johnson,G.P., Pincus,S.E.,
Cox,M.I., Audonnet,J.-C.Prancis. and Gettig,R.Robert.
Modified recombinant vaccinia virus and expression vectors thereof
Patent: US 5762938-A 336 09-UUN-1998;
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1 (bases 1 to 20)

(Chao, Y.-C.

Hz-1 virus persistence-associated-gene 1 (PAGI) promoter uses therefor, and compositions containing same or products therefrom Patent: US 5911982-A 24 15-JUN-1999;
unidentified
unclassified.

E unclassified.

E 1 (bases 1 to 20)
S Bardosa,N.N., De,B.B., Borja,T.M., Pons,A.F. and Torres,P.V.
Procedure for the detection and identification of viral and subviral pathogens
L Patent: EP 0574345-A 9 15-DEC-1993;
INST NACIONAL DE INVESTIGACION (ES)
Other publication JP 6062900 940308
Other publication AV 4120093 931223
Other publication ES 2044784 940101.
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Pred. No. 89;
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AR011463.1 GI:3969453
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Sequence 24 from patent US 5911982.
AR071524
AR071524.1 GI:7222412
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84.2%; Pred. No. 89;
iive 0; Mismatches
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1 (bases 1 to 20)

Bennett, C. Frank., Ackermann, E.J. and Cowsert, L.M.
Antisense modulation of X-linked inhibitor of apoptosis expression Patent: US 6081173-A 12 11.JUL-2000;
Location/Qualifiers
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Bennett.(C.Frank. and Dean,N.
Antisense oligomucleotides against human protein kinase C
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84.2%; Pred. No. 89;
:ive 0; Mismatches
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                                                                                          Query Match
1.3%; Score 14.2; D
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches
                                      1. .20
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Sequence 86 from patent US 5959096.
AR076721
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Synthetic construct

Synthetic construct

other sequences; artificial sequences.

CE I (bases 1 to 20)

RS Yamaguchi, T. and Tajima, M.

RS Yamaguchi, T. and Tajima, M.

Cell cycle regulatory protein

AL Patent: JD 200210891-A 6 09-APR-2002;

NIPPON SHINYAKU CO LITD

OS Artificial Sequence

PN JP 2002101891-A/6

PD 09-APR-2002

PP 02-OCT-2000 JP 2000302674

PP 02-OCT-2000 JP 2000302674

PP 02-OCT-2000 PP 2000302674

PP 02-OCT-2000 PP 2000302674

PP 02-OCT-2000 PP 2000302674

PP 03-OCT-2000 PP 2000302674

PP 03-OCT-2000 PP 2000302674

PP 03-OCT-2000 PP 2000302674

PP 04-OCT-2000 PP 2000302674

PP 05-OCT-2000 PP 2000302674

PP 05-
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    .20
    /organism='Artificial Sequence'.

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Location/Qualifiers
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1.3%; Score 14.2; D
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches
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JP 2002253248-A/5.
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BD144123.1 GI:27849881
JP 2002101891-A/6.
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433 AAGAGGAGATGATTTTAGC 451
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synthetic construct
                                                                                    Best Local Similarity
Matches 16; Conserv
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                                                                       Query Match
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CQ764016
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Patent: WO 02072815-A 147 19-SEP-2002;
EIICHI SOEDA,TAKESHI KUKITA
OS Artificial Sequence
PN WO 02072815-A/147
PD 19-SEP-2002
PF 12-MAY-2001 WO 2001JP004139
PR 12-MAR-2001 JP 01P 68285
PI EIICHI SOEDA
PC C12N15/09,C12Q1/68
CC Description of Artificial Sequence: Synthetic DNA FH KA Location/Qualifiers
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1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels
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Antisense modulation of 1rh1 expression
Patent: Wo 2004003201-A 2516 08-JAN-2004;
Pharmacia Corporation (US)
1. .20
Location/Qualifiers
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    .20
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synthetic construct
other sequences; artificial sequences.
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synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 20)
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1.3%; Score 14.2; D
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches
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A method of arraying genome clone.
BD176347 GI:29122053
WO 02072815-A/147.
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BD176347/c
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Antisense modulation of 1rh1 expression
Parent: WO 2004003201-A 2634 08-JAN-2004;
Pharmacia Corporation (US)
Location/Qualifiers
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/db_xref="texon.32630"
/noTe="Human LRH1 antisense"
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1.3%; Score 14.2; D
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches
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Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches
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Pred. No. 89;
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1 Similarity 84.2%;
16; Conservative (
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PAT 20-APR-2002

ORGANISM REFERENCE AUTHORS

KEYWORDS

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FEATURES

DEFINITION ACCESSION VERSION

RESULT 132

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CQ764722

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1 (bases 1 to 20)
Bennett, C. Frank., Dean, N.M., Cook, P. Dan. and Hoke, G.
Antisense oligonuclectides which have phosphorothioate linkages of
high chiral purity and which modulate .beta.I, .beta.II, .gamma.,
delta., .EPSILON., .zeta. and .eta. isoforms of human protein
kinase C
Unclassified.

1 (bases 1 to 20)

Nuno Bardess Nolasco,G., De Blas Beorlegui,C., Borja Tome,M.Jose.,

Nuno Bardesso,F. and Torres Pascual,V.

Procedure for the detection and identification of viral and
subviral pathogens

Patent: US 5714312-A 9 03-FEB-1998;

Location/Qualifiers
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Baker, B.F. and Freier, S.M.
Antisense modulation of interleukin 12 p35 subunit expression
Patent: US 6399379-A 4 04-JUN-2002;
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1.3%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3;
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Location/Qualifiers
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Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches
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Sequence 86 from patent US 6339066.
AR182778
AR182778.1 GI:20225985
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AR212037
AR212037.1 GI:21515517

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    /organism="unknown"
    /mol_type="unassigned DNA"

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/organism="unknown"
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1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels
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Pred. No. 89;
0; Mismatches 3; Indels
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="texon:32630"
/noTe="Human LRH1 antisense"
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synthetic construct
other sequences; artificial sequences.
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Sequence 9 from patent US 5714312.
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183386.1 GI:3406916
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/organism="unknown"
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771 GAAACCTTTTGCTTGGGGA 789
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Freier,S.M. and Wyatt,J.
Antisense modulation of syntaxin 4 interacting protein expression
Patent: US 6503756-A 208 07-JAN-2003;
Location/Qualifiers
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(S Cohen,D., Chumakov,I. and Blumenfeld,M.

Biallelic markers for use in constructing a h
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Best Local Similarity 84.2%; Pred. No. 89;
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Sequence 208 from patent US 6503756.
AR272138
AR272138.1 GI:29703706
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Sequence 86 from patent US 6537973.
AR300858.
AR300858.1 GI:31688425
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/organism="unknown"
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Sequence 9409 from patent US
AR297674
AR297674.1 GI:31684958
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19 AGAACTCCAGAATGTGAAG 1
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                      822 GCCTCTCATGACCCAGGAA 840
                                    1 GCCACTCCAGACCCAGGAA 19
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16; Conservative
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Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,L.D.
Chlamydia pneumoniae polymucleotides and uses thereof
Patent: US 655224-A 2125 06-MAY-2003;
Location/Qualifiers
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Unclassified.

I (bases I to 20)
Griffals,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Pletcher,L.D.
Chlamydia pneumoniae polynucleotides and uses thereof Patent: US 6559294.A 4121 06-MAY-2003;
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Unclassified.

1 (bases 1 to 20)

Bennett, C.F., Dean, N.M., Holmlund, J.T. and Dorr, F.A. Oligonucleotide inhibition of protein kinase C
Patent: us 6537973-A 86 25-MAR-2003;
Location/Qualifiers
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84.2%; Pred. No. 89;
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Sequence 4121 from patent
AR313584
AR313584.1 GI:31707010
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AR311588
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Best Local Similarity 84.2<sup>1</sup>
Matches 16; Conservative
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Best Local Similarity 84.2<sup>†</sup>
Matches 16; Conservative
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Best Local Similarity 84.29
Matches 16; Conservative
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PAT 08-OCT-2004
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Griffais, R., Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D. Chlamydia pneumoniae polynucleotides and uses thereof Patent: US 6559294-A 6581 06-MAY-2003; Location/Qualifiers
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Unclassified.
Unclassified.
1 (Dases I vo. 20)
Sukumar.S., Byron,E., Dooley,W.C., Sacchi,N. and Davidson,N. Sukumar.S., Byron,E., Dooley,W.C., Sacchi,N. and Janancy Aberrantly methylated genes as markers of breast malignancy Patent: US 6756200-A 79 29-JUN-2004;
Location/Qualifiers
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Atkinson, R. M. and Tuomanen, E. I.
Diagnostic assay for antibiotic tolerance
Patent: US 6623931-A 12 23-SEE-2003;
Location/Qualifiers
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ilarity 84.2%; Pred. No. 89;
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Sequence 79 from patent US 6756200.
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Sequence 12 from patent US 6623931.
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Griffais, R., Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D.
Chlamydia pneumoniae polynucleotides and uses thereof Patent: US 655224-A 5159 06-MAY-2003;
Location/Qualifiers
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Sequence 5166 from patent US 6559294.
AR314629
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Sequence 5159 from patent US 6559294.
AR314622 AR314622.1 GI:31708048
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1.3%; Score 14.2; D.
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches
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RESULT 142 AR314622

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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Matches 16; Conservative 0; Mismatches 3; Indels
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Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3;
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Sequence 189 from Patent W002086113.
AX590749.1 GI:27949298
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Patent: WO 0121822-A 47 29-MAR-2001;
Plant Bioscience Limited (GB)
Location/Qualifiers

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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

                     20 bp
Sequence 47 from Patent WO0121822.
AX101073
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 56 from Patent WO0172822.
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                                                            AX101073.1 GI:13619929
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AX259829/c
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AX590749/c
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Oreochromis niloticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Labroidei; Cichlidae; Oreochromis.
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Patent: WO 02092851-A 237 21-NOV-2002;
ANIMAL HEALTH TRUST (GB); The British Horseracing Board (GB)
Location/Qualifiers
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                                   Cookson, W.O., Moffat, M.F., Allen, M. and Lench, N. Enzyme and snp marker for disease Patent: WO 02086113-A 189 31-OCT-2002; Isis Innovation Limited (GB)
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Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/hote="primer"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"
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other sequences; artificial sequences.
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Sequence 1061 from Patent WO03060160.
AX804893
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Sequence 237 from Patent WO02092851.
AX601142
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Pred. No. 89;
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BD016204/c
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Spring buoleous and process artificial sequences.

Synthetic construct synthetic construct other sequences; artificial sequences.

The sequences artificial sequence of protein kinase C-epsilon of patent. JP 2001224386-A 94 21-AUG-2001;

The sequence of artificial s
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hardge,T., Schellander,K. and Wimmers,K. Genetic markers for the diagnosis of the expression of inverted nipples in pets, breeding animals and domestic cattle patent: WO 03066891-A 144 14-AUG-2003; Poerdervorein Biotechnologieforschung der deutschen Schweineproduktion e.V. (DE)
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/organism="Oreochromis niloticus"
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/db_xref="taxon:8128"
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Sequence 144 from Patent WO03066891.
AX815889
AX815889.1 GI:39646569
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1.3%; Score 14.2; D
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches

    .20
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9823"

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Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches
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BD016085/c
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AX815889/c
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cother sequences; artificial sequences.

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B Ennett, F.C., Boggs, R.T. and Dean, N.M.
Coligonuclectide modulation of protein kinase C-zeta
Oligonuclectide modulation of protein kinase C-zeta

L Patent: JP 2001224387-A9 4 21-AUG-2001;
CONTINIONAL SOURCE SEA ALTIFICIALS INC
COS Artificial Sequence
N JP 2001224387-A9 94
DD 21-AUG-2001
PF 13-DEC-2000 JP 2000379249
PP 13-DEC-2000 JP 2000379249
PP 13-DEC-2000 JP 2000379249
PR 09-JUL-1993 US 08/08996,22-FEBB-1994 US 08/199779 PI
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Oligonucleotide modulation of protein kinase C-eta. BD017356
BD017356.1 GI:22558532
JP 2001231579-A/94.
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                                                              /organism='Artificial Sequence' Location/Qualifiers
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/organism="synthetic construct"
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/db_xref="taxon:32630"
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/organism="synthetic construct"
/mol type="genomic DNA"
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ilarity 84.2%; Pred. No. 89;
Conservative 0; Mismatches
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JP 2001224387-A/94.
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E 1 (bases 1 to 20)

Bennett,F.C., Boggs,R.T. and Dean,N.M.
Oligonucleotide modulation of protein kinase C-eta
Patent: JP 2001231579-A 94 28-AUG-2001;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2001231579-A/94

PD 28-AUG-2001
PP 13-DEC-2000 JP 2000379234

PP 13-DEC-2000 JP 2000379234

PRANK C BENNETT,RUSSELL T BOGGS,NICHOLAS M DEAN PC
C12N15/09/AG1X31/711,AG1X31/712,AG1X31/7125,AG1X48/00,AG1P29/ PC
OO.AG1P35/00,
PC AG1P43/00,CO7H21/00,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50, PC
G01N33/50,
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Patent: JP 2001321190-A 1511 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
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1 Similarity 84.2%; Pred. No. 89;
16; Conservative 0; Mismatches 3; Indels
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84.2%; Pred. No. 89;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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    forganism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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JP 2001321190-A/1511
20-NOV-2001
12-MAR-2001 JP 2001068285
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JP 2001321190-A/1511.
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12-WAR-2001 JP 2001068285
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C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
                                                                                                           PAT 27-AUG-2002
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Patent: WO 2004072293-A 43 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
Scientifique (CNRS) (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jockers, R., Couturier, C. and Uhlmann, E. Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the
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Patent: JP 2001321190-A 2513 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
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/organism='Artificial Sequence'.
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    .20
    /organism="synthetic construct"
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/db_xref="taxon:32630"

    .14
    forganism="synthetic construct"
|mol type="unassigned DNA"
|db_xref="taxon:32630"

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Sequence 43 from Patent WO2004072293.
CQ860131
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JP 2001321190-A/2513.
synthetic construct
synthetic construct
other sequences; artificial sequences.

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JP 2001321190-A/2513
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/organism="Homo sapiens"
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BD208420-1-A/2039.

SB blatt, ... Mcwaiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
SB blatt, ... Mcwaiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
SB blatt, ... Mcwaiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
SB blatt, ... Mcwaiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
SB blatt, ... Mcwaiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
SB blatt, ... Mcwaiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
SB blatt, ... Mcwaiggen, J.A., Roberts, P.A. and Macejak, D.
SE bacent: JP 2002512791-A/2039
SB HEDATH, SOUGS12791-A/2039
SP JOSONAY-2002
SP Z6-APR-1999 US 60/083217, 18-SEP-1999 US 60/100842 PR 25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/257608, 23-MAR-1999 US 09/257608, 23-MAR-1999 US DAVCO, PAVCO, P
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/organism='Hepatitis virus (hepatitis C FT

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1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
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Sequence 460 from patent US 5616488.
139422
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       /note="Artificiel"
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1 (bases 1 to 15)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
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Telerman, A., Amson, R. and Tuijnder, M.

Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines

Patent: WO 03025175-A 5418 27-MAR-2003;

Molecular Engines Laboratories (FR)

Location/Qualifiers
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Sullivan, S., Draper, K.G., McSwiggen, J. and Stinchcomb, D.T. IL-5 targeted ribozymes Patent: US 5616488-A 460 01-APR-1997; Location/Qualifiers
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                                                                                                                                                                                          1.3%; Score 14; DB 1; Length 15; 100.0%; Pred. No. 1.1e+02; ative 0; Mismatches 0; Indels
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RIBOZYME PHARMACEUTICALS, INC. (US)
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Sequence 2866 from Patent EP1260586.
AX635727
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Homo sapiens
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Best Local Similarity 100.0
Matches 14; Conservative
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Unclassified.

E 1 (bases 1 to 20)

KS Cohen,D., Chumakov,I. and Blumenfeld,M.

Biallelic markers for use in constructing a high density disequilibrium map of the human genome

AL Patent: US 6537751-A 4185 25-MAR-2003;

Location/Qualifiers
                                                                                                                                                                                                                                                               1 (bases 1 to 18)
Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density disequilibrium map of the human genome Patent: US 6537751-A 5553 25-MAR-2003;
Location/Qualifiers
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1e+02;
hes 0; Indels
                                   Query Match 1.3%; Score 14; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 14; Conservative 0; Mismatches 0; Indels
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Sequence 5553 from patent US 6537751.
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1.3%; Score 14; DB
Best Local Similarity 100.0%; Pred. No. 96;
Matches 14; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                         1. .18
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AR292450/c
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                                                                                                                      1 (bases 1 to 20)
Cohen, D., Chumakov I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
Patent: US 6537751-A 5624 25-MAR-2003;
Location/Qualifiers
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Dean,N.M., Marcusson,E.G. and Wyatt,J.
Antisense modulation of Fas mediated signaling
Patent: US 6653133-A 156 25-NOV-2003;
Location/Qualifiers
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Cowsert, L. M. and Dobie, K. W.
Antisense modulation of PTPN12 expression
Patent: US 6743909-A 55 01-JUN-2004;
Location/Qualifiers
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96;
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Sequence 5624 from patent US 6537751.
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AR432356
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1.3%; Score 14; DB
Best Local Similarity 100.0%; Pred. No. 96;
Matches 14; Conservative 0; Mismatches
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Sequence 55 from patent US 6743909.
ARS42543
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AR293889.1 GI:31681173
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PAT 01-SEP-2000
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                 PAT 16-JUL-2002
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Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hardge,T., Schellander,K. and Wimmers,K. Genetic markers for the diagnosis of the expression of inverted nipples in pets, breeding animals and domestic cattle patent: WO 03066891-A 82 14-AUG-2003; Foerderverein Biotechnologieforschung der deutschen Schweinsproduktion e.V. (DE)
                                                                                                                                                                                                                1. .20 /vorganism="synthetic construct" /nol type="unassigned DNA" /db xref="taxon:32630" /nofe="Antisense ODN directed against alphaV integrin chain"
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                                                                                                                                                    Kronenwett,R., Graef,T., Haas,R. and Nedbal,W.
Antisense nucleic acid against alphav integrin
Patent: WO 0231142-A 11 18-APR-2002;
A3D GmbH, Antisense Design & Drug Development (DE)
Location/Qualifiers
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1.3%; Score 14; DB 1;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 14; Conservative 0; Mismatches (
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Sequence 64 from patent US 5976798.
AR083038

    .20
    /organism="Sus scrofa"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9823"

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Sequence 82 from Patent WO03066891.
AX815827
                 20 bp
Sequence 11 from Patent WO0231142.
AX467285
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                                                                      AX467285.1 GI:21900563
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synthetic construct
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Sus scrofa
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/mol_type="unassigned DNA"
/db_xref="leaxon:32630"
/note="Antisense ODN directed against alphaV integrin
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.ive 0; Mismatches 0; Indels
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Sequence 7 from Patent WO0231142.
AX467281
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Sequence 7 from Patent EP1197553.
AX417278
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AX467281/c
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AX417278/c
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Unclassified.

I (bases 1 to 17)
Parker, W. Davis., Herrnstadt, C., Ghosh, S. and Fahy, B.D.
Parker, W. Davis., Herrnstadt and tochondrial mutations diagnostic for Methods for detecting mitochondrial methods for determining heteroplasmy of mitochondrial nucleic acid
Patent: US 5976798-A 64 02-NOV-1999;
Location/Qualifiers
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Herrnstadt, C. and Parker, W. Davis.
Method of targeting conjugate molecules to mitochondria
Patent: US 6171859-A 140 09-JAN-2001;
Location/Qualifiers
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Herrnstadt, C. and Parker, W. Davis.
Method of targeting conjugate molecules to mitochondria
Patent: US 6171859-A 151 09-JAN-2001;
Location/Qualifiers
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Sequence 140 from patent US 6171859.
AR124365
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    .17
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/wol_type="unassigned DNA"
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AR124365/c
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AR124376/c
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Herrnstadt, C. and Parker, W. Davis.
Method of targeting conjugate molecules to mitochondria
Patent: US 6171859-A 185 09-JAN-2001;
Location/Qualifiers
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Hermstadt,C. and Parker,W.Davis.
Method of tergeting conjugate molecules to mitochondria
Patent: US 6171859-A 186 09-JAN-2001;
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Sequence 186 from patent US 6171859.
AR124411.
AR124411.1 GI:14109772
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Sequence 188 from patent US 6171859.
AR124413
AR124413.1 GI:14109774
                                                                                     Sequence 185 from patent US 6171859.
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/organism="unknown"
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/mol_type="unassigned DNA"
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Herrnstadt, C. and Parker, W.Davis.
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562 TGGGTTTTTAATACCT 578
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AR124410/c
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AR124411/c
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AR124413/c
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BD198972
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BD1989721-A/1998.
Homo sapiens (human)
Hom sapiens (human)

Hom sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Rethod and reagent for treating diseases or conditions concerning

Method and reagent for treating diseases or conditions concerning

Method and reagent for treating 102-APR-2002;

REDOZYME PHARNACEVITCALS INC

REDOZYME PHARNACEVITCALS INC

OS Homo sapiens (human)

PN JP 2002509721-A/1998

PD 02-APR-2002

PF 24-MAR-1999 UP 200541291

PR 27-MAR-1999 UP 200541291
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Regulation of repressor genes using nucleic acid molecules.
BD256418
BD256418.1 GI:33066188
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PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00,
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Method of targeting conjugate molecules to mitochondria Patent: US 6171859-A 188 09-JAN-2001; Location/Qualifiers
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Location/Qualifiers
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llarity 88.2%; Pred. No. 1.1e+02;
Conservative 0; Mismatches 2; Indels
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participating in vasculogenic response
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                                                                                                                                              1.2%; Score 13.8; DB 1; 88.2%; Pred. No. 1.1e+02; iive 0; Mismatches 2;
                                                                      1. .17
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Best Local Similarity 88.2'
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(C12P21/02,C12R1:91), (C12P21/02,C12R1:91),C12N15/00,C12N5/00,A61K37/02,(C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C1
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Regulation of repressor genes using nucleic acid molecules.
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AGIN37/02,
(C12NS/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH
Location/Qualifiers
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PN JP 2002541795-A/4659
PD 10-DEC-2002
PP 11-APR-2000 JP 2000611654
PF 12-APR-1999 US 60/129390
PI LAMRENCE BLATT,MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN F CLAN15/09, A61K38/00, A61K48/00, A61P43/00, C12N5/10, PC C12P21/02,
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PN JP 2002541795-A/4211
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PT LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PT LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PT C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC C12P21/02,
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Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Bregulation of repressor genes using nucleic acid molecules Patent: JP 2002541795-A 4659 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
unidentified
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unclassified.
1 (bases 1 to 17)
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 4211 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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88.2%; Pred. No. 1.1e+02;
tive 0; Mismatches 2;
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BD256866.1 GI:33066636
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TITLE JOURNAL

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ACCESSION VERSION KEYWORDS SOURCE

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PAT 06-FEB-1997
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                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Shannon,M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 17)
Parker, W.Davis. and Herrnstadt, C.
Cytochrome oxidase mutations aiding diagnosis of sporadic
alzheimer's disease
Patent: US 556322-A 12 15-OCT-1996;
Location/Qualifiers
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Aeomica, Inc. (US)
Location/Qualifiers
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88.2%; Pred. No. 1.1e+02;
tive 0; Mismatches 2; Indels
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LOCUS AR458886 17 bp DNA
DEFINITION Sequence 2563 from patent US 6686188.
                                                                                                                                                                                            DNA
                                                                                                                                                                                        CQ622009 17 bp DN
Seguence 6749 from Patent WO0192524.
CQ622009

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127376
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/mol_type="unassigned DNA"
                                                        744 GGCAGCTGCCACCTTAT 760
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Homo sapiens
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Best Local Similarity 88.2
Matches 15, Conservative
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Myosin-like gene expressed in human heart and muscle
Patent: WO 019254-A 2563 06-DEC-2001;
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Shannon,M.E.
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Patent: WO 0192524 A 2564 06-DEC-2001;
Aeomica, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tch 17; Score 13.8; DB 1; Length 17; al Similarity 88.2%; Pred. No. 1.1e+02; 15; Conservative 0; Mismatches 2; Indels
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                  /organism='Eukaryote'.
Location/Qualifiers
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Pred. No. 1.1e+02;
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                                                                      /organism="unidentified"
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Location/Qualifiers
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CQ617824.1 GI:41668042
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RESULT 182 CQ617824/c

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Indels

Length 17;

PAT 07-SEP-2001

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Hugot, J.P., Thomas, G., Zouali, M., Lesage, S. and Chamaillard, M. eners involved in intestinal inflammatory diseases and use thereof Patent: WO 0172822-A 64 04-0CT-2001; Pondation Jean Dausset-Ceph (FR)
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 2567 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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1.2%; Score 13.8; DB 1;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2;
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/noTe="Nucleic Acid"
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    17 '17 'organism="Homo sapiens" 'mol_type="unassigned DNA" 'db_xref="taxon:9606"

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Sequence 2567 from Patent WO0159103.
AX217125
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Sequence 64 from Patent WO0172822.
AX259837
                            /mol_type="genomic DNA"
1. .17
/organism="unknown"
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2 (Ly., Ji.Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Gu,Y., Ji.Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. E Shannon,M.E.
Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle Patent: 105 (686188-A 6749 03-FEB-2004;
Location/Qualifiers
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
Patent: US 6686188-A 2564 03-FEB-2004;
                                                                             Unknown.
Unknown.
Unknown.
Unclassified.
Unclassified.
Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Shannon,M.E.
Shannon,M.E.
Polymuclectide encoding a human myosin-like polypeptide expressed prodominantly in heart and muscle predominantly in heart and muscle Patent: US 6666188-A 2563 03-FEB-2004;
Location/Qualifiers
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Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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1.2%; Score 13.8; DB 1; Length 17;
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6686188.
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/organism="unknown"
/mol_type="genomic DNA"
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/organism="unknown"
/wol_type="genomic DNA"
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RESULT 190 AX273034 DEFINITION ACCESSION VERSION KEYWORDS

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C1201/68,C07H21/04
Strandedness: Double;
Topology: Linear;
Methods for dejecting mitochondrial mutations diagnostic for
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WILLIAM DAVIS PARKER, CORINNA HERRNSTADT, SOUMITRA GHOSH, EOIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Luciosu, linear PAT 27-Al Methods for detecting mitochondrial mutations dispnostic for Alzheimer's disease and methods for determining heteroplasmy mitochondrial nucleic acid.
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Parker,W.D., Herrnstadt,C., Ghosh,S. and Fahy,E.D.
Methods for detecting mitochondrial mutations diagnostic for Alzhaimer's disease and methods for determining heteroplasmy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease and methods for determining heteroplasmy of mitochondrial nucleic
                                                                                                                                                                                                                                                                                                               1.2%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 1.18+02; ive 0; Mismatches 2; Indel8
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/organism='Unidentified'
                                                                                                                                                 Human testis expressed patched like protein
Patent: EP 1229046-A 4243 07-AUG-2002;
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Patent: JP 2001514500-A 64 11-SEP-2001;
                                                                                                                                                                                                                                            /organism="Homo sapiens"
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/db_xref="taxon:9606"

    .17
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/db_xref="taxon:32644"

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JP 2001514500-A/64
11-SEP-2001
27-FEB-1998 JP 1998537738
28-FEB-1997 US 08/81059
                                                                                                                                                                                     Aeomica, Inc. (US)
Location/Qualifiers
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BD070507.1 GI:22616110
     AX502936.1 GI:23385229
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                                      Homo sapiens (human)
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Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
                                                          Homo sapiens
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                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Rendi, A.M.
Method and reagent for the inhibition of erg
Patent: WO 0188124-A 2055 22-NOV-2001;
RIBOZYME PHARMACHICALS, INC. (US); GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Ellis, J.H.
Method and reagent for the inhibition of grid
Patent: WO 0162911-A 603 30-AUG-2001;
PRIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED
Location/Qualifiers
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88.2%; Pred. No. 1.1e+02;
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88.2%; Pred. No. 1.1e+02;
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AX502936

    17 .17
    /organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

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/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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                                                                                                        17 bp 1
Sequence 603 from Patent WO0162911.
AX273034
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1 GCCATCTCCCCAAGCCC 17
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Homo sapiens
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Best Local Similarity 88.2
Matches 15; Conservative
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Matches 15; Conservative
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KEYWORDS SOURCE ORGANISM

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/organism="synthetic construct"
/orl_type="unassigned DNA"
/db xref="taxon:32630"
/note="Detection oligonucleotide
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88.2%; Pred. No. 1.1e+02;
iive 0; Mismatches 2;
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88.2%; Pred. No. 1.1e+02;
rative 0; Mismatches 2;
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Patent: Wo 2004035803-A 1135 29-APR-2004;
Epigenomics AG (DE)
Location/Qualifiers
5;
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CQ807685
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                                                                                                                                                                                 Sequence 499 from Patent WO2004031413.
CQ799849.1 GI:46848796
                                                                                                                                                                                                                                                                                                                                           other sequences; artificial sequences.
Mismatches
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                                           566 TTTTTTAATACCTTTAT 582
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Matches 15; Conservative
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CQ807685
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AUTHORS
TITLE
JOURNAL
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(c) Lasting High type
(c) Lasting High type
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Pred. No. 1.1e+02;
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88.2%; Pred. No. 1.1e+02;
tive 0; Mismatches 2;

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    ^17
    ^2rganism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

                                                                                                                                                            17 bp DNA
Kit and method for determining HLA type.
BD104790
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/organism="unknown"
/mol_type="unassigned DNA"
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WO 0192572-A/894.
                      562 TGGGTTTTTAATACCT 578
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Best Local Similarity 88.2
Matches 15; Conservative
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Unclassified.
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Best Local Similarity
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ACCESSION
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ORGANISM
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AR071523/c
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ACCESSION
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/mol_type="unassigned DNA"
/db xref="taxon:32630"
/note="Artificially synthesized S-oligonucleotide sequence for antisense method"
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Method and nucleic acids for the improved treatment of breast cell
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PAT 28-APR-2004
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Method for diagnosing non-small cell lung cancers
Patent: WO 2004031413-A 499 IS-APR-2004;
Oncotherapy Science, Inc. (UP); Japan as represented by the
president of the university of Tokyo (JP)
Location/Qualifiers
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Patent: US 6537751-A 6041 25-MAR-2003;
Location/Qualifiers
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Matches 15; Conservative
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Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserv
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Unclassified.

E 1 (bases 1 to 18)

AS Parker, W. Davis. and Herrnstadt, C.
Cytochrome oxidase mutations aiding diagnosis of sporadic
alzheimer's disease
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alzheimer's disease
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1 (bases 1 to 18)

2 (oben,D., Chumakov,I. and Blumenfeld,M.
Biallelic markers for use in constructing a high density disequilibrium map of the human genome
Patent: US 6537751-A 4732 25-MAR-2003;
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Unclassified.
1 (bases 1 to 18)
Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density disequilibrium map of the human genome
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1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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1.2%; Score 13.8; DB 1;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2;
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AR292997
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6537751.
                                              18 bp Sequence 23 from patent US 5565323.
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Sequence 6041 from patent US
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127387.1 GI:1818163
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AR294306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 18)
Cohen,D., Chumakov,I. and Blumenfeld,M.
Biallelic markers for use in constructing a high density disequilbrium map of the human genome Patent: US 6537751-A 11352 25-MAR-2003;
Location/Qualifiers
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/noTe="Primer C375"
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Sequence 11352 from patent US 6537751.
AR299617.1 GI:31686901
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synthetic construct
other sequences; artificial sequences.
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Sequence 6 from Patent W00146696.

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AX181724.1 GI:15133047
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Method and nucleic acids for the analysis of colon cancer
Patent: WO 03014388-A 277 20-FEB-2003;
Epigenomics AG (DE)
Location/Qualifiers
                                                                                                                                                                                              Distler,J., Model,F. and Taubert,H.
Method and nucleic acids for the analysis of colon cancer
Patent: WO 03014388-A 275 20-FEB-2003;
Epigenomics AG (DE)
Location/Qualifiers
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/noTe="Detection oligonucleotide for PGR"
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/db_xref="taxon:32630"
/noTe="Detection oligonucleotide for PGR"
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synthetic construct
other sequences; artificial sequences.
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Sequence 277 from Patent W003014388.
AX705608.1 GI:29562273
                                                                            AX705606 18 bp DN
Sequence 275 from Patent W003014388.
AX705606.1 GI:29562271
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//organism="unidentified"
//mol_type="unassigned DNA"
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Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and Masuho,Y.
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/organism='Artificial Sequence'.
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                                                                                                                                                                                                                1.2%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 1.1e+02; arive 0; Mismatches 2; Indels
                                                              Full-length cDNA sequences Full-length cDNA sequences Farent: BP 13470464.8 5064 24-SEP-2003; Research Association for Biotechnology (JP) Location/Qualifiers
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TGAACATCACGCCCAAC 18
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AX348064.1 GI:18614174
   synthetic construct
synthetic construct
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PC C12N15/55
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BD012154
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CC PCR
FH Key
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ribozyme therapy for the treatment of proliferative skin and diseases
Patent: WO 0130362-A 649 03-MAY-2001;
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Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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IMMUSOL, INC. (US)
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                              AX129431
Sequence 649 from Patent WO0130362.
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Sequence 354 from Patent W00136625.
AX149152. GI:14347676
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Rolyma,N., Okui,T., Takakura,H., Asada,K. and Kato,I.
Polypebtide
L Patent: WO 0109348-A 7 08-FEB-2001;
TAKARA SHUZO CO LID,NOBUTO KOYAMA,TOSHITAKE OKUI,HIKARU TAKAKURA,
KIYOZO ASADA,TKUNOSHIN KATO
OS Artificial Sequence
NN WO 0109348-A/7
PD 08-FEB-2001
PF 26-JUL-2000 WO 2000JP004956
PR 02-AUL-1099 JP 99P 218778
PI NOBUTO KOYAMA,TOSHITAKE OKUI,HIKARU TAKAKURA,KIYOZO ASADA, PI
                                            Wright, J.A., Young, A.H. and Dugourd, D.
Antisense oligonucleotide sequences derived from groel and groes as inhibitors of microorganisms
Patent: WO 0136625-A 354 25-MAY-2001;
GeneSense Technologies Inc. (CA)
Location/Qualifiers
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1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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    .19
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other sequences; artificial sequences
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448 TAGCTGGCAGCAGTG 462
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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A method for direct genetic analysis of target cells by using flourescence probes
Patent: WO 0206524-A 3 24-JAN-2002;
Praenadia GmbH (DE)
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Wiebusch, H., Schmitt-John, T. and Weidner, J.
Wiebusch, H., Schmitt-John, T. and Weidner, J.
Method for direct genetic analysis of target cells by using fluorescence probes
Patent: EP 117248-2 16-JAN-2002;
Praenadia GmbH (DE)
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1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 93.3%; Pred. No. 1.40+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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Sequence 354 from patent US 5599706.
135386
135386.1 GI:2088354
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synthetic construct
other sequences; artificial sequences.

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Sequence 3 from Patent WO0206524.
AX540329
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JP 2002514431-A/20.

unidentified

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unclassified.

Losses 1 to 17)

Gorochov, G., Piquexas, B., Doussal, J.M.L. and Debre, P.

Gorochov, G., Piquexas, B., Doussal, J.M.L. and Debre, P.

Gorochov, G., Piquexas, B., Doussal, J.M.L. and Debre, P.

Gorochov, G., Piquexas, B., Doussal, J.M.L. and Debre, P.

Gorochov, G., Piquexas, B., Doussal, J.M.L. and Debre, P.

Gorochov, G., Piquexas, B., Doussal, J.M.L. and Debre, P.

Gorochov, G., Piquexas, B., Doussal, J.M.L. and Debre, P.

Gorochov, G., Piquexas, B., Doussal, J.M.L. and Debre, P.

Gorochov, G., Piquexas, J. and D
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Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T. C-myb ribozymes having 2'-5'-linked adenylate residues Patent: US 5817796-A 1915 06-OCT-1998;
Location/Qualifiers
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1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.38+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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misc_feature (1) . .(17).
Location/Qualifiers
1. .17
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Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1;
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1. .16
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C12R1:91)
C (C12P21/02,C12R1:91), (C12P21/02,C12R1:91),C12N15/00, PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH Key Location/Qualifiers
FT source Location/Qualifiers
FT /Organism='Eukaryote'.
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PN JP 2002541795-A/2413
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHARL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN 12-D215/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC PC C12P21/02,
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BD254795-A/2413.
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
                                                                                                             Score 13.4; DB 1;
Pred. No. 1.3e+02;
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1.2%; Score 13.4; D
Best Local Similarity 93.3%; Pred. No. 1.3e
Matches 14; Conservative 0; Mismatches
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17 bp DNA linear PAT 17-JUL-2003
BD256555
BD256555,1 GI:33066325
JP 2002541795-A/4348.
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(C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH
Location/Qualifiers
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A61K37/02,
(C12N5/00,C12R1:91)
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PN JP 2002541795-A/4348
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PF 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N15/09, A61X38/00, A61X48/00, A61P43/00, A61P43/00, C12N5/10, PC C12P21/02,
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Regulation of repressor genes using nucleic acid molecules Patent: JP 2002541795-A 4210 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC OS BUKARYOTE
PN JP 2002541795-A/4210
PD 10-DEC-2002
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Batt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Begulation of represent genes using nucleic acid molecules
Patent: 17 2002541795-A 4348 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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Location/Qualifiers
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Regulation of repressor genes using nucleic acid molecules.
BD257003
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מארבות מאוחם מאוחם האוחם ה
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(C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    unclassified.

unclassified.

1 (bases 1 to 17)

S Blatt, L., Zwick,M., Pavco,P. and Mcswiggen,J.

S Blatt, L., Zwick,M., Pavco,P. and Mcswiggen,J.

Regulation of repressor genes using nucleic acid molecules

Regulation of repressor genes using nucleic acid molecules

RIBOZYME PHARMACEUTICALS INC

OS EURATYOTE

PD 10-DEC-2002

PF 11-APR-2000 JP 2000611654

PR 11-APR-1999 US 60/129390

PI LAWRENCE BLATT,MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC

CINIS,O9,A61K38/00,A61K48/00,A61P43/00,CL2N5/10, PC
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C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
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1 (bases 1 to 17)

1 bases 1 to 17)

2 Zwick,M., Pavco,P. and Mcswiggen,J.

Regulation of repressor genes using nucleic acid molecules

Patent: JP 2002541795-A 4796 10-DEC-2002;
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1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
                                         / Match 1.2%; Score 13.4; DB 1; Length 17; Local Similarity 93.3%; Pred. No. 1.3e+02; les 14; Conservative 0; Mismatches 1; Indels
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Location/Qualifiers

    .17
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

             /db_xref="taxon:32644"
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PC A61K37/
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CC Regulat
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KEYWORDS
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AUTHORS
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PN JP 2002541795-A/4796

PN JP 2002541795-A/4796

PD 10-DEC-2002

PF 11-APR-2000 JP 2000611654

PR 12-APR-1999 US 60/1239390

PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N15/09, A61K38/00, A61R43/00, A61P43/00, C12N5/10, PC C12P21/02, C12P21/02, A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC C12R1:91), (C12P21/02, PC C12R1:91), (C12R1:91), (C12R1
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(C12NS/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Myosin-like gene expressed in human heart and muscle Patent: WO 0192524-A 2567 06-DEC-2001;
Aeomica, Inc. (US)
Location/Qualifiers
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Sequence 6287 from Patent WO0192524.
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/mol_type="unassigned DNA"
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/organism="unidentified"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
                                                                           Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
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                                                                                      Shannon,M.E.
Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 6287 06-DEC-2001;
Aeomica, Inc. (US)
Location/Quallfiers
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Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 6289 06-DEC-2001;
                                                                                                                                                                                                                                            Query Match
1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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Patent: WO 0192524-A 6288 06-DEC-2001;
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Sequence 6289 from Patent WO0192524.

    1.17
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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CQ621549.1 GI:41671767
Homo sapiens (human)
Homo sapiens
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Homo sapiens
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Bscobedo, J.
Pavco, P., McSwiggent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 4443 20-MAY-2003;
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Unclassified.
1 (bases 1 to 17)
Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T. C-myb targeted ribozymes
Patent: US 5646042-A 1915 08-JUL-1997;
Location/Qualifiers
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                                                                                                                             Length 17;
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93.3%; Pred. No. 1.3e+02;
tive 0; Mismatches 1;
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llarity 93.3%; Pred. No. 1.3e+02;
Conservative 0; Mismatches 1;
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Inc. (US)
Location/Qualifiers
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Polymucioned encoding a human myosin-like polypeptide expressed predominantly in heart and muscle Patent: US 6686188-A 6289 03-FEB-2004; Location/Qualifiers
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Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
patent: WO 0159103-A 818 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle Patent: US 6686188-A 6288 03-FEB-2004; Location/Qualifiers
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Unclassified.
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1 (bass 1 to 17)
6u, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
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/mol type="unassigned RNA"

/db xref="taxon:32630"

/noTe="Nucleic Acid"
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synthetic construct
other sequences, artificial sequences.
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Sequence 6289 from patent US 6686188.
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AR462612.1 GI:42697669
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Sequence 818 from Patent WO0159103.
AX215376
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Unclassified.
1 (bases 1 to 17)
GL,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
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                                                                                                                                                     Unknown.
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QL,Y., Ji.Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
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US 6686188.
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                                                   AR458890 17 bp DNA
Sequence 2567 from patent US 6686188.
AR458890 GI:42693947
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Sequence 6288 from patent
AR462611
AR462611.1 GI:42697668
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PAT 20-FEB-2004

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PAT 07-SEP-2001

PAT 18-JUN-2002

Matches

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REFERENCE AUTHORS TITLE

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FEATURES

RESULT 232

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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                                                                                                                               Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Mclaughlin, F.G. and Randi, A.M.
Rethod and reagent for the inhibition of erg
Patent: WO 0188124-A 1047 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.2%; Score 13.4; DB 1; Length 17; Best Local Similarity 93.3%; Pred. No. 1.3e+02; Matches 14; Conservative 0; Mismatches 1; Indels
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Pred. No. 1.3e+02;
0; Mismatches 1;
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EP1229046.
                                   AX422711 17 bp RNA
Sequence 1047 from Patent WO0188124.
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Sequence 4244 from Patent EP1229046.
AX502937
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                                                                                       AX422711.1 GI:21526093
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Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 819 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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Patent: WO 0159103-A 2566 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US)
McSwiggen, James (US); Chowrira, Bharat M. (US)
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Sequence 2566 from Patent WO0159103.
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Best Local Similarity 93.3
Matches 14; Conservative
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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                                                    Zhan,J.
Human testis expressed patched like protein
Human testis expressed patched like protein
Patcht: EP 1229046-A 4245 07-AUG-2002;
Pacmica, Inc. (US)
Location/Qualifiers
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Patent: WO 03004526-A 3085 16-JAN-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 3085 from Patent WO03004526.
AX674640
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Aeomica, Inc. (US)
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Matches 14; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 93.3%; Pred. No. 1.38+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No. 1.3e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                   Parent: WO 03025175-A 1463 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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WO03025177.
  Sequence 1463 from Patent WO03025175
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Seguence 2012 from Patent
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Matches 14; Conservative
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Patent: WO 03025176-A 5707 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 1496 from Patent WO03025176.
AX723809
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    17 .17 /organism="Mus musculus" /mol_type="unassigned DNA" /db_xref="taxon:10090"

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Mus musculus
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AX728020.1 GI:30507363
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CCCAGAGACCAAGAG 15
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo sapiens
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Matches 14; Conservative
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AX754466/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicamente Patent: WO 3025177-A 4165 27-MAR-2003; Molecular Enginee Laboratories (FR)
Location/Qualifiers
                                    Telerman, A., Amson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicamente patent: WO 03025177-A 2012 27-WAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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         Aammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 03037931-A 812 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
Location/Qualifiers
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Sequence 4165 from Patent WO03025177.
AX738575
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Sequence 812 from Patent WO03037931.
AX754465
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Homo sapiens
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AX754465/c
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 93.3%; Pred. No. 1.38+02;
Matches 14; Conservative 0; Mismatches 1; Indels
Length 17;
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Human angiomotin-like protein 1

Patent: WO 03037931-A 814 08-MAY-2003;

Amersham Blosciences SV Corp. (US)

Location/Qualifiers
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Human angiomotin-like protein 1
Patent: WO 03037931-A 813 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
Location/Qualifiers
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/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
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PAT 17-0CT-2001

SOURCE ORGANISM

AUTHORS TITLE

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AX759999/c DEFINITION ACCESSION VERSION KEYWORDS

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FEATURES

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Unclassified.

1 (bases 1 to 18)

Keating,M.T., Sanguinetti,M.C. and Splawski,I.

Mutations in the KCNEI gene encoding human minK which cause
arrhythmia susceptibility thereby establishing KCNEI as an LQT gene
Patent: US 6274332-A 43 14-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 18)

Keating, M.T., Sanguinetti, M.C., Karan, M.E., Landes, G.M.,

Connors, T.D., Burn, T.C. and Splawski, I.

KVLQTI-QT extension syndrome
Patent: JP 2002251045-A 41 16-JUL-2002;

UNIVERSITY OF UTAH RESEARCH FOUNDATION, GENZYME CORP

OS Homo sapiens (human)

N JP 2002521045-A/41
                                                                                         Unclassified.

1 (bases 1 to 18)
Splawski, I. and Keating, M.T.
Homozygous mutation in KVLQT1 which causes Jervell and Lange Nielsen syndrome
Patent: US 6150104-A 41 21-NOV-2000;
                                                                                                                                                                                                                                                                                                                Length 18;
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Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1;
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Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                      /organism="unknown"
/mol_type="unassigned DNA"
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    .18
    /organism="unknown"

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JP 2002521045-A/41.
Homo sapiens (human)
Homo sapiens
                  GI:14101188
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
Molecular Bogines Laboratories (FR)
Location/Qualifiers
                                                                                                                                                                                                                                                                                         Telerman, A., Amson, R. and Tuijnder, M. Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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                                                                                             AX759999 17 bp DNA Sequence 3320 from Patent WO03040369.

    17 .17
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    /db_xref="taxon:9606"

    .17
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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15 TCATTTTCCTTTCAA
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RESULT 251 AX762004

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PAT 17-JUL-2003

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van Lohuizen, M.M., Berns, A.J., Martins, C.P., Mikkers, H.M., Lenz, J.R., Lund, A.H. and de Koning, J.P.
Use of genes identified to be involved in tumor development for the development of anti-cancer drugs between WO 2004012817-A 16 12-FEB-2004;
Kylix B.V. (NL)
                                                                                                                                        PAT 06-MAR-2004
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Method for diagnosing non-small cell lung cancers
Patent: WO 2004031413-A 491 15-APR-2004;
Oncotherapy Science, Inc. (1, Japan as represented by the
president of the university of Tokyo (JP)
Location/Qualifiers
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/not="taxon:32631"
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for antisense method"
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 18)

RS Gallbert, F. and Andre, C.

Total genome radiation hybrid map of canine genome and its use for identification of interesting genes identification of interesting genes identification of interesting genes identification of interesting genes consistent DP 200230091-A122 17-SEP-2002;

PD PATERNI NATIONAL DE LA RECHERCHE SCIENTIFIQUE OS Canis familiaris (dog)

PP 17-SEP-2002

PP 17-S
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C12N15/00,
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PC
CI2NI/21, CI2NS/10, C12P21/08, C12Q1/02, C12Q1/68, G01N33/15, G01N33/ PC
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                          PD 16-JUL-2002
PF 12-MAY-1999 JP 2000562052
PR 29-JUL-1998 US 60/094477,17-AUG-1998 US 09/135010 1
MARK T KEATING,MICHAEL C SANGUINETTI,MARK E KARAN,GREGORY M
                                                                                                                                  PI TIMOTHY D CONNORS, TIMOTHY C BURN, IGOR SPLAWSKI PC CL2N15/09, A01K67/027, C07K14/46, C07K14/47, C07K16/18, C12N1/15,
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/organism='Canis familiaris (dog)'.
Location/Qualifiers
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Key Location/Qualifiers
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/organism="Canis familiaris"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .18
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JP 2002530091-A/122.
Canis familiaris (dog)
Canis familiaris
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Best Local Similarity 93.3
Matches 14; Conservative
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PI TI
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

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BD230253/c LOCUS DEFINITION

RESULT 255

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Patent: US 6420124-A 43 16-JUL-2002;
Location/Qualifiers
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/organism="unknown"
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                                                                                                                                      Marx, A.

Method and nucleic acids for the improved treatment of breast cell
proliferative disconders

Patent: WO 2004035803-A 1300 29-APR-2004;

Epigenomics AG (DE)
Location/Qualifiers
Lorganism="synthetic construct"
//organism="synthetic construct"
//mol_type="unassigned DNA"
//db_xref="taxon:32630"
//note="Detection oligonucleotide for X51730 PGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (Chases 1 to 18)
Wessler,S.R. and Casa,A.M.
Wessler,S.R. inverted repeat transposable elements and methods of use Patent: US 6420117-A 6 16-JUL-2002;
Location/Qualifiers
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                                                                                                                Foekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F.,
Nimmrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and
                                                                                                                                                                                                                                                                                                                                            Gaps
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Unclassified.
1 (John 18)
Keating, M.T., Sanguinetti, M.C., Curran, M.E., Landes, G.M.,
Connors, T.D., Burn, T.C. and Splawski, I.
KVLQT1--a long qt syndrome gene
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93.3%; Pred. No. 1.3e+02;
tive 0; Mismatches 1; Indels
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1.2%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1;
Sequence 1300 from Patent WO2004035803.
CQ807850
                                                                                    other sequences; artificial sequences.
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/organism="unknown"
/mol_type="genomic DNA"
                              CQ807850.1 GI:47113244
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synthetic construct
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Best Local Similarity
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1 (bases 1 to 18)
Keating,M.T., Sanguinetti,M.C. and Splawski,I.
Mutations in the KCNE1 gene encoding human mink which cause arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene Patent: US 6432644-A 43 13-AUG-2002;
Location/Qualifiers
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Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
Connors,T.D., Burn,T.C. and Splawski,I.
KVLQT1--- long QT syndrome gene
Patent: US 6451534-A 43 17-SEP-2002;
Location/Qualifiers
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                                    1.2%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 1.3e+02; ative 0; Mismatches 1; Indels
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Sequence 43 from patent US 6432644.
AR223111
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Sequence 43 from patent US 6451534.
AR229873.1 GI:27269751
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/mol_type="genomic DNA"
/mol_type="genomic DNA"

    18
    /organism="unknown"

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Matches 14; Conservative
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                                                                                                                           Unknown.
Unknown.
Unclassified.

I (bases I to 18)

Keating,M.T., Sanguinetti,M.C. and Splawski,I.

Keating,M.T., Sanguinetti,M.C. and Splawski,I.

Keating,M.T., Sanguinetti,M.C. and Splawski,I.

Keating,M.T., Sanguinetti,M.C. and Splawski,I.

Reating,M.T., Sanguinetti,M.C. and Splawski,I.

Reations in the KCNEI gene encoding human mink which cause

Arrhythmia susceptibility thereby establishing KCNEI as an LQT gene
arrhythmia susceptibility thereby establishing KCNEI as an LQT gene
Patent: US 6323026-A 43 27-NOV-2001;
Patent: US 6323026-A 43 27-NOV-2001;
Patent: Incation/Qualifiers
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Cohen, D., Chumakov, I. and Blumenfeld, M.
Bjalleljic markers for use in constructing a high density disequilibrium map of the human genome patent: US 6537751-A 5744 25-MAR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknow...
Unclassified.
Unclassified.
1 (bases 1 to 18)
Cohen,D., Chumakov,I. and Blumenfeld,M.
Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
Patent: US 6537751-A 5495 25-MAR-2003;
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Sequence 5744 from patent US 6537751.
AR294009.1 GI:31681293
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Sequence 5495 from patent US 6537751.
AR293760. GI:31681044
                                      18 bp 18 Sequence 43 from patent US 6323026. AR262129 GI:28073490
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AR293760/c
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Keating, M.T., Sanguinetti, M.C., Curran, M.E., Landes, G.M.,
Connors, T.D., Burn, T.C. and Splawski, I.
Diagnostic method for KVLQTI--a long QT syndrome gene
Patent: US 6582913-A 43 24-JUN-2003;
Location/Qualifiers
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Sequence 139 from Patent WO0129251.
AX119482
AX119482.1 GI:14036401
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Sequence 43 from patent US 6582913.
AR344567
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/wol_type="genomic DNA"
1. .18
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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PN JP 2002516657-A/346
PD 11-JUN-2002
PP 22-DEC-1998 US 60/099658 PI
PN 22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PI
DANIEL COHEN, MARTA BLUMENFELD, ILYA CHUMAKOV, LYDIE BOUGUELERET PC C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC C12N1/19, C12N1/19, C12N1/10,C12N5/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10,C12N2/10
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PC C12N5/00,C12N15/00
CC upstream amplification primer for SEQ 251, SEQ 328 FH
Location/Qualifiers
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                                                                Sequence 195 from Patent WO0129251.

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JP 2002516657-A/346.
Homo sapiens (human)
Homo sapiens
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BD196757
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                    RESULT 268
AX119538/c
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                                                                                            DEFINITION
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BD196757/c
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AUTHORS
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        PAT 05-MAY-2004
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C12N15/09,C12N1/19,C12N9/02,(C12N1/19,C12R1:865),(C12N9/02,
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                                                                                                                                                                                             Schrenzel, J., Francois, P., Charbonnier, Y., Jacquet, J.G., Utinger, D., Kresbach, G.M., Abel, A. and Ehrat, M. Analytical chip for the detection of 16s-rrna from clinically relevant bacteria and analytical method based thereon Patent: WO 2004033720-A 256 22-APR-2004; Hopitaux Universitaires de Geneve (CH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Akiyoshi, M., Yabusaki, Y., Sakaki, T., Murakami, H. and Okawa, H. BOVING ADRENAL ADRENODOXIN PRODUCING STRAIN
PREDRIE: JP 199506767-A 4 14-MAR-1995;
SUMITOMO CHEM CO LTD
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PI AKIYOSHI MEGUMI, YABUSAKI YOSHIYASU, SAKAKI TOSHIYUKI,
MURAKAMI HIROKO,
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           linear
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="texon:32630"
/note="Probe for Bacteroides fragili"
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Sequence 256 from Patent WO2004033720. CQ801939
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                                                                                                                                                          other sequences; artificial sequences.

    .19
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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Artificial sequences.
JP 1995067667-A/4
14-MAR-1995
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                                                                       CQ801939.1 GI:47058520
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JP 1995067667-A/4.
unidentified
unidentified
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synthetic construct
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1 (bases 1 to 19)
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AR299591.1 GI:31686875
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AX132453
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KEYWORDS
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AR452230/c
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TITLE
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                                                                                                                                                                                                                                           Unknown:
Unclassified.
Unclassified.
1 (bases 1 to 19)
Wilson, J.M., Goldman, M., Bals, R., Stolzenberg, E.D., Anderson, M.,
Zasloff, M. and Kari, P.
Compositions and methods for use of defensin
Patent: US 6399370-A 23 04-JUN-2002;
Location/Qualifiers
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                                            Gaps
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Unknown.
Unclassified.
Unclassified.
(Lases 1 to 19)
Cohen, D., Chunakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
disequilibrium map of the human genome
Location/Qualifiers
Location/Qualifiers
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                   Query Match
1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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93.3%; Pred. No. 1.3e+02;
tive 0; Mismatches 1;
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Sequence 4387 from patent US 6537751.
AR292652
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/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                         AR211777 19 bp Sequence 23 from patent US 6399370. AR211777
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15 TCAAAAGGGGAGCCT 1
                                                                        1100 CTGCTCATTTGTTTA 1114
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nes 14; Conservative
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AR299591
LOCUS
DEFINITION
ACCESSION
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AR292652/c
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AUTHORS
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PAT 15-MAY-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ribozyme therapy for the treatment of proliferative skin and diseases
Patent: WO 0130362-A 3671 03-MAY-2001;
IMMUSDL, INC. (US)
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Unknown.
Unknown.
Unclassified.
I (bases 1 to 19)
Cohen, D., Chunakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
patent: US 6537751-A 11336 25-MAR-2003;
Location/Qualifiers
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Unclassified.
Unclassified.
I (bases 1 to 19)
Janjio, N., Bullard, J.M., McHenry, C.S. and Kery, V.
Thermophilic polymerase III holoenzyme
Patent: US 6677146-A 80 13-JAN-2004;
Location/Qualifiers
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1.2%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1;
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93.3%; Pred. No. 1.3e+02;
tive 0; Mismatches 1;
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    19
    organism="Homo sapiens"
/mol_type="unassigned DNA"

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AR452230
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Homo sapiens
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Best Local Similarity 93.3
Matches 14; Conservative
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AUTHORS
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PN 17 2001502891-A/13
PD 06-MAR-2001
PP 20-AUG-1997 JP 1998510921
PP 22-AUG-1996 US 60/023424,01-OCT-1996 US 60/027334 PR 18-PEB-1997 US 60/038685
PI JAMES M WILSON,MITCHELL GOLDMAN,ROBERT BALS,
PI ETHAN D STOLZENBERG,
PI MARK ANDERSON,MICHAEL ZASLOFF,PRASAD KARI
PC C12N5/00,C12N15/00,C07H21/04,A61K38/00,A61K48/00,C07K2/00, PC
                                                                                                                                                                                                                                  PAT 26-OCT-2001
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synthetic construct
synthetic construct
other sequences; artificial sequences.
other sequences; artificial sequences.
other sequences; artificial sequences.
i (bases 1 to 19)
Wilson,J.M., Goldman,M., Bals,R., Stolzenberg,E.D., Anderson,M.,
Zasloff,M. and Kari,P.
Compositions and methods for use of defensin
patent: JP 2001520291-A 13 06-MAR-2001;
THE TRISTEES OF THE UNIVERSITY OF PENNSYLVANIA, AGAININ
PHARMACEUTICALS INC
OS Artificial Sequence
                                                                                    Gaps
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/mol type="unassigned DNA"
/db. tref="texton:32630"
/noTe="reverse/antisense ATG primer #p133-A1237"
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0
                                              Query Match
1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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/db_xref="taxon:9606"
/note="Cdc25 hs ribozyme binding site"
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Compositions and methods for use of defensin.
BD009904
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                                                                                                                                                                                                                                                                                                              synthetic construct
synthetic construct
other sequences; artificial sequences.
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Sequence 80 from Patent WO0173052.
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JP 2001502891-A/13.
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Synthetic construct DNA, reverse primer for human STS sts-stSG4211
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Patent: JP 2001321190-A 584 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
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      /organism='Artificial Sequence'
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Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1;
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Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1;
                                                        1. .19
/organism="synthetic construct"
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/db_xref="taxon:32630"

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        <pri>forganism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"</pr>

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1 (bases 1 to 19)
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AB068097
AB068097.1 GI:15128901
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JP 2001321190-A/584.
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AR018185/c
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Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H., Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A. and Soeda, E.
A BAC-based STS-content map spanning a 35-Mb region of human Gromosome 1p35-p36 Genomics 74 (1), 55-70 (2001)
                                                                                                                                                            Direct Submission
Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology, 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (B-mail:horii@mail.cc.tohoku.ac.jp,
Tel:81-22-717-8042, Fax:81-22-717-8047)
Location/Qualifiers
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1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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unidentified
unclassified.
1 (bases 1 to 18)
Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLICONUCLEOTIDE PREPARATION METHOD
Patent: WO 9833904-A 6 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
LOCATION/Qualifiers
                                                                                                                                                                                                                                                          /organism="synthetic construct"
/mol_type="genomic DNA"
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    18 / Organism="unidentified"
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Sequence 6 from Patent EP0856579.
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Sequence 6 from Patent WO9833904.
A87858
A87858.1 GI:6736428
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2 (bases 1 to 19)
Horii,A.
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Pedersen,F. Skou., Lund,A. Henrik., Lovmand,J., J.O
Pedersen,F. Skou., Lund,A. Henrik., Lovmand,J., J.O
slashed.rgensen,P. and Duch,M.
Retroviral vector, a replication system for said vector and avian or mammalian cells transfected with said vector
Patent: US 5866411-A 3 02-PEB-1999;
Location/Qualifiers
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Guntaka,R.V., Weber,K.Theodore., Kovacs,A. and Kandala,J.
Gligomers which inhibit expression of collagen genes
Patent: US 5780611-A 12 14-JUL-1998;
Location/Qualifiers
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1 (bases 1 to 18)
Brysch, W.D. and Schlingensiepen, K.D.
An antisense oligonuclectide preparation method
Patent: EP 0856579-A 6 05-AUG-1998;
BIOGNOSTIK GES (DE)
Location/Qualifiers
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83.3%; Pred. No. 1.4e+02;
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Sequence 12 from patent US 5780611.
AR018185
AR018185.1 GI:3973788
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Sequence 3 from patent US 5866411.
AR031775
AR031775.1 GI:5946064
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/organism="unidentified"
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/organism="unknown"
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Best Local Similarity 83.3
Matches 15; Conservative
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                                                                                                                                                   Unknown.
Unclassified.
1 (bases 1 to 18)
11 (bases 1 to 18)
11 (by Waratase
Nitrile hydratase
Patent: US 5807730-A 34 15-SEP-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unclassified.
1 (bases 1 to 18)
1 (bases 1 to 18)
1 Lo,K., Yamaki,T., Arii,T., Tsuruoka,M. and Nakamura,T.
Nitrile hydratase
Patent: US 5910432-A 34 08-JUN-1999;
Location/Qualifiers
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1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels
                                                                                     linear
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                                                                                     DNA
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                                                                                Sequence 34 from patent US 5807730. AR039068.1 GI:5958431
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/organism="unknown"
/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                   /organism="unknown"
/wol_type="unassigned DNA"
192 TCCACGCCATCTCCCCA 209
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1 TCCCGGCATCTCCACCA 18
                                                                                                                                                                                                                                                                                                                                        17 CTGCCCGGCCGTGGCAG 34
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AR071248/c
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AR039068/c
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AR076370/c
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Bedersen, F. Skou., Lund, A. Henrik., Lovmand, J., J. o. slashed. rgensen, P. and Duch, M.

Retroviral vector, a replication system for said vector and avian or mammalian cells transfected with said vector

Patent: US 6107478-A 3 22-AUG-2000;

Location/Qualifiers
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Akong, M.Anthony., Harpold, M.Miller., Velicelebi, G. and Brust, P. Aktomated analysis equipment and assay method for detecting cell surface protein function using same Patent: US 612713.3-A 2 03-007-2000;
Location/Qualifiers
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Bennett, C. Frank., Ackermann, B.J. and Cowsert, L.M.
Antisense inhibition of cellular inhibitor of apoptosis-1
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Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels
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Patent: US 5958772-A 37 28-SEP-1999;
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
/wol_type="unassigned DNA"
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Sequence 2 from patent US 6127133.
AR111390.1 GI:12828238
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                                                                                          Location/Qualifiers
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/organism="unknown"
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Best Local Similarity 83.3%;
Matches 15; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

ICE 1 (bases 1 to 18)

RS Landers,J.E., Jordan,B., Housman,D.E. and Charest,A.

Methods and products related to genotyping and DNA analysis

Methods and products related to genotyping and DNA analysis

Patent: JP 200252127-A 16 13-AUG-2002;

MASSACHUSETTS INSTITUTE OF TECHNOLOGY

OS Homo sapiens (human)

PN JP 200252127-A/16

PN JP 200252127-A/16

PN JP 200252127-A/16

PR 25-SEP-1999 US 60/101757

PR 25-SEP-1999 US 60/101757

PR 25-SEP-1999 US 60/101757

PR 25-SEP-1999 US CONIN3/53,GOIN33/58,GOIN37/00, PC CI2N15/09,CI2Q1/68,GOIN33/53,GOIN33/58,GOIN37/00, PC CI2N15/09
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                                                                                            18 bp DNA linear PAT 17-JUL-2003
Antisense modulation of expression of cellular inhibitor of
apoptosis-1.
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Bennett, F.C., Ackermann, E.A. and Cowsert, L.M.
Bennett, F.C., Ackermann, E.A. and Cowsert, L.M.
Is Bennett, F.C., Ackermann, E.A. and Cowsert, L.M.
La placet, 10 2002531469-A 37 24-SEP-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
No 24-SEP-2002
PR 19-200231469-A/37
PR 03-DEC-1998 US 09/205204
PR 03-DEC-1998 US 09/205204
PI FRANK C BENNETT, ELIZABETH A ACKERMANN, LEX M COWSERT PC
AGIRSA(00, AGIRS1/7115, AGIRS1/7112, AGIRS1/7125, AGIPS9/00 PC
AGIRSA(00, AGIRS1/7115, AGIRS1/7115, AGIRS1/7125, AGIPS9/00 PC
C Synthetic
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Methods and products related to genotyping and DNA analysis.
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/organism="synthetic construct"
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/db_xref="taxon:32630"
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JP 2002525127-A/16.
Homo sapiens (human)
Homo sapiens
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JP 2002531469-A/37.
       Query Match 1.23
Best Local Similarity 83.33
Matches 15; Conservative
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BD241069/c
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Synthetic construct
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cher sequences; artificial sequences.
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cher sequences; artificial sequences.

I (bases 1 to 18)
S Fan, J.B., Hirschhorn, J.N., Huang, X., Kaplan, P., Lander, E.S.,
Cockhart, D.G., Ryder, T. and Sklar, P.
Universal arrays
AL Patent: JP 2002539849-A 398 26-NOV-2002;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH, AFFYMETRIX INC
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH, AFFYMETRIX INC
OS Artificial Sequence
FOR JPARA JOSO JP 2006608794
FR 26-MAR-1399 US 60/126473,23-JUN-1999 US 60/140359 PI
PR 26-MAR-1999 US 60/126473,23-JUN-1999 US 60/140359 PI
BR 26-MAR-1999 US 60/126473,23-JUN-1999 US 60/140359 PI
FI DAVID J LOCKHART, THOMAS RYDER, PAMELA SKLAR
PI DAVID J LOCKHART, THOMAS RYDER, PAMELA SKLAR
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Methods and products related to genotyping and DNA analysis FH _{\rm L}
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                                                                                              organism='Homo sapiens (human)'.
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[ve 0; Mismatches 3; Indels
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PI DAVID J LOCKHART, THOMAS RYDER, PAMELA SKLARR
C C12Q1/68,C12M1/00,C12N15/09,C12N15/09,C12N15/00
G01N33/566,
PC G01N37/00,C12N15/00,C12N15/00
CC Primer
FH Key
I. 18
FT source
Organism='Artificial Sequ
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/organism="synthetic construct"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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BD266398.1 GI:33076166
JP 2002539849-A/398.
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                                                                                                                                        C Artificial sequences.

1 JP 1997275978-A/32

2 26-OCT-1997

F 29-JAN-1997 JP 1997015295

F 14-FEB-1996 JP 96P 27004

I TO KIYOSHI, YAWAKI TOSHIBUMI, ARII TERUO, TSURUOKA MIYUKI, PI
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29-JAN-1999 EP 9910125:8
HOSEN W P PAN MYLIBERT IE W ZENDOWAN
C12N15/09,C07K14/82,C07K16/32,C12P21/02,C12Q1/68,G01N33/566,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        other sequences; artificial sequences.

1 (bases 1 to 18)

Myulen, N. P. F. and Zendoman, A. I. W.
Novel gene regulated and decreased in metastatic human melanoma utilization of the same

Patent: JP 200021788-A 5 08-AUG-2000;

P. HOFFWANN LA ROCHE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel gene regulated and decreased in metastatic human melanoma cell and protein thereof, process for producing the same and utilization of the same.
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unidentified
unidentified
unidentified
unclassified.
1 (bases 1 to 18)
Ito,K., Yamaki,T., Arii,T., Tsuruoka,M. and Nakamura,T.
NEW NITRILE-HYDRAPASE
Patent: JP 1997275978-A 32 28-OCT-1997;
MITSUI TOATSU CHEM INC
OS None
OC Artificial sequences.
PN JP 1997275978-A/32
PD 28-OCT-1997
PP 29-JAN-1997 JP 1997015295
PR 14-FEB-1995 JP 96P 27004
PR 14-FEB-1995 JP 96P 27004
PR 14-FEB-1995 JP 96P 27004
PR 14-FEB-1997 JP 1997015295
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Location/Qualifiers
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Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3;
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Btrandedness: Single;

topology: Linear;

hypothetical: No;

anti-sense: No;
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JP 2000217585-A/5
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JP 2000217585-A/5.
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C12R1:19),
PC (C12N1)
CC (CC topold
CC hypotl
CC anti-I
FH Key
FT source
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Unclassified.

(bases 1 to 18)

Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,

Baveracce,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.

Lawrence,D.A., Levine, and unclaic acids encoding same

Patent: US 6387657-A 131 14-MAY-2002;

Location/Qualifiers
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Unclassified.
1 (bases 1 to 18)
Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density disequilibrium map of the human genome
Patent: US 6537751-A 5708 25-MAR-2003;
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/organism='Artificial Sequence'
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13.3%; Pred. No. 1.4e+02;
ve 0; Mismatches 3;
                                                                                                                               1.2%; Score 13.2; DB 1;
83.3%; Pred. No. 1.4e+02;
ative 0; Mismatches 3;
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83.3%; Pred. No. 1.4e+02;
7ative 0; Mismatches 3;

    18. 18
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Seguence 5708 from patent US 6537751.
AR293973
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/organism="unknown"
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Best Local Similarity
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    1. .18
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Location/Qualifiers
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AR482570/c
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Bancroft, F.C., Fliss, M. and Clelland, C.L.

Brolactin regulatory element binding protein and uses thereof Patent: N 58565811A 29 01-JUL-2003;

Location/Qualifiers
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Harpold,M.M. and Brust,P.
Assay methods and compositions useful for measuring the transduction of an intracellular signal patent: US 5401629-A 3 28-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                       Offices 1 to 18)
Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density disequilbrium map of the human genome patent: US 6537751-A 9959 25-MAR-2003;
Location/Qualifiers
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1.2%; Score 13.2; DB 1;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3;
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                                                  AR298224 18 bp DN.
Sequence 9959 from patent US 6537751.
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Sequence 3 from patent US 5401629.
AR364672
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1. .18
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/ordanism="synthetic DNA"
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/note="Description of Combined DNA/RNA Molecule:
Endonuclease protected sequence~Detection oligonucleotide"
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Enzymatically catalysed signal amplification
Patent: WO 0055365-A 4 21-SEP-2000;
MULROONEY CONOR (GB) ; OULTRAM JOHN DOUGLAS (GB) ; TEPNEL MEDICAL
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Landers, J. Jordan, B., Housman, D.E. and Charest, A.
Methods and products related to genotyping and DNA analysis
Patent: US 6703228-A 16 09-MAR-2004;
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Length 18;
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1.2%; Score 13.2; DB 1;
83.3%; Pred. No. 1.4e+02;
ative 0; Mismatches 3;
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Sequence 16 from patent US 6703228.
AR482570
AR482570.1 GI:47245093
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Sequence 4 from Patent WO0055365.
AX035247
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                                                                                                           synthetic construct synthetic construct
            Query Match
Best Local Similarity 83.3
Matches 15; Conservative
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Unclassified.
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Best Local Similarity
Matches 15; Conserv
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73

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synthetic construct other sequences.
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Matches 15; Conservative
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Matches 15; Conserv
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                                                          PAT 22-FEB-2001
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                Bukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels
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Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels
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Patent: WO 0105963-A 37 25-JAN-2001;
McGill University (CA)
Location/Qualifiers
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Patent: WO 0202630-A 10 10-JAN-2002;
SMITHKLINE BEECHAM PLC (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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    .18
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                                                         AX078863 18 bp
Sequence 37 from Patent W00105963.
AX078863
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                                                                                                   AX078863.1 GI:13158480
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                                                                                                                                   Homo sapiens (human)
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AX348093
                            RESULT 302
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                          /note="Residue mutated with respect to the corresponding position in Par jl.0102"
                                                                                                                                                                                                                                                                                                  /note="Residue mutated with respect to the corresponding
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Geraci, D., Colombo, P., Duro, G., Izzo, V. and Costa, M.A.
Parietaria judaica ns-ltp antigen variants, uses thereof and compositions comprising them

Eatent: WO 0220790-A 13 14-WAR-2002;

CONSIGLIO NAZIONALE DELLE RICERCHE (IT)

Location/Qualifiers
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83.3%; Pred. No. 1.4e+02;
tive 0; Mismatches 3;
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83.3%; Pred. No. 1.4e+02;
tive 0; Mismatches 3;

    18
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Patent: WO 02077272-A 1131 03-OCT-2002;
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other sequences; artificial sequences.
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AX599792
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Sequence 1131 from Patent WO02077272.
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                                                                                                                                                                                                                                                    /note="Oligonucloetide"
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synthesized primer se q"
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
AUTHORS
Schlingensiepen, K.H. and Brysch, W.
TITLE
An antisense oligonucleotide preparation method
TITLE
An antisense oligonucleotide preparation
BICGNOSTIK GESELLSCHAFT FUR BICMOLEKULARE DIAGNOSTIK MBH
WENT
OS UNKNOWN
PN 10 2001511000-A/6
PP 30-JAN-1998 UP 1998532533
PR 31-JAN-1999 RP 971015-7
PI KARL HERRANN SCT.
CC 7-
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10-2011

10-301-1994 BT 1998532533

13-13A-1997 EP 97101531.8

KARL HERMANN SCHLINGENSIEBEN, WOLFGANG BRYSCH

C12N15/11, C7H21/04, AG1K31/70

An antisense oligonucleotide preparation method FH

Location/Qualifiers
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Pred. No. 1.4e+02;
0; Mismatches 3;
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                                      Full-length cDNA sequences
Patent: EP 1347046-A 4925 24-SEP-2003;
Research Association for Biotechnology
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Sequence 16 from patent US 5858981.
AR028977
AR028977.1 GI:5940950
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                                                                                      Location/Qualifiers
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Unclassified.
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AR028977/c
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BD065371/c
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Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
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                                                           Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J., Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, E., Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T., Mellet, C. and Ziebarth, H.
Methods and nucleic acids for the analysis of hematopoietic cell proliferative disorders

Patent: WO 02077272-A 1132 03-OCT-2002;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db.zref="taxon:32630"
/noTe="Detection oligonucleotide for Me491/TD63"
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83.3%; Pred. No. 1.4e+02;
iive 0; Mismatches 3; Indels
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                    synthetic construct other sequences.
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Sequence 4925 from Patent EP1347046.
AX837801 GI:39921493
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    .18
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Location/Qualifiers
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Sus scrofa
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Schreiber, A.D. and Park, J.-G.
Methods of inhibiting phagocytosis
Patent: US 62427-A 16 05-JUN-2001;
Location/Qualifiers
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Schreiber,A.D. and Park,J.-G.
Methods of inhibiting phagocytosis
Patent: US 6638764-A 16 28-OCT-2003;
Location/Qualifiers
1 (bases 1 to 16)
Schreiber, A.D. and Park, J.-G.
Method of inhibiting phagocytosis
Patent: US 5858981-A 16 12-JAN-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                               Sequence 16 from patent US 6242427.
AR156859
AR156859.1 GI:15125563
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    .16
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    16
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AR156859/c
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AR412057/c
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8 Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.

8 Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.

8 Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.

8 Regulation of repressor genes using nucleic acid molecules

8 Regulation of repressor genes using nucleic acid molecules

8 RIBOZYNE PHARMACEUTICALS INC

8 SUKARYOCE

8 D 10-DEC-2002

9 D 10-DEC-2002
Regulation of repressor genes using nucleic acid molecules. BD558394
BD258394.1 GI:33068164
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Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 1811 16-AUG-2001;
RIBOZYME PHARMCEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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/db xref="taxon:32630"
/noTe="Nucleic Acid"
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Sequence 1811 from Patent WO0159103.
AX216369
AX216369.1 GI:15526430
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xrefe"taxon:32644"
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AX227245/C
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RESULT 317
AX226888/c
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Patent: WO 0157206-A 259 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Fattaey, Ali R. (US)
Location/Qualifiers
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Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 2387 16-AUG-2001;
RIBOZYME PHARMACHULALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
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/organism="synthetic construct"
/mol type="unassigned RNA"
/db_xref="taxon:32630"
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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Sequence 2387 from Patent WO0159103.
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PAT 10-SEP-2001
                                                                                                                                                                      Fattaey, A.R., Jarvis, T., Mcswiggen, J., Booher, R.N. and Holman, P.S. Method and reagent for the inhibition of checkpoint kinase-1 (chk
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        Patent: WO 0157206-A 260 09-AUG-2001;
        Patent: WO 0157206-A 260 WO-AUG-2001;
        RIBOZYME PHARMACEUTICALS, INC. (US);
        Fattaey, Ali R. (US)
        Location/Qualifiers

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100.0%; Pred. No. 1.5e+02;
:ive 0; Mismatches 0;
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Sequence 618 from Patent WO0157206.
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/db_xref="taxon:9606"
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Pattaey, A.R., Jarvis, T., Mcswiggen, J., Booher, R.N. and Holman, P.S. Method and reagent for the inhibition of checkpoint kinase-1 (chk l) enzyme
Patent: WO 0157206-A 618 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Fattaey, Ali R. (US)
Location/Qualifiers
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Method and reagent for the inhibition of checkpoint kinase-1 (chk
1) enzyme
Patent: WO 0157206-A 767 09-AUG-2001,
RIBOZYME PHARMACEUTICALS, INC. (US); Fattaey, Ali R. (US)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                              /organism="synthetic construct"
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/organism="synthetic construct"
/mol type="unassigned RNA"
/db_xref="taxon:32630"
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Sequence 1413 from Patent WO03025177.
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/mol_type="unassigned DNA"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
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100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0; Indels
Query Match 1.2%; Score 13; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 13; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.5e+02;
7ative 0; Mismatches 0; Indels
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AX758667
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Homo sapiens
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Matches 13; Conservative
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Search completed: August 19, 2005, 10:52:32 Job time : 7 secs
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Patent: WO 03072831-A 132 04-SEP-2003;
Epigenomics AG (DE)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Ammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0; Indels
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1.2%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
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Sequence 132 from Patent WO03072821.
AX825880
AX825880.1 GI:39751394
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    .18
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Best Local Similarity 100.
Matches 13; Conservative
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          13 AGCCGGAAGCAGC 1
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AX825880/c
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Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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100.0%; Pred. No. 2.2e+02;
ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                           Patent: WO 03025176-A 4476 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
Sequence 4476 from Patent W003025176.
AX726789
AX726789.1 GI:30506132
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/mol type="unassigned DNA"
/db_xref="taxon:10090"
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Best Local Similarity 100.
Matches 12; Conservative
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

- nucleic search, using sw model OM nucleic

August 19, 2005, 10:37:46; Search time 0.001 Seconds (without alignments) 352.024 Million cell updates/sec Run on:

US-10-774-721-21 1114 Title: Perfect score:

1 gtctggcttgggcaggctgc......gttacctgctcatttgttta 1114 Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 0.5

9 segs, 158 residues Searched: Total number of hits satisfying chosen parameters:

18

seq length: 0 seq length: 200000000 88 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 9 summaries

estdb:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	ACCESSION: AZ457101	ACCESSION: D44776	ACCESSION: AZ579189	ACCESSION: AU060353	ACCESSION:AI446372	ACCESSION: AJ588273	ACCESSION: BH169716	ACCESSION: CA851710	ACCESSION: AJ727978
ΩI	AZ457101	D44776	AZ579189	AU060353	AI446372	AJ588273	BH169716	CA851710	AJ727978
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* Query Match Length DB ID	22	19	19	20	16	18	14	15	15
Query Match	1.4	1.3	1.3	1.3	1.1	1.1	1.1	1.1	1.1
Score	15.6	14.8	14.8	14.8	12.8	12.8	12.4	12.4	12
ult No.	٦	0	ო	4	ß	9	7	æ	σ
Result No.	υ	U				υ			υ

## ALIGNMENTS

Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomicleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 k range using preparative agarese gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AP129072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance." É ö /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, Gaps ; 0 1.4%; Score 15.6; DB 1; Length 22; 11.8%; Pred. No. 1.4; ve 0; Mismatches 4; Indels Rm. 300, 188 5606
Fax: 801 585 5606
Fax: 801 585 7177
Email: ddunn&genetics.utah.edu
Insert Length: 10000 Std Broor: 0.00
Plate: 0260 row: J column: 17
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
High quality sequence stop: 22.
Location/Qualifiers /organism="Mus musculus" /mol type="genomic DNA" /strain="C57BL/6J" /db xref="taxon:10090" /clone="UUGCIMO260J17" Contact: Robert B. Weiss University of Utah Genome Center University of Utah /sex="Male" Unpublished (2000) source JOURNAL FEATURES

Query Match
Best Local Similarity 81.8%;
Matches 18; Conservative

D44776 1998 HUMSUPY214 Human brain cDNA Homo Bapiens CDNA clone MF51-S-2, mRNA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 19)
Hadano,S., Ishida,Y., Tomiyasu,H., Yamamoto,K., Bates,G.P. and Transcript map of the human chromosome 4p16.3 consisting of 627 cDNA clones derived from 1 Mb of the Huntington's disease locus DNA Res. 3 (4), 239-255 (1996) 97101646 D44776.1 GI:1572251 Homo sapiens (human) Homo sapiens sequence. RESULT 2 D44776/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

MEDLINE PUBMED JOURNAL

TITLE

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Matches 16; Conserv
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1M0363112F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0363112 F, genomic survey sequence.
      Japan Science and Technology Corporation, NeuroGenes Project, ICORP Univ. of Tokai School of Med.

Bohseidai, Isehara, Kanagawa 259-1193, Japan
Tel: 81-463-91-4993
Email: shinji@nga.med.u-tokai.ac.jp.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid inserts
University of Utah
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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1 (Dases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Neilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                  1.3%; Score 14.8; DB 1; Length 19; 88.9%; Pred. No. 1.7; 2; Indels :ive 0; Mismatches 2; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0363 row: I column: 12
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Location/Qualifiers
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Contact: Shinji Hadano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                     16; Conservative
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was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil | 4732114 | gb | AF129972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dictyostellum discoideum
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.

I (bases I to 20)
Norio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.
Developmental cDNA in Dictyostellum discoideum
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 20-MAY-1999
Dictyostelium
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/db_xref="taxon:44689"
/clone="gij384"
/dev_stage="slug"
/clone_lib="Dictyostelium discoideum SL (H.Urushihara)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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PROJECT = Dictyostelium discoideum cDNA project in Japan.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                              1.3%; Score 14.8; DB 1; Length 19; 88.9%; Pred. No. 1.7; ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU060353 Dictyostelium discoideum SL (H.Urushihara) discoideum cDNA clone SLJ384, mRNA sequence.
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Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
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Best Local Similarity 88.9
Matches 16; Conservative
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/mol_type="genomic_DNA"
/ecotype="Col-0"
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Location/Qualifiers
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Best Local Similarity 77.8%;
Matches 14; Conservative
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BH169716
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                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., M.D., Ph.D.,
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="poorly differentiated adenocarcinoma with signet ring call features"
/lab host="DHIOB"
/clone lib="NCI CGAP Gas4"
/note="Torgan: stomach; Vector: pCMV-SPORT6; Site 1: Sall; Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"
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GSS; right border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chavin, S., Bechlerdi, N., Craud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T_DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 16)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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  element MSR1 repetitive element ;, mRNA sequence.
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Insert Length: 1948 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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EMBO Rep. 3 (12), 1152-1157 (2002)
22363535
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/clone="IMAGE:2141098"
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                     AI446372
AI446372.1 GI:4294748
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Unpublished (1997)
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Direct Submission

Submitted (123-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue daston Cremieux, 91057 Bvry cedex, FRANCE

Gaston Cremieux, 91057 Bvry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 14)
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Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shina,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ынт69716 Arabidopsis thaliana TDNA linear GSS 03-OCT-200
SALK 001788 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK 001788, genomic survey sequence.
BH169716
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This is single pass sequence recovered from the left border of
TDNA.
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Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
The Salk Institute for Biological Studies
The Salk Institute For Biological Studies
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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/mol type="genomic DNA"
cultivar="Wassillewskija"
/db xref="taxon:3702"
/clone="529E06"
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/organism="Arabidopsis thaliana"

    18 / note="T-DNA flanking sequence

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Pred. No. 4;
0; Mismatches
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AJ727978
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Alkharouf, N. W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                                                                                          CA651710 11.abl cDNA Peking library 2, 4 day SCN3 Glycine max clone D16F12 5', mRNA sequence.
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            /db xref="taxon:3702"
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/clone="Jb="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/clone_lib="cDNA Peking library 2, cDNA clones from mRNA
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."
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Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
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/organism="Glycine max"
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/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D16F12"
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Contact: Caldwell RB
GSF - Forschungszentrum, Institut fuer Molekulare Strahlenbiologie
Ingolstaedter Landstr. 1, D-85764 Neuherberg, GERMANY.
Location/Qualifiers
Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

1 (bases 1 to 15)
Caldwell,R.B., Kierzek,A.M., Arakawa,H., Bezzubov,Y., Zaim,J., Fiedler,P., Kutter,S., Blagodatski,A., Kostovska,D., Koter,M., Plachy,J., Carninci,P., Hayashizaki,Y. and Buerstedde,J.M.
Full-jength cDNAs from bursal lymphocytes to facilitate gene
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100.0%; Pred. No. 4.5;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="32b1388"
/cell type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
                                                                                                                                                                                                                                                                                                                                                                                                 1. .15
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="riken1"
/note="CB inbred strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: August 19, 2005, 10:37:47 Job time : 0.001 secs
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Matches 12; Conserv
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

August 19, 2005, 10:56:24; Search time 8 Seconds (without alignments) 2.891 Million cell updates/sec

US-10-774-721-21 1114 1 gtctggcttgggcaggctgc.....gttacctgctcatttgttta 1114 Title: Perfect score: Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 0.5

536 segs, 10381 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

1072

ngsdb: \* Database :

N-Genesea Post-processing: Minimum Match 0% Maximum Match 100% Listing first 537 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		Query				
Š.	Score	Match	Length	8	QI .	Description
1	09	5.4	9	Т	ACA56897	an cDNA e
Ö	51	4.6		Н	AAH90177	
c)	49.4	4.4	51	-	AAH90178	Human clone cg4392
ο 4	1 22	2.0	22	Н	ADR27689	OB-RGRP antisense
υ u	5 21	1.9	21	7	ADT71352	Reverse primer for
Ψ	20.2	1.8	25	Н	ACK10810	Human microarray D
7	20	1.8	20		AAV17684	PCR primer P1 used
ω	3 20	1.8	20	٦	AAV17685	PCR primer P2 used
o o	9 20	1.8		Н	AAK95054	Human cDNA clone-s
c 10		1.8		Н	ADL32266	Clone specific PCR
7		1.8		н	ADR27690	OB-RGRP antisense
c 12		1.8		ч	ADR27680	OB-RGRP antisense
-	3 20	1.8	20	Н	ADR27685	OB-RGRP antisense
c 14		1.8	20	ч	ADR27653	OB-RGRP antisense
c 15	5 20	1.8	20	Н	ADR27682	OB-RGRP antisense
-		1.8	20	ч	ADR27688	OB-RGRP antisense
c 17		1.8	20	н	ADR27681	OB-RGRP antisense
7	8 20	1.8	20	ч	ADR27687	OB-RGRP antisense
c 19		1.8	. 20	-	ADR27679	OB-RGRP antisense
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7	3 20	1.8	20	Н	ADR27684	OB-RGRP antisense
~		1.8	20	-	ADR27691	OB-RGRP antisense
~	5 20	1.8	20	~	ADT71351	Forward primer for
°	19	1.8	25	Н	ABK39905	Human Parathyroid
7	7 19	1.7	19	-	AAT64982	Human OB receptor
5	œ	1.7	25	٦	ACK10811	Human microarray D
ر د	9 18.2	1.6	25	-	ACI63081	Human microarray D
ĕ		1.6	18	-	AAT64981	Human OB receptor
33	1 18	1.6	18	-	AAT85600	on.
m	2 18	1.6	18	Н	AAT85601	Antisense oligonuc
ω ω		1.6	18	Н	ACA75490	Human WSX receptor

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Forward primer for Human biallelic ma Human biallelic ma	Human long QT synd nog genomic marker	Human KVLOTI exon	Neurofibromatosis Neurofibromatosis	PCR primer used to	PCR primer used to	FCR DITHEI USED CO	Himan cyclin-depen	PCR primer 2 used	Oligonucleotide of	Monge hera defensi	pre primer for PG1	CAC OF he ribozyme	thiman biallelic ma	umman biallelic ma	Thomas thermorhil	Thermus chermophiti	Caczs ns ribozyme	Human chromosome 1	Human ERG2-targete	Human ERG2-targete	TCPTP2 siRNA #1.	TCPTP2 siRNA #2.	Analytical probe c	Analytical probe c	Himan and inoprote	Human apolipoprote	Human aportogod W	HHV-6 associated M	Collagen gene prom	Transforming grown	Human WISP-2 PCR p	Human c-IAP-1 mRNA	Murine tRNA gene f	Mouse tRNA-Ala(g)	Murine Ala tRNA 3'	Human genomic SNP	Collagen promoter	CMV GlyB detection	Murine tRNA oligon	Human biallelic ma	Human biallelic ma	TM7XN1 cDNA antise	PCR primer used to	Reverse primer #96	Human mGluR1beta G	Human HCN1 DNA amp	Human glial cell d	Haematopoietic cel	Haematopoietic cel	DNA fragment B amp	PGC-1 mutational a	TCV RdRP mutagenic	Xenopus axis dupli	Mammalian inverted	Human PCR primer S	Human CIAP-1 DNA a		CENPCI extend prim	nydratas	Modernia injurated with the deter	יייים לייים ליין	Tanınat.								
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13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	4.6	* • • • •	# C C	* * * * *	13.4	13.4	13.4	13.4	13.4	13.4	13.2	13.2	13.2	10.	4.6	10.6	177	13.2	13.2	13.2	13.2	13.2	13.2	13.2	13.2	13.2	13.6	4.66	7	13.4	10.01	1.0	13.6	2.6	10.0	1.5			13.2	13.2	13.2	13.2	13.2	13.2	12								
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1 AAX76902 1 AAZ71685					_	·	٦.			٠.	4 -	4 -	٠,	٠,	٠,	н,	_	Н	н	н	_	بس ا	-	-	4 +	٠,	н,	н	Н	Н	н	Н	Н	Н		-	-	1	-	١,	۱ -	-	-	-	Н	Н	Н	Н	Н	Н	-	Н	-	٦	_	Н	_	-	_	-11	٦,									
18	18	18	18	81	18	8 6	B C	7 6	9 6	n 0	7 -	7 -	η r	7 .	4.	13	19	19	19	19	19	61	, r	ן ני	1 6	1. 1.	15	15	16	16	16	17	17	17	17	1 -	17	17	17	17	17	17	1	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17
1.2	-i-	i	ri r	4	H	.i	٠,	i -	-		٠,	٠,	٠,	٠,	٠,	-	-1	-	-		-	٠.	٠.	4 -	٠,	_	-	-	-	_		_	-	'-	-	1 -	' -	-	1 -	' -		' -	, ,					•	•																			7.7	1.2	1.2
13.8	13.8	13.8	13.8	13.0	13.8	13.8	13.8	5 T T	0.0	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	8	3	2 0	9 0		10.7	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	4.61	13.4	 	10.1		. 4	10.4		† c	7.00	12.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4
																																																																						c 471

AAH90177 standard; cDNA; 51 BP.

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The invention relates to a complex between two interacting proteins in adipocyte cells, given in the specification. The proteins are identified by selecting a bait protein from a known adipocyte marker and then performing a yeast 2-hybrid selection to isolate prey proteins encoded by members of an adipocyte cDNA library. The proteins are designated SID (RTM) (selected interacting demains) proteins. Also included are a polymucleotide encoding a polypeptide in the adipocyte cells, a recombinant host cell expressing at least one of the interacting colls, a SID (RTM) polypeptide comprising any of the 738 amino acid sequences given in the specification (including its fragment or variant), a such (RTM) polymucleotide comprising any of the 738 mucleotide sequences given in the specification (including its fragment or variant), a vector comprising the SID (RTM) polymucleotide, a recombinant host cell comprising the vector, a protein chip comprising the polypeptides and a recombinant host cell comprising all or part of the data, listed in the specification. The complex, polypeptides, polymorleotides and compounds are useful for the order subsetty of the data, higher are useful for the polymorleotide are useful as the polymorleotides are useful to the maniant of the data and compounds are useful to the maniant mate or diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complex between two interacting proteins in adipocyte cells, useful identifying selected interacting domains that modulate protein gractions, or for preventing or treating metabolic disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The polymucleotides are useful as probes or primers. The complex is particularly useful for identifying selected interacting domains (SID (RTM)) for screening drugs that modulate the protein interaction, thus exhibiting the therapeutic effect. The present sequence encodes a bait
                                                                                                                                                                              Human, 88; gene, bait, adipocyte, SID; selected interacting domain,
anorectic, antidiabetic, protein-protein interaction, diabetes,
yeast 2-hybrid assay, metabolic disorder, obesity.
                                                                                                                                     Human cDNA encoding an adipocyte bait protein, OBRGRP_v2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein used to generate the complexes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 60 BP; 18 A; 15 C; 15 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 41; 382pp; English.
  路
                                                                                                                                                                                                                                                                                                                                                                                                              14-MAR-2002; 2002WO-EP003768
                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAR-2001; 2001US-0275734P
ACAS6897 standard; cDNA; 60
                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Legrain P, Daviet L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2003-103412/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYBR-) HYBRIGENICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       obesity or diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; ABU70363
                                                                                                                                                                                                                                                                                                                      WO200286122-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interactions,
                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                        10-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                   31-OCT-2002
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ö 0; Gaps DB 1; Length 60; 0; Indels 5.4%; Score 60; DB 1; Le 100.0%; Pred. No. 1.5e-06; iive 0; Mismatches 0; Query Match
Best Local Similarity 100.
Matches 60; Conservative

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RESULT 2 AAH90177/c

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Sequences AAH90121-AAH90700 represent 580 human cDNA sequences which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 568 (AAH90121-AAH90688) are consecutive pairs of nucleotides which contain silent SNPs. Sequences 569 to 580 (AAH90689-AAH90700) are consecutive pairs of nucleotides containing SNPs which result in changes in the corresponding amino acid sequences (AAG64751-AAG64752). The SNPs in sequences 569 to 574 (AAH90689-AAH90609) result in changes, while those in sequences 575 to 578 (AAH90698) result in non-conservative changes. The SNP in sequences 579 and 580 (AAH90699) result in non-conservative changes. The SNP in sequences 579 and 580 (AAH90699) result in non-conservative changes of two nucleic acids in a nucleic acid and a method of detecting a polymorphic site in a nucleic acid and a method of detecting polymorphic proteins/ peptides using the antibodies. The nucleic acids are useful for gene therapy of an individual having, suspected of having, or at risk of developing a pathological condition due to the presence of a sequence polymorphism. Such treatment would comprise administration of the wild-type nucleic acid sequence polymorphise administration of the wild-type nucleic acid sequence polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides containing single nucleotide polymorphisms, for detecting the presence of polymorphism, detecting a polymorphic site, and treating a patient suffering from a pathology ascribed to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                              chromosome 1; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             870
                                                                                                                                                                                                                                                                                          /standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  · 51 AGCCTCTCATGACCCAGGAAGGCCGGGGTGGATCCCTCTTTGTGTTGTAG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               820 AGGCCTCTCATGACCCAGGAAGGCCGGGGTGGATCCCTCTTTGTGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 51 BP; 13 A; 17 C; 13 G; 8 T; 0 U; 0 Other;
                                                                                                                                            Human; single nucleotide polymorphism; SNP; chromos identification; gene therapy; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. No. 6.1e-05; ive 0; Mismatches 0;
                                                                                                         Human clone cg43922807 SNP site, SEQ ID NO:57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in the treatment of such individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 51;
                                                                                                                                                                                                                                    Location/Qualifiers
replace(26,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 69; 295pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         27-DEC-2000; 2000WO-US035387.
                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-00472865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-425617/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                WO200147942-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                            27-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymorphism.
                                                                                                                                                                                                    Homo sapiens
                                                                       08-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2001
                                                                                                                                                                                                                                                       variation
                                  AAH90177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nsed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
ð
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AAH90178/c

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New polynucleotides containing single nucleotide polymorphisms, for detecting the presence of polymorphism, detecting a polymorphic site, and treating a patient suffering from a pathology ascribed to the
                                                            Human; single nucleotide polymorphism; SNP; chromosome 1; detection; identification; gene therapy; genetic disorder; ss.
                                                                                                                         /*tag= a
/standard name= "single nucleotide polymorphism"
                                            Human clone cg43922807 SNP site, SEQ ID NO:58.
                                                                                                       Location/Qualifiers replace (26, C)
                                                                                                                                                                                                                                                                                                           Claim 1; Page 69; 295pp; English.
AAH90178 standard; cDNA; 51 BP
                                                                                                                                                                                27-DEC-2000; 2000WO-US035387
                                                                                                                                                                                                 99US-00472865
                                (first entry)
                                                                                                                                                                                                                                  Leach M;
                                                                                                                                                                                                                  (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                  WPI; 2001-425617/45.
                                                                                                                                                  WO200147942-A2
                                                                                                                                                                                                                                                                                            polymorphism.
                                                                                                                                                                                                  27-DEC-1999;
                                                                                                                                                                                                                                  Shimkets RA,
                                                                                          Homo sapiens
                                 08-OCT-2001
                                                                                                                                                                  05-JUL-2001
                                                                                                                  variation
                AAH90178;
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Sequences AAH90121-AAH90700 represent 580 human cDNA sequences which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 568 (AAH90121-AAH90688) are consecutive pairs of nucleotides which contain single nucleotides solved to silent SNPs. Sequences 569 to 580 (AAH90689-AAH90700) are consecutive pairs of nucleotides containing SNPs which result in changes in the corresponding amino acid sequences (AAG64751-AAG64762). The SNPs in corresponding amino acid sequences (AAG64751-AAG64762). The SNPs in an in non-conservative changes. The SNP in sequences 559 to 574 (AAH90689-AH90699) result changes, while those in sequences 575 to 578 (AAH90699) result changes, while those in sequences 575 to 578 (AAH90699) result conservative changes. The SNP in sequences 579 and 580 (AAH90699) containing the relatedines of two nucleic acids. It also encompasses of determining the relatedines of two nucleic acids. It also encompasses containing polymorphic sites, antibodies raised against such chantibodies. The nucleic acids are useful for gene therapy of an individual having, suspected of having, or at risk of developing a individual comprise administration of the wild-type nucleic acids acids are useful for gene therapy of an individual would comprise administration of the wild-type nucleic acids acids equence polymorphism. Such treatment would comprise administration of the wild-type nucleic acids acids equence. Antibodies raised against polymorphic peptides can also be used in the treatment of such individuals

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                                              Gaps
                                              ;
                      Length 51;
                                             1; Indels
Sequence 51 BP; 13 A; 16 C; 13 G; 9 T; 0 U; 0 Other;
                       Score 49.4; DB 1;
Pred. No. 0.00012;
0; Mismatches 1;
                        4.4%;
                                                50; Conservative
                                       Local Similarity
                            Query Match
                                                    Matches
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TTGTGTTGTAG 870 820 AGGCCTCTCATGACCCAGGAAGGCCGGGGTGGATCCCTCT 51

RESULT 4 ADR27689/c

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The present invention relates to a leptin receptor related protein (OBCRGRP) antisense oligonucleotide (ON; ADR27653), that hybridises

CRGRP) antisense oligonucleotide (ON; ADR27653), that hybridises

CRGRP) antisense of leptin receptors on the cell surface and may

CRG specifically with and inhibits the expression of ADR27652. The ON

CRG contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a

CRG triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA

CRG (IRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit

CRG (IRNA) of 16-25 nt that hybridize specifically with ADR27672, and inhibit

CRG coding sequences comprising OB-RGRP or WY047 (thought to be a member of

CRG (IRNA) for detecting compounds that OB-RGRP), and a protein that

CRG (IRNA) for detecting compounds that Modify the interaction between

CRG (IRNA) for detecting compounds that modify the interaction between

CRG (IRNA) for detecting compounds that modify the interaction between

CRG (IRNA) for detecting compounds that modify the interaction between

CRG (IRNA) for detecting compounds that modify the interaction between

CRG (IRNA) for detecting compounds that modify the interaction between

CRG (IRNA) for detecting compounds that modify the interaction between

CRG (IRNA) for detecting compounds that modify the interaction between

CRG (IRNA) for detecting compounds that modify the interaction between

CRG (IRNA) for detecting compounds that modify the compound Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory; Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic; Leptin receptor related protein; Ob-RGRP; leptin receptor; Pleptin-related disorders; osteoporosis; calcification; obesity; diabetes; anorexia; sexual maturity disorder; haematopoiesis; anglogenesis; thrombus formation; immunity; inflammation; fetal development; cancer; New oligonucleotides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and angiogenesis. triethyleneglycol spacer" (AVET ) AVENTIS PHARMA SA. (INRM ) INSERM INST NAT SANTE & RECH MEDICALE. /mod\_base= OTHER /note= "Optional thioester" "mod\_base= OTHER
'note= "2' O-methylation"
8. .22 O-methylation" OB-RGRP antisense oligonucleotide, AS 11. Ξ. Ξ Location/Qualifiers Uhlmann Example 6; Fig 1; 104pp; French. /mod\_base= OTHER /note= "2' O-metl OTHER BP. 10-FEB-2003; 2003FR-00001543. 10-FEB-2003; 2003FR-00001543. /mod\_base= (/note= "3' ADR27689 standard; DNA; 22 Б ಗ \*tag= c Jockers R, Couturier C, Д (first entry) /\*tag= \*tag= \*tag= WPI; 2004-595751/58. modified base antisense; ss modified base modified base modified base FR2850971-A1 13-AUG-2004. 04-NOV-2004 Synthetic. ADR27689; 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for identifying compounds (1) that are active against loss or gain of weight or diabetes in humans or animals. The method comprises measuring the effect of a test compound on the expression of at least one of the genes LEPROTL1 (leptin receptor overlapping transcript-like 1) or OB-RGRP (leptin receptor gene related protein). Alternatively the method comprises measuring the effect of the compound on intracellular transport as far as the cell membrane (CM), the presence at CM, and internalisation from the membrane of proteins (X) encoded by the specified genes, or parts of them. Compounds of the invention are used to treat or prevent obesity, weight loss and diabetes.
                calcification; obesity; diabetes; anorexia; disorders of sexual maturity, hematopolosess, anglogenesis, thrombus formation, regulation of immunity and inflammation, fetal development and cancer. The present OB-RGRP antisense oligonucleotide was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antidiabetic; anorectic; weight loss; weight gain; diabetes; LEPROTL1; leptin receptor overlapping transcript-like 1; OB-RGRP; leptin receptor gene related protein; intracellular transport; obesity;
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            current sequence represents a primer for the amplification of OB-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying compounds useful for treating loss or gain of weight or diabetes, from their ability to modulate expression or transport of proteins related to the leptin receptor.
osteoporosis (or other conditions involving reduced bone density);
                                                                                                                                                                            ö
                                                                                                                                       DB 1; Length 22; 7.9;
                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21 BP; 4 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Reverse primer for amplifying OB-RGRP, seq id 15.
                                                                                                      Sequence 22 BP; 7 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Belouzard
                                                                                                                         2.0%; Scc.
v 100.0%; Pred. No. .
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; SEQ ID NO 15; 38pp; French.
                                                                                                                                                                                                             285
                                                                                                                                                                                                                                 22 CCTGTCGGGAACTGGCATATTT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seron K,
                                                                                                                                                                                                             264 CCTGTCGGGAACTGGCATATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CNRS ) CNRS CENT NAT RECH SCI
                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-2003; 2003FR-00002931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAR-2003; 2003FR-00002931
                                                                                                                                                                                                                                                                                                                    .352/c
ADT71352 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                       Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rouille Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-671009/66.
                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR; primer; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FR2852397-A1
                                                                                                                                                                                                                                                                                                                                                                                                         16-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bailleul B,
                                                                                                                                                                                                                                                                                                                                                                        ADT71352;
                                                                                                                                                                                                                                                                                                                    ADT71352/
                                                                                                                                                                                                                                                                                                    RESULT 5
SKSSSXX
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific acid probes is useful in in situ hybridisation, in Southern, Northern or dotones to hybridisation of any gene, in mapping the 5' termini of mRNA melecules by containing of additional subclones containing segments of DNA that have been containing segments of DNA that have been contained in electronic format directly from ucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from the necessarial contains and the microarray. Note: The sequence of the contains of any sequence of the contains of any sequence of the contains of any sequence of the sequence of the contains patent can also be obtained in electronic format directly and recontains of any sequence. The sequence of the contains and the microarray. Note: The sequence of the contains and the microarray of the contains patent can also be 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapa
                                                                                                                                                                                                                                                                                                                                                                  EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 20.2; DB 1; Length 25; 8.0%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                    Human microarray DNA oligonuclectide SEQ ID NO 110791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25 BP; 3 A; 9 C; 4 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 110791; 9pp; English.
353 AAATGGGGAGCCTGCGGCCTT 373
                            AAATGGGGAGCCTGCGGCCTT
                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-2002; 2002US-00098263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-2001; 2001US-0276759P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.04;
                                                                                                                                                                    ACK10810 standard; DNA; 25
                                                                                                                                                                                                                                                                   14-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-567953/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003104410-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ното варіелв.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mittmann MP;
                                           21
                                                                                                                                                                                                                     ACK10810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                   RESULT 6
ACK10810
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179 TTCGTCCTGATTTTCCACGCCATCT 203

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Gaps

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0; Indels

DB 1; Length 21; 12;

Query Match 1.9%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 12; Matches 21; Conservative 0; Mismatches

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08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001
                                                  Homo sapiens
                                                                      WO9805792-A2
                                                                                                                                             15-APR-1997;
                                                                                                                                                                                      Akerblom IE;
                                                                                          12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK95054;
                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAK95054
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                                                                                                                                                                                                                                                                                                                                                                                                                     PCR primers AAV17684-87 are used in a reverse transciptase PCR (RT-PCR) reaction to amplify DNA encoding human leptin receptor gene-related protein (LRGRP). The CDNA sequence was first isolated in Incyte clone 492703 from the NHV2 cell line CDNA library through a computer generated search for amino acid sequence alignments. The LRGRP protein has some homology to the membrane associated proteins of Caenorhabditis elegans of RT C308. The agonists of LRGRP can be used to treat metabolic, reproductive and developmental disorders, whilst antagonists of LRGRP can be used for treatment of cancer or connective tissue disorders e.g. rheumatoid arthritis and Sjogren's syndrome. Polymucleolides which hybridise to the LRGRP nucleotide sequence can be used for detection
                                                                                                                                      Human; leptin receptor gene-related protein; LRGRP; Incyte clone 492703; treatment; cancer; connective tissue disorder; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primer P2 used to amplify a leptin receptor gene-related protein.
                                                                                                                                                                                                                                                                                                                                                            DNA encoding human leptin receptor gene-related protein - useful for, e.g. screening for drugs used in treatment of metabolic, reproductive, developmental and connective tissue disorders or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                 PCR primer P1 used to amplify a leptin receptor gene-related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 17;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;
     TICATCCIGAGITICCACGCCGICT 25
                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 36; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354 AATGGGGAGCCTGCGGCCTT 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                         BP.
                                                                                                                                                                                                                                                                      96US-00691071.
                                                                                                                                                                                                                                                  97WO-US014191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV17685 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                         AAV17684 standard; DNA; 20
                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                    (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                              WPI; 1998-145624/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUL-1998
                                                                                                                                                                                                                                                                      01-AUG-1996;
15-APR-1997;
                                                                                                                                                                                                                                                  25-JUL-1997;
                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                           WO9805792-A2
                                                                                                                                                                                                                                                                                                                            Akerblom IE;
                                                                                                                                                                                                                               12-FEB-1998.
                                                                                                    10-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                            Synthetic
                                                                                AAV17684;
                                      RESULT 7
AAV17684/c
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EXEXEXE
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PCR primers AAV17684-87 are used in a reverse transciptase PCR (RT-PCR) reaction to amplify DNA encoding human leptin receptor gene-related protein (LRGRP). The CDNA sequence was first isolated in Incyte clone 492703 from the NHTZ cell line CDNA library through a computer generated search for amino acid sequence alignments. The LRGRP protein has some homology to the membrane associated proteins of Canorhabditis alone one one used to treat metabolic, reproductive and developmental disorders, whilst antagonists of LRGRP can be used for treatment of cancer or connective tissue disorders e.g. rheumatoid archritis and Sjogren's syndrome. Polynucleotides which hybridise to the LRGRP nucleotide sequence can be used for detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; full length cDNA; cDNA synthesis; oligo-capping; PCR primer; ss.
Human; leptin receptor gene-related protein; LRGRP; Incyte clone 492703;
treatment; cancer; connective tissue disorder; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding human leptin receptor gene-related protein - useful for, e.g. screening for drugs used in treatment of metabolic, reproductive, developmental and connective tissue disorders or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 17;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA clone-specific primer, SEQ ID NO: 4299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 3 A; 9 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 36; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCAGCCGCGCCCCAGTTC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 AGCAGCCGCGCCCCAGTTC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                054/c
AAK95054 standard; DNA; 20 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99JP-00194486.
                                                                                                                                                                                                                                                                                                                               97WO-US014191
                                                                                                                                                                                                                                                                                                                                                                                          96US-00691071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-145624/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1130094-A2
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Example 18; SEQ ID NO 4299; 1340pp; English.
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                                                                                                                                                                                                                                                                                                        RESULT 11
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                                                                                                                                                                                                 clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' - and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a primer used to amplify a human cDNA clone provided in the invention
                                                                                                                          830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone specific PCR primer to amplify human full length cDNA SeqID 4299.
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New oligonucleotide primers (830 cDNAs) useful for synthesizing full
length human cDNAs.
                                                                           Ξ
                                                                                                                                                                                       synthesising full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawai Y;
T, Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human, medicine; signal transduction; glycoprotein, transcription;
oligo-capping method; ss; PCR; primer.
                                                               hii S, Kawai Y,
Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                       Score 20; DB 1; Length 20;
Pred. No. 17;
                                                                                                                                                               Example 18; Page 129; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ishii S,
S, Otsuki
                                                               Ishii S,
                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 2 A; 3 C; 6 G; 9 T; 0 U; 0 Other;
                                                              Hayashi K, Isl
K, Kojima S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ai T, Hayashi K, Is
Nagai K, Kojima S,
                                                                                                                                                                                                                                                                                                                                            The invention relates to primers for
                                                                           Wakamatsu A, Sugiyama T, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                        1029 GAGAAGTAAACATCACACCC 1048
                                                              Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                        20 GAGAAGTAAACATCACACCC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nishikawa T, Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000EP-00114089.
11-JAN-2000; 2000JP-00118774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUL-2000; 2003EP-00025638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-00194486
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                       (HELI-) HELIX RES INST
                                                              Nishikawa T,
                                                                                                 WPI; 2001-524255/58.
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
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                                                                                  glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This oligonucleotide sequence is a human clone specific PCR primer used in an exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic; Leptin receptor related protein; OB-RGRP; leptin receptor; leptin receptor; leptin-related disorders; osteoporosis; calcification; obesity; diabetes; anorexia; sexual maturity disorder; haematopolesis; anglogenesis; thrombus formation; immunity; inflammation; fetal development; cancer;
                     it refers
This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refer to secretory or membrane proteins that are potential therapeutic agents/target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction,
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                      1.0%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 17;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= d
/mod_base= OTHER
/note= "3' triethyleneglycol spacer"
                                                                                                                                                                                             Sequence 20 BP; 2 A; 3 C; 6 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AVET ) AVENTIS PHARMA SA.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Optional thioester"
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/*tag= a
/mod_base= OTHER
/note= "2' O-methylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= c
/mod_base= OTHER
/note= "2' O-methylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OB-RGRP antisense oligonucleotide, AS 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                1029 GAGAAGTAAACATCACACCC 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .20
/*tag= b
/mod base= OTHER
                                                                                                                                                                                                                                                                                                                                ч
                                                                                                                                                                                                                                                                                                                    20 GAGAAGTAAACATCACACCC
                                                                                                                                                                                                                                                                                                                                                                                                10-FEB-2003; 2003FR-00001543
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                                                                                                                                                                                                                                                                20; Conservative
                                                                                                                                                                                                                          Query Match
Best Local Similarity
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The present invention relates to a leptin receptor related protein (OB-RGRP) antisense oligonucleotide (ON; ADRZ7653), that hybridises rGRP) antisense oligonucleotide (ON; ADRZ7653), that hybridises preditically with and inhibits the expression of ADRZ7652. The ON promotes expression of leptin receptors on the cell surface and may critathylaneglycol residue at the 3'-end. Also claimed are interfering RNA triathylaneglycol residue at the 3'-end. Also claimed are interfering RNA (IRNA) of 15-25 nt that hybridize specifically with ADRZ7672, and inhibit companies of 15-25 nt that hybridize specifically with ADRZ7672, and inhibit companies of 15-25 nt that hybridize specifically with ADRZ7672, and inhibit confined are fusion proteins (FPS) and their expression of OB-RGRP. Also claimed are fusion proteins (FPS) and their coding sequences comprising OB-RGRP or NY047 (thought to be a member of coding sequences comprising OB-RGRP or NY047) (thought to be a member of the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that it is a donor or acceptor of energy e.g. luciferase or yellow fluorescent or the leptin receptor and OB-RGRP proteins, which can be used to prevent or the leptin receptor and OB-RGRP proteins, which can be used to prevent or creat leptin-related disorders. On also related disorders, e.g. osteoporosis (or other conditions involving reduced bone density);

calcification, obseity, diabetes, anorexia; disorders of sexual maturity, and inflammation, fetal development and cancer. The present OB-RGRP antisense oligonucleotide was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory; Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic; Leptin receptor related protein; OB-RGRP; leptin receptor related protein; OS-RGRP; leptin receptor; Desity; antiportarion; obesity; diabetes; anorexia; sexual maturity disorder; haematopoiesis; angiogenesis; thrombus formation; immunity; inflammation; fetal development; cancer;
                                                                      New oligonuclectides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20; DB 1; Length 20;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Scc., No. 1.0.0%; Pred. No. 1...
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/note= "Optional thioester"
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/mod_base= OTHER
/note= "2' O-methylation"
16. 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OB-RGRP antisense oligonucleotide, AS 02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
Uhlmann E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 CGGGAACTGGCATATTTCTT 1
                                                                                                                                                                                 Example 6; Fig 1; 104pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1680/c
ADR27680 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 CGGGAACTGGCATATTTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ...20
*tag=
Couturier C,
                                        WPI; 2004-595751/58
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modified_base
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                                                                                                                                               angiogenesis.
    Jockers R,
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Gaps

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The present invention relates to a leptin receptor related protein (OB-RGRP) antisense oligomucleotide (ON; ADR27653), that hybridises CC RGRP) antisense oligomucleotide (ON; ADR27653), that hybridises pecifically with and inhibits the expression of ADR27652. The ON contain phosphorothioate bonds; 2'-on-dethyl nucleotides and/or a criterhyleneglycol residue at the 3'-end. Also claimed are interfering RNA triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA (IRNA) of 15-25 nt that hybridize specifically with ADR2767, and inhibit companies sequences comprising OB-RGRP or MY047 (thought to be a member of coding sequences comprising OB-RGRP or MY047 (thought to be a member of the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that the OB-RGRP family, shares 68% homology with OB-RGRP), and observed to receptor and OB-RGRP proteins, which can be used to prevent or the leptin receptor and OB-RGRP proteins, which can be used to prevent or treat leptin-related disorders OF, also osteoporosis (or other conditions involving reduced bone density), calcification; obesity, diabetes; anorexia; disorders of sexual maturity, had and inflammation, feed domestic of a protein of a protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New oligonucleotides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, anorexia, hematopolesis, and
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Pred. No. 17;
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                                                                                                       OTHER triethyleneglycol spacer"
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(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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                                   O-methylation"
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                  OTHER
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Best Local Similarity
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Pred. No. 17;

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1.8%; Score 20; DB 1; Length 20;
Query Match
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Leptin receptor related protein; OB-RGRP; leptin receptor; leptin receptor; leptin receptor; leptin receptor; leptin-related disorders; osteoporosis; calcification; obesity; diabetes; anorexia; sexual maturity disorder; haematopoiesis; angiogenesis; thrombus formation; immunity; inflammation; fetal development; cancer; antisense; ss. Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;

Synthetic

Location/Qualifiers Ω Key modified\_base

'note= "Optional thioester" mod\_base= OTHER .... \*tag≃ modified base

O-methylation" mod\_base= OTHER 2 ಥ .20 note= modified\_base

O-methylation" OTHER 20 /\*tag= د تمط أممة /\*tag= c /mod\_base= ( /note= "2' ( modified\_base

triethyleneglycol spacer"

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FR2850971-A1

13-AUG-2004

10-FEB-2003; 2003FR-00001543

10-FEB-2003; 2003FR-00001543

(INRM ) INSERM INST NAT SANTE & RECH MEDICALE. (AVET ) AVENTIS PHARMA SA

Uhlmann E; Couturier C, Jockers R,

WPI; 2004-595751/58

oligonucleotides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and angiogenesis. New

Example 6; Fig 1; 104pp; French.

The present invention relates to a leptin receptor related protein (OB-RGRP) antisense oligonuclectide (ON; ADR27653) that hybridises apecifically with and inhibits the expression of ADR27652. The ON promotes expression of leptin receptors on the cell surface and may contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a rise state at the 3'-end. Also claimed are interfering RNA (IRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit expression of OB-RGRP. Also claimed are fusion proteins (FPS) and their coding sequences comprising OB-RGRP or MY047 (thought to be a member of the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that is a donor or acceptor of energy e.g. luciferase or yellow fluorescent protein (YFP) for detecting compounds that modify the interaction between the leptin receptor and OB-RGRP proteins, which can be used to prevent or treat leptin-related disorders. Proteins in the leptin receptor and OB-RGRP proteins, which can be used to prevent or treat leptin-related disorders of sexual maturity, calcification; obseity; diabetes; anorexia; disorders of sexual maturity, and the latest of the maturity of the latest o The present OB-RGRP antisense oligonucleotide was used to illustrate the invention fetal development and cancer. inflammation,

Sequence 20 BP; 7 A; 7 C; 2 G; 4 T; 0 U; 0 Other;

The present invention relates to a leptin receptor related protein (OB-RGRP) antisense oligomucleotide (ON; ADR27653), that hybridises gpecifically with and inhibits the expression of ADR27652. The ON promotes expression of ADR27652. The ON promotes expression of Leptin receptors on the cell surface and may contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA (IRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit expression of OB-RGRP. Also claimed are fusion proteins (FPS) and their coding sequences comprising OB-RGRP or WY047 (thought to be a member of the OB-RGRP family, shares 68thomology with OB-RGRP), and a protein that is a donor or acceptor of energy e.g. luciferase or yellow fluorescent protein (YPP) for detecting compounds that modify the interaction between the leptin receptor and OB-RGRP proteins, which can be used to prevent or treat leptin-related disorders. On, also related disorders, e.g. used for prevention and/or treatment of leptin-related disorders. Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory; Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic; Leptin receptor related protein; OB-RGRP; leptin receptor; leptin-related disorders; osteoporosis; calcification; obesity; diabetes; anorexia; sexual maturity disorder; heamatopoises; angiogenesis; thrombus formation; immunity; inflammation; fetal development; cancer; Gaps New oligonucleotides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and ö Indels ö (INRM ) INSERM INST NAT SANTE & RECH MEDICALE. OB-RGRP antisense oligonucleotide, SEQ ID 2. Mismatches 図; Claim 4; SEQ ID NO 2; 104pp; French Uhlmann 143 TGTGCCTTAGAGGATTATGG 162 100.0%; TGTGCCTTAGAGGATTATGG 1 Bb 10-FEB-2003; 2003FR-00001543. 10-FEB-2003; 2003FR-00001543 ADR27653 standard; DNA; 20 (first entry) (AVET ) AVENTIS PHARMA SA 20; Conservative Couturier C, WPI; 2004-595751/58. Best Local Similarity angiogenesis. 04-NOV-2004 FR2850971-A1 13-AUG-2004. Jockers R, Synthetic. 20 ADR27653; Matches ઠે 셤 

Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

and inflammation, fetal development and cancer

haematopoiesis, angiogenesis, thrombus

osteoporosis (or other conditions involving reduced bone density); calcification; obesity; diabetes; anorexia; disorders of sexual maturity, haematopoiesis, angiogenesis, thrombus formation, regulation of immunity

Query Match

DB 1; Length 20; 1.8%; Score 20;

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ADR27688,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a leptin receptor related protein (OBRGRP) antisense oligonuclectide (ON; ADR27653), that hybridises specifically with and inhibits the expression of ADR27652. The ON promotes expression of leptin receptors on the cell surface and may contain phosphorothicate bonds; 2'-0-methyl nuclectides and/or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New oligonucleotides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and angiogenesis.
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            Indels
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/note= "3' triethyleneglycol spacer"
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(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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note= "2' O-methylation"
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    Best Local
              Matches
                                                                           RESULT 15
                                                                                    ADR27682/
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triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA (IRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit expression of OB-RGRP. Also claimed are fusion proteins (FPS) and their coding sequences comprising OB-RGRP or MYO47 (thought to be a member of the OB-RGRP family, shares 68* homology with OB-RGRP), and a protein that the OB-RGRP family, shares 68* homology with OB-RGRP), and a protein that is a donor or acceptor of energy e.g. ludiferase or yellow fluorescent protein (YFP) for detecting compounds that modify the interaction between the leptin receptor and OB-RGRP proteins, which can be used to prevent or treat leptin-related disorders or used for prevention and/or treatment of leptin-related disorders, e.g. osteoporosis (or other conditions involving reduced bone density); calcification; obesity; diabetes, anoreaxis; disorders of sexual maturity, and inflammation, fetal development and cancer. The present OB-RGRP and inflammation, fetal development and cancer. The present OB-RGRP antisense oligonucleotide was used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADR27688;
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ADR27687;
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ADR27687/c
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  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   요
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                                                                                                                                                                                                                                                                                The present invention relates to a leptin receptor related protein (OB-RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises respecifically with and inhibits the expression of ADR27652. The ON promotes expression of leptin receptors on the cell surface and may contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a ritethylaneslycol residue at the 3'-end. Also claimed are interfering RNA (IRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit expression of OB-RGRP. Also claimed are fusion proteins (FPB) and their coping sequences comprising OB-RGRP or MV047 (thought to be a member of the OB-RGRP family, shares 68 th homology with OB-RGRP), and a protein that is a donor or acceptor of energy eq. luciferase or yellow fluorescent protein (YFP) for detecting compounds that modify the interaction between treat leptin receptor and OB-RGRP proteins, which can be used to prevent or treat leptin related disorders. Ow, also related interfering RNA, are used for prevention and/or treatment of leptin-related disorders, e.g. cateoporosis (or other conditions involving reduced bone density, calculation; obesity; diabetes; anorexia; disorders of sexual maturity, hand interfering candinal development and cancer. The present OB-RGRP and inflammation fermation, regalation of immunity and interfering conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Osteopathic, Anorectic, Antidiabetic; Cytostatic; Antinflammatory; Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic; Leptin receptor related protein; OB-RGRP; leptin receptor; leptin-related disorders; osteoporosis; calcification; obseity; diabetes; anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombus formation; immunity; inflammation; fetal development; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                            New oligonucleotides that inhibit expression of the leptin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antisense oligonucleotide was used to illustrate the invention
                                                                                                                                                                    related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.8%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 17; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
(AVET ) AVENTIS PHARMA SA.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .20
/*tag= b
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/note= "Optional thioester"
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                                                              Couturier C, Uhlmann E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 TGCCTGTCGGGAACTGGCAT 281
                                                                                                                                                                                                                                                  Example 6; Fig 1; 104pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 TGCCTGTCGGGAACTGGCAT 1
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ADR27681 Btandard; DNA; 20 BP.
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                                                                                                                                                                                                         angiogenesis.
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                                                              Jockers R,
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The present invention relates to a leptin receptor related protein (OB-
KGRP) antisense oligonucleotide (ON; ADR27653), that hybridises

CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises

CC specifically with and inhibits the expression of ADR27652. The ON

CC promotes expression of leptin receptors on the cell surface and may

CC contain phosphorothioate bonds; 2'-on-ethyl nucleotides and/or a

CC (IRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit

CC (IRNA) of 15-25 nt that hybridize specifically with ADR27673, and inhibit

CC coding sequences comprising OB-RGRP or WY047 (thought to be a member of

CC coding sequences comprising OB-RGRP or WY047 (thought to be a member of

CC coding sequences comprising OB-RGRP or WY047 (thought to be a member of

CC coding sequences comprising OB-RGRP or WY047 (thought to be a member of

CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that

CS a donor or acceptor of energy e.g. luciferase or yellow fluorescent

CS the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that

CC treat leptin-related disorders. ON, also related interfering RNA, are

CC treat leptin-related disorders of sexual maturity,

CC calcification; obseity; diabetes, anorexis, disorders of sexual maturity,

CC aclicitation, eteral development and cancer. The present OB-RGRP

CC antisense oligonucleotide was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New oligonucleotides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
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                                                                                                                                                                                                                                                                                                            triethyleneglycol spacer"
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(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                 O-methylation"
                                                                                                                                                                        O-methylation"
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                                                                                                                                                                                                                                                                                   OTHER
/mod_base= OTHER
/note= "2' O-metl
                                                                                                                                       OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6; Fig 1; 104pp; French.
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Sequence 20 BP; 8 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

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Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic; Leptin receptor related protein; OB-KGRP; leptin receptor; leptin-related disorders; osteoporosis; calcification; obesity; diabetes; anorexia; sexual maturity disorder; haematopoiesis; angiogenesis; thrombus formation; immunity; inflammation; fetal development; cancer;
                                   Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            triethyleneglycol spacer"
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(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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OB-RGRP antisense oligonucleotide, AS 09.
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/*tag= c
/mod_base= OTHER
/note= "2' O-meth)
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mod base= OTHER
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                                                                                                                                                                                                                    Synthetic
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related protein, useful for treatment and prevention of e.g.
related protein, useful for treatment and prevention of e.g.
related protein, useful for treatment and prevention of e.g.
angiogenesis.

Example 6; Fig 1; 104pp; French.

Example 6; Fig 1; 104pp; French.

The present invention relates to a leptin receptor related protein (OBGRARP) antisense oligonuclectide (ON: ADR27653), that hybridises
ppecifically with and inhibits the expression of ADR27652. The ON
promotes expression of leptin receptors on the cell surface and may
contain phosphorothicate bonds; 2.0-enchyl nucleotides and/or a
triethyleneglycol residue at the 3'-end. Also claimed are innerfering RNA
triethyleneglycol residue at the 3'-end. Also claimed are innerfering (IRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
cypression of OB-RGRP. Also claimed are fusion proteins (FPS) and their
coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
the OB-RGRP family, shares 68\* homology with OB-RGRP), and a protein the leptin receptor of energy e.g. ludiferase or yellow fluorescent
protein (YPP) for detecting compounds that modify the interfering RNA, are
treat leptin-related disorders. ON, also related interfering RNA, are
treat leptin-related disorders. ON, also related disorders, e.g.
osteoporosis (or other conditions involving reduced bone density);
calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
and inflammation, fetal development and cancer. The present OB-RGRP
antisense oligonucleotide was used to illustrate the invention.

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                                                                                                                                                                                                                                                diabetes;
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                                                                                                                                                                                                                        Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic; Leptin receptor related protein; OB-RGRP; leptin receptor; leptin related disorders; osteoproseis; calcification; obesity; diabete anorexia; sexual maturity disorder; haematopoiesis; angiogenesis; thrombus formation; immunity; inflammation; fetal development; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New oligonucleotides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and anglogenesis.
                      Gaps
                                                                                                                                                                                                              Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
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DB 1; Length 20; 17;
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           triethyleneglycol spacer"
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(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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             Pred. No. 17;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           OTHER
O-methylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O-methylation"
                                                                                                                                                                                             OB-RGRP antisense oligonucleotide, AS 01.
   1.8%; Score 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Uhlmann E;
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                              161 GGCGTTTACTGGCCCTTATT 180
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                                                                                                                                                                                                                                                                                                                                                                mod_base= OTHER
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                                                            GGCGTTTACTGGCCCTTATT 1
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                          Conservative
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               Similarity
                                                                                                                                                                                                                                                                                        antisense; ss.
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                                                                                                                                                                                                                                                                                                            Synthetic.
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specifically with and inhibits the expression of ADR27652. The ON promotes expression of leptin receptors on the cell surface and may contain phosphorochioate bonds; 2'-O-methyl nucleotides and/or a triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit expression of OB-RGRP. Also claimed are fusion proteins (FPS) and their coding sequences comprising OB-RGRP or MYO47 (thought to be a member of the OB-RGRP family, shares 68* homology with OB-RGRP), and a protein that is a donor or acceptor of energy e.g. luciferase or yellow fluorescent protein (FPS) for detecting compounds that modify the interaction between the leptin receptor and OB-RGRP proteins, which can be used to prevent or treat leptin-related disorders. ON, also related interfering RNA, are used for prevention and/ob-rarement of leptin-related disorders, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                       osteoporosis (or other conditions involving reduced bone density); calcification; obesity; diabetes; anorexia; disorders of sexual maturity, haematopoiesis, anglogenesis, thrombus formation, regulation of immunity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antisense oligonucleotide was used to illustrate the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fetal development and cancer.
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'note= "Optional thioester"
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/mod_base= OTHER
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/note= "2' (
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AC ADR2765
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DD 09-RGHE
DD 09-RGHE
DD 09-RGHE
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Matches
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The present invention relates to a leptin receptor related protein (OB-RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises gpecifically with and inhibits the expression of ADR27652. The ON promotes expression of leptin receptors on the cell surface and may contain phosphorothioate bonds; 2'-one thy luncleotides and/or a contain phosphorothioate bonds; 2'-one the OB-RGRP, and an interfering RNA (IRNA) of 15-25 in that hybridize specifically with ADR27672, and inhibit expression of OB-RGRP. Also claimed are fusion proteins (FPB) and thair colling sequences comprising OB-RGRP or MY047 (thought to be a member of the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that contain the contain of OB-RGRP proteins, which can be used to prevent or treat leptin-related disorders on allowed the conditions involving reduced bone density, are calcification; obesity, diabetes; anorexia; disorders of sexual maturity, chammatopolesis, anglogenesis, thrombus formation, regulation of immunity and inflammation, fetal development and cancer. The present OB-RGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Osteopathic, Anorectic, Antidiabetic; Cytostatic; Antinflammatory; Immunomodulatory; Anabolic; Endocrine; Antianemic; Antianglogenic; Leptin receptor related protein; OB-RGRP; leptin receptor; leptin-related disorders; osteoporossis; calcification; obesity; diabetes; anorexia; sexual maturity disorder; haematopoiesis; angiogenesis; thrombus formation; immunity; inflammation; fetal development; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                   New oligonucleotides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
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100.0%; Pred. No. 17;
ive 0; Mismatches 0; Indels
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                                                         (AVET ) AVENTIS PHARMA SA.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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                                                                                                                    Couturier C, Uhlmann E;
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ID ADR27683 standard; DNA; 20 BP.
                   10-FEB-2003; 2003FR-00001543
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OB-RGRP antisense oligonucleotide, AS 08.
             04-NOV-2004 (first entry)
The present invention relates to a leptin receptor related protein (OB-RRP) antiennse oligonuclectide (ON; ADR27653), that hybridises graps antiennse oligonuclectide (ON; ADR27653), that hybridises promotes expression of leptin receptors on the cell surface and may contain phosphorothicate bonds; 2.0-methyl nuclectides and/or a contain phosphorothicate bonds; 2.0-methyl nuclectides and/or a contain phosphorothicate bonds; 2.0-methyl nuclectides and/or a contain phosphorothicate specifically with ADR27672, and inhibit expression of OB-RGRP. Also claimed are fusion proteins (FPB) and inhibit expression of OB-RGRP and OB-RGRP of Claimed are fusion proteins (FPB) and a protein that is a donor or acceptor of energy e.g. luciferase or yellow fluorescent protein (FPP) for detecting compounds that modify the interaction between the leptin receptor and OB-RGRP proteins, which can be used to prevent or treat leptin-related disorders. ON, also related disorders, e.g. creat leptin-related disorders. ON, also related blooders, e.g. calcification; obesity; diabetes; anorexia; disorders of sexual maturity, hemantopolesis, angiogenesis, thrombus formation, regulation of immunity continued the context of the present one familiammation, feel development and cancer. The present OB-RGRP protein that the mation of immunity and cancer.
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(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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      'note= "Optional thioester"
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ADR27686 standard; DNA; 20 BP

ADR27686/c

RESULT 22

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ADR27686

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The present invention relates to a leptin receptor related protein (OBCRGRP) antisense oligonucleotide (ON; ADR27653), that hybridises

CC specifically with and inhibits the expression of ADR27652. The ON

CD promotes expression of leptin receptors on the cell surface and may

CC promotes expression of leptin receptors on the cell surface and may

CC contain phosphorothioate bonds; 2'-one thyl nucleotides and/or a

CC (IRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit

CC (IRNA) of 16-25 nt that hybridize specifically with ADR27672, and inhibit

CC coding sequences comprising OB-RGRP or WY047 (thought to be a member of

CC chops sequences comprising OB-RGRP or Juciferase or yellow fluorescent

CC coding sequences comprising OB-RGRP or Juciferase or yellow fluorescent

CC the OB-RGRP for detecting compounds that modify the interaction between

CC treat leptin receptor and OB-RGRP proteins, which can be used to prevent or

CC treat leptin receptor and OB-RGRP proteins, which can be used to prevent or

CC treat leptin related disorders ON, also related interfering RNA, are

CC used for prevention and/or treatment of leptin-related disorders, or

CC used for prevention and/or treatment of leptin-related disorders,

CC used for prevention and/or treatment of leptin-related disorders,

CC calcification; obesity, diabetes; anorexia, disorders of sexual maturity,

CC harmal popularity in angiogenesis, thrombus formation, regulation of immunity
Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory; Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic; Leptin receptor related protein; Ob-RGRP; leptin receptor related disorders; osteoporosis; calcification; obesity; diabetes; anorexia; sexual maturity disorder; haematopoiesis; anglogenesis; thrombus formation; immunity; inflammation; fetal development; cancer;
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(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                                                                                                                             Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic; Leptin receptor related protein; OB-RGRP; leptin receptor; leptin-related disorders; osteoporosis; calcification; obesity; diabetes; anorexia; sexual maturity disorder; haematopoiesis; angiogenesis; thrombus formation; immunity; inflammation; fetal development; cancer;
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New oligonucleotides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
and inflammation, fetal development and cancer. The present OB-RGRP
                                                                                                                                                                                                                                                    Osteopathic, Anorectic, Antidiabetic, Cytostatic, Antiinflammatory;
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          antisense oligonucleotide was used to illustrate the invention
                                                  DB 1; Length 20;
17;
                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              triethyleneglycol spacer"
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                             Sequence 20 BP; 7 A; 7 C; 2 G; 4 T; 0 U; 0 Other;
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                                                 Query Match 1.8%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 17; Matches 20; Conservative 0; Mismatches
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/note= "Optional thioester"
                                                                                                                                                                                                                                OB-RGRP antisense oligonucleotide, AS 06.
                                                                                                                                                                                                                                                                                                                                                                                                                                            O-methylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O-methylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Uhlmann B;
                                                                                                                                                                                                                                                                                                                                                          cocation/Qualifiers
                                                                                          152 GAGGATTATGGCGTTTACTG 171
                                                                                                                                                                                                                                                                                                                                                                                         OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER
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                                                                                                        20 GAGGATTATGCCGTTTACTG 1
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                                                                                                                                                                 ADR27684 standard; DNA; 20 BP
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                                                                                                                                                                                                                                                                                                                   antisense;
                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                       ADR27684;
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The present invention relates to a leptin receptor related protein (OBROBE) antisense oligomucleotide (ON; ADR27653), that hybridises appecifically with and inhibits the expression of ADR27652. The ON promotes expression of Leptin receptors on the cell surface and may contain phosphorothicate bonds; 2'O-methyl nucleotides and/or a contain phosphorothicate bonds; 2'O-methyl nucleotides and/or a propersion of OB-RGRP. Also claimed are interfering RNA (IRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit expression of OB-RGRP. Also claimed are fusion proteins (FPP) and their coding sequences comprising OB-RGRP or WY047 (thought to be a member of the OB-RGRP family, shares 68 homology with OB-RGRP), and a protein that is a donor or acceptor of energy e.g. luciferase or yellow fluorescent protein (FPP) for detecting compounds that modify the interaction between the leptin receptor and OB-RGRP proteins, which can be used to prevent treat leptin related disorders. ON, also related interfering RNA, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leptin-related disorders; osteoporosis; calcification; obesity; diabetes; anorexia; sexual maturity disorder; haematopoiesis; angiogenesis; thrombus formation; immunity; inflammation; fetal development; cancer;
                                                                                                                                                                                                                                                                                                                                    used for prevention and/or treatment of leptin-related disorders, e.g. osteoporosis (or other conditions involving reduced bone density); calcification; obesity, disbetes; anorexia; disorders of sexual maturity, haematopolesis, angiogenesis, thrombus formation, regulation of immunity and inflammation, fetal development and cancer. The present OB-RGRP antisense oligonucleotide was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory; Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic; Leptin receptor related protein; OB-RGRP; leptin receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 8 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O-methylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTATGCTGGGATGTGCCTT
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The present invention relates to a leptin receptor related protein (OB-RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises content antisense oligonucleotide (ON; ADR27653), that hybridises content and inhibits the expression of ADR27652. The ON promotes expression of leptin receptors on the cell surface and may contain phosphorothioate bonds; 2'-o-methyl nucleotides and/or a crietchyleneglycol residue at the 3'-end. Also claimed are interfering RNA triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit content of the OB-RGRP place of the OB-RGRP place of the OB-RGRP place of the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that is a donor or acceptor of energy e.g. luciferase or yellow fluorescent correct leptin receptor of energy e.g. luciferase or yellow fluorescent creat leptin-related disorders. ON, also related interfering RNA, are created for prevent or the leptin receptor and OB-RGRP proteins, which can be used to prevent or creat leptin-related disorders. ON, also related interfering RNA, are created for other conditions involving reduced bone density).

Cued for prevention and/or treatment of leptin-related disorders, e.g. osteoporosis (or other conditions involving reduced bone density), chaematopoiesis, angiogenesis, thrombus formation, regulation of immunity and inflammation, fetal development and cancer. The present OB-RGRP cand inflammation, fetal development and cancer. The present on.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                            New oligonucleotides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
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100.0%; Pred. No. 17;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                 Couturier C, Uhlmann E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   370 CCTTGTGTTGGCAGGCAATG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Fig 1; 104pp; French.
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                                                    10-FEB-2003; 2003FR-00001543
                                                                                                              10-FEB-2003; 2003FR-00001543
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                                                                                                                                                                            (AVET ) AVENTIS PHARMA SA
                                                                                                                                                                                                                                                                                                                                  WPI; 2004-595751/58
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 angiogenesis.
13-AUG-2004
                                                                                                                                                                                                                                                                          Jockers R,
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Human; ss; PCR; embryonic stem cell; differentiation; primer; transplantation; heart muscle damage; kidney tissue degeneration; skin damage; liver degeneration; brain degeneration; spinal cord injury; anaemia; immunodeficiency; adrenal degeneration; biomedical engineering human development.

01-AUG-2000; 2000US-0222160P. 09-FEB-2001; 2001US-0267559P.

(YISS ) YISSUM RES & DEV CO.

WPI; 2002-180078/23.

Benvenisty N;

31-JUL-2001; 2001WO-IB001719.

WO200210347-A2.

07-FEB-2002.

Homo sapiens

Human Parathyroid hormone 3' RT-PCR primer.

(first entry)

21-MAY-2002

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ABK39905;

BP.

ABK39905 standard; DNA; 25

RESULT 26 ABK39905,

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The invention relates to a method for identifying compounds (I) that are active against loss or gain of weight or diabetes in humans or animals. The method comprises measuring the effect of a test compound on the expression of at least one of the agaes LEBROTL1 (leptin receptor verlapping transcript-like 1) or OB-RGRP (leptin receptor gene related protein). Alternatively the method comprises measuring the effect of the protein). Alternatively the method comprises measuring the effect of the presence at CM, and internalisation from the membrane of proteins (X) encoded by the specified genes, or parts of them. Compounds of the invention are used to treat or prevent obesity, weight loss and diabetes. The current sequence represents a primer for the amplification of OB-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                          Identifying compounds useful for treating loss or gain of weight or diabetes, from their ability to modulate expression or transport of proteins related to the leptin receptor.
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Pred. No. 17;
0; Mismatches 0; Indels
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                                                                                                          Belouzard S;
                                                                                                                                                                                                                                                        Example 3; SEQ ID NO 14; 38pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Scc.
100.0%; Pre
                                                                                                            Seron K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 AGCAGCCGCGGCCCCAGTTC 63
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                                                                         (CNRS ) CNRS CENT NAT RECH SCI
10-MAR-2003; 2003FR-00002931.
                                        10-MAR-2003; 2003FR-00002931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 20; Conservative
                                                                                                              Bailleul B, Rouille Y,
                                                                                                                                                   WPI; 2004-671009/66.
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WPI; 1997-435085/40.

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The invention relates to mapping a pathway of differentiation of a population of embryonic cells, comprising (a) selecting: (i) a set of gene expression products, where each gene expression products, in the set of a characteristic of a cell type that has undergone differentiation, so that several differentiated cell types are represented in the set and (i) an exogenous factor in the set and caracterising the exogenous factor to the population of embryonic cells, (c) characterising the effect of the exogenous factor on the differentiation products in the set and (d) mapping the pathway of differentiation of products in the set and (d) mapping the pathway of differentiation of cells. The method is useful for annipulating cells. The method is useful for annipulating differentiation of embryonic stem cells. The method is particularly useful for manipulating differentiation of human embryonic stem cells to provide a uniform population of precursors and differentiated cells of a desired lineage. The differentiated cells may be used for treating a medical condition in pathologies, (e.g. heart muscle damage, kidney tissue degeneration, skin and it muscles in the set and condition in the set and condition in the pathologies, (e.g. heart muscle damage, liver degeneration, skinners, it muscles in the pathologies of the pathologies o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
Mapping a pathway of or directing differentiation of human embryonic cells, comprises exposing cells to an exogenous factor and measuring gene expression products characteristic of the particular cell type or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anaemia, immunodeficiency, and adrenal degeneration) or as a component in
biomedical engineering as well as providing clues on early stages of
human development. The present sequence is an RT-PCR (reverse
transcriptase PCR) primer used to amplify the one member of the set of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ob receptor; obesity; leptin; rat; rodent; animal model; ligand; fatty; fa mutation; therapy; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression products from embryonic stem cells in the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human OB receptor 5' untranslated region PCR primer HOBR 1F-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 19.8; DB 1; Length 25; 91.3%; Pred. No. 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   794 CTTGGAGAGGCAGATAACGCTGA 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 CTTGGAGAGGCAGACAAAGCTGA 1
                                                                                                                                  5; 52pp; English
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96US-0013969P.
96GB-00008473.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-US002397
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Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MERI ) MERCK & CO INC.
                                                                                                                            Example 1; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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22-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9731015-A1
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                                                                                                                                            based on the 5' untranalated region (5'UTR) of the human ob receptor (OB R) sequence. Primers HOBR IF (AAT64981) and HOBR IF-2 were paired with rat OB-R specific reverse primers ROBR 11 (AAT64983) or ROBR 12 (AAT64984) to amplify the 5' end of rat OB-R CDNA. The largest product, obtained with HOBR IF-2 and ROBR11, was a 500 bp fragment that covered the 5' region and included a Met codon. Pull-length sequences for lean rat OB-R CDNA (AAT64961) and fatty (fa) mutant rat OB-R CDNA (AAT64061) and fatty (fa) mutant rat OB-R CDNA (AAT64062).
                               Rat wild-type and mutant ob receptor protein - useful in identification of new ligands for prevention and treatment of obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                This oligonuclectide comprises forward PCR primer HOBR 1F-2, which is
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
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                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 19; . 26;
                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human microarray DNA oligonucleotide SEQ ID NO 110792.
                                                                                                                                                                                                                                                                                                                     Sequence 19 BP; 3 A; 5 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                          1.7%; Score 19; DB
100.0%; Pred. No. 26;
iive 0; Mismatches
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                                                                                           Example 6; Page 13; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                        90 TCGTGGCATTATCCTTCAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAR-2002; 2002US-00098263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACK10811 standard; DNA; 25
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                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cross-species comparison.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-567953/53.
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nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, cor family members of a gene and a cross-species comparison. Bach of the concleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-plot hybridisation to identify or detect the sequence or specific blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening soments of DNA that have been for additional subclones containing segments of DNA that have been consolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence can directly data for this patent can also be obtained in electronic format directly from USPTO at sequence.html 88888888888888888888888

Sequence 25 BP; 4 A; 9 C; 4 G; 8 T; 0 U; 0 Other;

ö 1.7%; Score 18.6; DB 1; Length 25; 84.0%; Pred. No. 34; 4; Indels 0; Mismatches 179 TICGICCIGATITICCACGCCAICT 203 1 TTCATCCTGAGTATCCACGCCGTCT 25 Query Match Best Local Similarity 84.0° Matches 21, Conservative 8

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Gaps

ACI63081 standard; DNA; 25 BP. ACI63081; ACI63081/

13-OCT-2003 (first entry)

Human microarray DNA oligonucleotide SEQ ID NO 63072.

EST; 88; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.

Homo sapiens.

US2003104410-A1.

05-JUN-2003

LS-MAR-2002; 2002US-00098263.

16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC

Mittmann MP;

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 63072; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring 

gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dotbrook hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence.html ö Rat wild-type and mutant ob receptor protein - useful in identification of new ligands for prevention and treatment of obesity. Ob receptor; obesity; leptin; rat; rodent; animal model; ligand; fatty; fa mutation; therapy; PCR; primer; ss. Gaps ; Human OB receptor 5' untranslated region PCR primer HOBR 1F. DB 1; Length 25; Indels Sequence 25 BP; 8 A; 3 C; 5 G; 9 T; 0 U; 0 Other; 1.6%; Score 18.2; D 37.0%; Pred. No. 40; ive 0; Mismatches Hess JW, Caskey CT, Liu Q, Phillips MS; 271 GGAACTGGCATATTTCTTCACTA 293 Example 6; Page 13; 35pp; English. 24 GGAACTGACATATCTCTTCATTA 2 96US-0013969P. 97WO-US002397. 96US-0090405P 87.0%; AAT64981 standard; DNA; 18 (first entry) 1.6 Best Local Similarity 87.0 Matches 20; Conservative (MERI ) MERCK & CO INC. WPI; 1997-435085/40. Homo sapiens. 18-FEB-1997; 22-FEB-1996; 22-MAR-1996; 25-APR-1996; WO9731015-A1 23-FEB-1998 28-AUG-1997 Synthetic AAT64981; AAT64981 RESULT 8¥33333333333 à 셤

This oligonucleotide comprises forward PCR primer HOBR IF, which is based on the 5' untranslated region (5'UTR) of the human ob receptor (OB-R) sequence. Primers HOBR IF and HOBR IF-2 (AAT64982) were paired with rat ober specific reverse primers ROBR II (AAT64983) or ROBR 12 (AAT64984) to amplify the 5' end of rat OB-R CDNA. Full-length sequences for lean rat OB-R cDNA (AAT64961) and fatty (fa) mutant rat OB-R CDNA (AAT64062), which differ by only 1 bp, were subsequently obtained 1.6%; Score 18; DB 1; Length 18; 100.0%; Pred. No. 38; Sequence 18 BP; 2 A; 4 C; 6 G; 6 T; 0 U; 0 Other; Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the sense oligonucleotide -47 for the human WSX receptor cDNA. The receptor can be used to identify and purify ligands and activators. An anti-WSX receptor antibody can be used as an agonist to activate the WSX receptor antibody can be used as an agonist differentiation of a cell expressing the WSX receptor. It can also be used to decrease body weight and/or fat-depot weight and/or food intake in an obese mammal. WSX receptor ligands can be used to enhance proliferation or differentiation of lymphoid, myeloid or erythroid blood cell lineages. This is useful when a mammal, especially a human, is suffering from decreased blood cell levels, i.e. anaemia, caused by chemotherapy, radiation therapy or bone marrow transplantation therapy. It can also be used to reappulate blood cells in a mammal. The products can also be used to treat, e.g. neoplastic disorders, arteriosclerosis, Type II diabetes, polycystic ovarian disease, cardiovascular diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WSX receptor and related antibodies and ligands - used to develop products for diagnosis and therapy, e.g. for improving haematopoiesis or
                                                                                                                                                                                                                                                                                                      Human; WSX receptor; identification; purification; ligand; activator; antibody; agonist; proliferation; obesity; differentiation; anaemia; treatment; neoplasia; arteriosclerosis; Type II diabetes; polycystic ovarian disease; cardiovascular disease; osteoarthritis; dermatological disorder; hypertension; insulin reeistance; hypercholesterolaemia; hypertriglyceridaemia; cancer; cholelithiasis;
 Gaps
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 Indels
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 8; Fig 7; 219pp; English.
                                   131 CTTATGCTGGGATGTGCC 148
                                                                   1 crrarecrecearcrece 18
                                                                                                                                                              BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-00667197
                                                                                                                                                          AAT85600 standard; DNA; 18
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18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-372864/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                     sense; ss
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Matches
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The present sequence is the antisense oligonucleotide +85 for the human WSX receptor cDNA. The receptor can be used to identify and purify and agonist to activators. An anti-WSX receptor antibody can be used as an agonist to activate the WSX receptor, leading to enhanced proliferation of a cell expressing the WSX receptor. It can also be used to decrease body weight and/or fat-depot weight and/or food intake in an obese mammal. WSX receptor ligands can be used to enhance proliferation or differentiation of lymphoid, myeloid or erythroid blood cell inneages. This is useful when a mammal, especially a human, is suffering from decreased blood cell levels, i.e. anaemia, caused by chemotherapy, radiation therapy or bone marrow transplantation therapy. It can also be used to repopulate blood cells in a mammal. The products can also be used to repopulate blood cells in a mammal. The products can also be used to repopulate blood cells in a mammal. The products can also be used to react, e.g. neoplastic disorders, arteriosclerosis, Type II diabetes, polycystic ovarian disease, cardiovascular diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor and related antibodies and ligands - used to develop lucts for diagnosis and therapy, e.g. for improving haematopoiesis or
                                                                                                                                                                                                                                                                                                      Human; WSX receptor; identification; purification; ligand; activator; antibody; agonist; proliferation; obesity; differentiation; anaemia; treatment; neoplasia; arteriosclerosis; Type II diabbetes; polycystic ovarian disease; cardiovascular disease; osteoarthritis; dermatological diseater; hypertension; insulin resistance; hypercholesterolaemia; hypertriglyceridaemia; cancer; cholelithiasis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chiang NY, Kim KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches
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136 GCTGGGATGTGCCTTAGA 153
                                      18 GCTGGGATGTGCCTTAGA 1
                                                                                                                                           AAT85601 standard; DNA; 18 BP
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Rodrigues ML;
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20-JUN-1996;
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0; Mismatches

Best Local Similarity 100. Matches 18; Conservative

Query Match

1.6%; Score 18; DB 1; Length 18; 100.0%; Pred. No. 38;

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The invention relates to an isolated cytokine receptor which plays a role in enhancing proliferation and/or differentiation of haematopoietic clus, termed WSX receptor comprising the amino acid sequence of mature cells, termed WSX receptor comprising the amino acid sequence of mature ceptor is useful for identifying a molecule which binds to and/or receptor is useful for identifying a molecule which binds to and/or creeptor is useful for identifying a molecule which binds to and/or creeptor is useful for identifying a molecule which binds to and/or creeptor is useful for undargostic cells (such as anaemia, thrombocytopaenia, decrease in hematopoietic cells (such as anaemia, thrombocytopaenia, hypoplasia, disseminated intravascular coagulation, myelodysplasia, climmune clutoimmune) thrombocytopaenic purpura (ITP) and HIV induced ITP), comporting repopulation of mature blood cell lineages in cells having condergone chemo- or radiation of mature blood cell lineages in cells having to the way receptor is useful for producing anti-WSX receptor antibodies, cor affinity purification of WSX ligand, for competitive screening of for affinity purification of WSX ligand, for competitive screening of consecutal weight markers, as reagents for mechanism studies of the WSX receptor or its ligands, to study the role of the WSX receptor and WSX ligand in normal growth and development, as well as abnormal growth and development, as standards or controls in assays
                                                                                                                                                                                                                                                                                                       Human; ss; WSX receptor; antianaemic; haemostatic; anticoagulant; neuroprotective; immunosuppressive; dermatological; anti-HIV; probe; antiinflammatory; anorectic; antidiabetic; cytostatic; antitumour; cytokine receptor; proliferation; differentiation; haematopoietic cell; anaminist thrombocytopaenia; hypoplasia; myelodysplasia; HIV induced ITP; disseminated intravascular coagulation; immune thrombocytopaenic purpura; ITP; myeloproliferative thrombocytotic disease; thrombocytosis; inflammatory condition; iron deficiency; obesity; diabetes; mature blood cell lineage; chemotherapy; radiation therapy; bone marrow transplantation; metabolic disorder; anorexia; eteroid-induced truncalobesity; stem cell tumour; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated cytokine receptor, termed WSX receptor, useful for
treating diseases characterized by a decrease in hematopoietic cells e.g.
anemia, or for treating myeloproliferative thrombocytotic diseases.
                                                                                                                                                                                                                                                                        Human WSX receptor -47nt antisense oligonucleotide.
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GCTGGGATGTGCCTTAGA 153
                      1 GCTGGGATGTGCCTTAGA 18
                                                                                                                                                    BP.
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                                                                                                                                                  ACA75490 standard; DNA; 18
                                                                                                                                                                                                                                        07-JUL-2003 (first entry)
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08-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                  ACA75490;
    136
                                                                                                            RESULT 33
                                                                                                                                     ACA75490,
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The invention relates to an isolated cytokine receptor which plays a role in enhancing proliferation and/or differentiation of haematopoietic cells, termed Wax receptor comprising the amino acid sequence of mature human Wax receptor variant 13.2 or its extracellular domain. The Wax receptor is useful for identifying a molecule which binds to and/or activates the Wax receptor, as a disanositic tool for measuring serum elevels of endogenous Wax ligand, for treating diseases characterised by a decrease in hematopoietic cells (such as anaemia, thrombocytopaenia, hypoplasia, disseminated intravascular coagulation, myelodysplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; ss; WSX receptor; antianaemic; haemostatic; anticoagulant; neuroprotective; immunosupressive; dermatological; anti-HIV; probe; antiinflammatory; anorectic; antidiabetic; cytostatic; antitumour; cytokine receptor; proliferation; differentiation; haematopoietic cell; disseminated intravascular coagulation; immune thrombocytopaenic purpura; ITP; myeloproliferative thrombocytotic disease; thrombocytopaenic purpura; inflammatory condition; iron deficiency; obesity; diabetes; mature blood cell lineage; chemotherapy; radiation therapy; bone marrow transplantation; metabolic disorder; anorexia; steroid-induced truncalobesity; stem cell tumour; tumour;
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for WSX receptor. A composition comprising the WSX polypeptide is useful as an antagonist for reducing activation of endogenous WSX receptor, and to treat metabolic disorders (e.g. anorexia or steroid-induced truncalobesity), stem cell tumours and other tumours which express WSX receptor. The present sequence represents a human WSX receptor probe used
                                                                                                                                                                                                              Gaps
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                                                                                                                                                                           1.6%; Score 18; DB 1; Length 18; 00.0%; Pred. No. 38;
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                                                                                                                                     Sequence 18 BP; 5 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
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                                                                                                           in an antisense inhibition assay
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97US-00780562.
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                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 18; Conservative
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Annual (auconfinance) in Doubocytotic diseases, thrombocytosis from inflammatory conditions and in iron deficiency, obesity or diabetes, inflammatory conditions and in iron deficiency, obesity or diabetes, cenhancing repopulation of mature blood cell lineages in cells having undergone chemo- or radiation therapy or bone marrow transplantation therapy, or for promoting kidney, liver and lung growth and/or repair. The WSX receptor is useful for producing anti-WSX receptor antibodies, for affinity purification of WSX ligand, for competitive screening of potential agonists or antagonists for binding to the WSX receptor, as molecular weight markers, as reagents for molecular weight markers, as reagents for molecular weight markers, as reagents for molecular weight markers, or study, the role of the WSX receptor and WSX ingand in normal growth and development, as well as abnormal growth and development, e.g., in malignancies, or as standards or controls in assays for WSX receptor. A composition comprising the WSX polypeptide is useful as an antagonist for reducing activation of endogenous WSX receptor, and truncalobesity), stem cell tumours and other tumours which express WSX traceptor. The present sequence represents a human WSX receptor probe used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leptin receptor; WSX receptor; metabolic disorder; ITP; ss; antisense; anoraxia; eteroid-induced truncalobesity; stem cell tumnour; tumnour; DIC; anaemia; thrombocytopaenia; hypoplasia; myelodysplasia; HIV-induced ITP; disseminated intravascular coaqulation; immune thrombocytopaenic purpura; myelopycliferative thrombocytotic disease; thrombocytopis; inflammatory condition; iron deficiency; disabetes; renal failure; haemacopoietic cell proliferation; bone marrow transplantation.
(autoimmune) thrombocytopaenic purpura (ITP) and HIV induced ITP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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38;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                  in an antisense inhibition assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 GCTGGGATGTGCCTTAGA 153
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Best Local Similarity 100.
Matches 18; Conservative
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proteins), a partial mouse WSX receptor and its encoding DNA sequence. The WSX receptor is useful for preparing a composition for treating diseases mediated by WSX receptor, especially diseases characterised by a decrease in haematopoletic cells, e.g., anaemia, thrombocytopaenia, hypoplasia, disseminated intravascular coagulation (DIC), myelodysplasia, immune (autoimmune) thrombocytopaenic purpura (ITP), and HIV induced ITP. The WSX receptor is also useful for treating metabolic disorders such as anorexia, obesity (e.g. steroid-induced truncalobeaity) tumours such as stem cell tumours, inflammatory conditions, iron deficiency, diabetes, renal failure, conditions related to haematopoietic cell proliferation (such as in bone marrow transplantation and for promoting kidney, lung and liver growth and/or repair. An experiment was performed to show antisense inhibition of human and mouse WSX receptors. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated leptin/WSX receptor comprising a sequence of mature human WSX receptor variant 12.1. Also disclosed are the 13.2 and 6.4 WSX receptor variants (and DNA molecules encoding all 3 proteins), a partial mouse WSX receptor and its encoding DNA sequence. The WSX receptor is useful for preparing a composition for treating decrease in haematopoietic cells, e.g., anaemia, thrombocytopsenia, hypoplasia, disseminated intravascular coagulation (DIC), myelodysplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leptin receptor; WSX receptor; metabolic disorder; ITP; ss; anorexia; steroid-induced truncalobesity; stem cell tumour; tumour; DIC; anaemia; thrombocycopaenia; hypoplasia; myelodysplasia; HIV-induced ITP; disseminated intravascular coagulation; immune thrombocytopaenic purpura; myeloproliferative thrombocytoic disease; thrombocytosis; inflammatory condition; iron deficiency; diabetes; renal failure; haematopoletic cell proliferation; bone marrow transplantation.
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                                                                                                                                                                                                                                                                    sequence is an antisense oligonucleotide used in the experiment
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38;
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Pred. No.
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Matches 18; Conservative
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Human; WSX receptor; 88; weight reduction; obesity; bulimia; metabolic disorder; diabetes; insulin level reduction; food consumption; type II adult onset diabetes; infertility; hypercholesterolaemia; hyperlipidaemia; cardiovascular disease; arteriosclerosis; polycystic ovarian disease; osteoarthritis; dermatological disorder; insulin resistance; hypertriglycertidaemia; cancer; cholelithiasis; hypertension; kidney ailment; lung dysfunction; emphysema; haemorrhage; anaemia; thrombocytopenia; hypoplasia; cachexia; anorexia; appetite loss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to agonist antibodies which specifically bind to the human WSX receptor. The agonist antibodies are useful for activating the WSX receptor and for enhancing proliferation or differentiation of a cell comprising the WSX receptor, by exposing the cell to an antibody. The antibodies are also useful for reducing weight, specifically in the
immune (autoimmune) thrombocytopaenic purpura (ITP), and HIV induced ITP. The WSX receptor is also useful for treating metabolic disorders such as such exanorexia, obesity (e.g. steroid-induced truncalobesity) tumours such as stem cell tumours, inflammatory conditions, iron deficiency, diabetes, renal failure, conditions related to haematopoietic cell proliferation and liver prometing kidney, lung and liver growth and/or repair. An experiment was performed to show antisense inhibition of human and mouse WSX receptors. The present sequence is a sense (control) oligonucleotide used in the experiment
                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                         DB 1; Length 18; 38;
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                              GCTGGGATGTGCCTTAGA 153
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les 18; Conservative
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MATTHEWS W.
RODRIGUES M I
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20-JUN-1996;
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(KIMK/)
(MATT/)
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                                                                                                                                                                                                                                                  Matches
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treatment of obesity, bulimia and other disorders associated with abnormal expression or functions of WSX receptor genes, for treating metabolic disorders such as diabetes, for reducing excessive levels of insulin in human patients and for treating patients suffering from food consumption and related pathological conditions such as type II adult onset diabetes, infertility, hypercholesterolemia, hyperlipidaemia, cardiovascular diseases, arteriosclercosis, polycystic ovarian disease, osteoarthitis, dermatological disorders, insulin resistance, osteoarthitis, dermatological disorders, insulin resistance, osteoarthitis, dermatological disorders, insulin resistance, osteoarthitis, dermatological fisher and allments, lung dysfunctions such as emphysema, hemorrhages, diseases characterised by decrease in blood cells such as anaemia, thrombocytopenia, hypoplasia, center tumour related disorders und anorexia and loss of appetite, and other tumour related disorders. This sequence represents a human WSX receptor DNA antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; WSX receptor; ss; weight reduction; obesity; bulimia; metabolic disorder; diabetes; insulin level reduction; food consumption; type II adult onset diabetes; infertility; hypercholesterolaemia; hyperlipidaemia; cardiovascular disease; arteriosclerosis; polycygtic ovarian disease; osteoarthritis; dermatological disorder; insulin resistance; hypertriglyceridaemia; cancer; cholelithiasis; hypertension; kidney ailment; lung dysfunction; emphysema; haemorrhage; anaemia; thrombocytopenia; hypoplasia; cachexia; anorexia; appetite loss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel agonist antibody useful for activating WSX receptor and for enhancing proliferation or differentiation of a cell comprising WSX receptor, which specifically binds to the WSX receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18; DB 1; Length 18;
Pred. No. 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
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96US-00667197.
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Matches 18; Conservative
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MATTHEWS W.
RODRIGUES M L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour; antisense
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20-JUN-1996;
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(KIMK/)
(MATT/)
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The invention relates to agonist antibodies which specifically bind to the human WSX receptor. The agonist antibodies are useful for activating the wax receptor and for enhancing profileration or differentiation of a cell comprising the WSX receptor, by exposing the cell to an antibody.

The antibodies are also useful for reducing weight, specifically in the treatment of obesity, bulinia and other disorders associated with a bnormal expression or functions of WSX receptor genes, for treating metabolic disorders such as diabetes, for reducing excessive levels of insulin in human patients and for treating patients suffering from food consumption and related pathological conditions such as type II adult onset diabetes, infertility, hypercholesterolaemia, hypertipidaemia, cardiovascular diseases, arteriosclerosis, polycystic ovarian disease, exteriosclerosis, polycystic ovarian disease, orteriosclerosis, insulin resistance, hypertriglyceridaemia, cancer, cholelithiasis and hypertension. The antibodies are also useful for treating kidney allments, lung decrease in blood calls such as anaemia, thrombocytopenia, hypoplasia, metabolic disorders such as cachexia, anorexia and loss of appetite, and other tumour related disorders. This sequence represents a human WSX receptor DNA antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method for analysing microsatellite loci. In method involves coamplifying a set of 3 microsatellite loci, comprising a specific mononucleotide repeat locus selected from the group consisting of BAT-25, BAT-26, BAT-40, MONO-11 and MONO-15 and two
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loci.
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microsatellite instability; MSI; cancer; gastrointestinal system;
endometrium; BAT-25 locus; PCR; primer; ss.
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Pred. No. 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 GCTGGGATGTGCCTTAGA 153
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nes 18; Conservative
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tetranucleotide repeat loci selected from FGA, DISSIB, DI7SI299 etc from a sample of genomic DNA and determining the size of the amplified fragments. The method is useful for analysing microsatellite loci and for detecting microsatellite instability (MSI) in genomic DNA. The instability in the set of microsatellite loci are used in prognostic tumour diagnosis for the diagnosis of familial tumour predisposition. It is also used to detect cancerous tumours in the gastrointestinal system and of the endometrium. The cancerous tumours are preferably from a colorectal cancer. The present DNA sequence is a PCR primer which is used for amplifying human BAT-25 locus. This primer is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method for determining the presence of neoplastic molecular markers in a host, involving the use of neoplastic molecular marker specific reagents to detect such markers and analysing the array of reagents, allowing the identification of the neoplastic disease present. This can be used to determine the best treatment for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining the presence of neoplastic molecular markers, by identifying the presence of markers in host test sample using array of neoplastic molecular marker specific reagents and analyzing the array of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, cancer, neoplastic disease, tumour specific marker, cytostatic,
transcription factor; PCR; primer, 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancers, in particular neural cell, lung and prostate tumours. The present sequence is a PCR primer useful for detecting the coding sequences of markers of the invention
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                                                                                                                                                                                                                                                   1.6%; Score 17.6; D
83.3%; Pred. No. 51;
ive 0; Mismatches
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0; Mismatches
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83.3%; Pred. No. 51;
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                                                                                                                                                                                 exemplification of the invention
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                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Palm K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                      ABT03742
   88888888888888
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09-AUG-2002

Human;

AAD36414;

RESULT 41 AAD36414/

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21-MAR-2002

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Human microsatellite locus PCR primer #60
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                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cross-species comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACI87101 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flanagan L,
                                                                                                                                                                                                                                                                                                                                                                                                                                (PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-830985/77
                                                                                                                                                                                   colorectal cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2003104410-A1.
                                                                                                                                                                                                                                                          US2003180758-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-OCT-2003
                                                                                                                                                                                                                         Homo sapiens
                                                   15-JAN-2004
                                                                                                                                                                                                                                                                                                  25-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacher JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACI87101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
               ADD31191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACI87101/c
ID ACI871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method of analysing microsatellite coloi. The method involves co-amplifying a set of three microsatellite loci loci. The method involves co-amplifying a set of three microsatellite loci comprising at least one mononcleotide repeat locus and at least two terra-nucleotide repeat loci from a sample of genomic DNA in a multiplex amplified DNA fragments obtained. The method is useful for analysing compositellite loci and for detecting microsatellite instability (MSI) in genomic DNA microsatellite loci of the second genomic DNA, where the MSI cresults are useful in prognostic tumour diagnosis, in diagnosis of familial tumour predisposition, to detect cancerous tumours of the cancerous tumours are tumours from a colorectal cancer. The method is useful for detecting or diagnosing diseases associated with MSI such as certain ctypes of cancer and predisposition for cancer and in diagnostic assays to types of cancer and predisposition for cancer and in diagnostic assays computed to determine treatment and prognosis of disease. The present DNA sequence is a primer which is used for amplifying human BAT-25 locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Analyzing micro-satellite loci for detecting or diagnosing cancer, by coamplifying set of three microsatellite loci from DNA sample in multiplex reaction using primers, and determining size of amplified fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                    microsatellite locus; microsatellite instability; MSI; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24 BP; 5 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       th 1.6%; Score 17.6; D
Similarity 83.3%; Pred. No. 51;
20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                    Human BAT-25 loci amplifying primer #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  921 AGAGCCTTATTAGAAATGCAGAAT 944
                         834 CCAGGAAGGCCGGGGTGGATCCCT 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agagccaragranaaargcagaar 1
                                               1 CCAGTATGGCCGGGATGGATACCT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nassif N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 73; 73pp; English.
                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-2001; 2001WO-US028647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-SEP-2000; 2000US-00663020
                                                                                                                                                        AAD36414 standard; DNA; 24
                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacher JW, Flanagan L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROM-) PROMEGA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-393975/42.
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                                                                                                                                                                                                                                                                                                                                 cancer; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                        WO200222879-A2
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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ADD31191 standard; DNA; 24 BP.

ADD31191/c ID ADD311

RESULT 42

24

Query Match

Matches

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The invention relates to a method of analysing microsatellite loci. The invention is used to detect microsatellite instability in prognostic tumour diagnosis, particularly a familial tumour prediagnosition especially to detect cancerous tumours of the gastrointestinal system or endometrium, most particularly colorectal cancer. The present sequence represents a human microsatellite locus PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Analyzing microsatellite instability by amplification of multiple loci including mono-nucleotide and tetra-nucleotide repeats useful to detect cancerous gastrointestinal or endometrium tumors particularly colorectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST; ss; probe; expressed sequence tag; microarray; gene expression;
genetic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
ss; PCR; primer; human; microsatellite locus; prognostic tumour diagnosis; familial tumour predisposition; cancerous tumour; gastrointestinal cancer; endometrial cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human microarray DNA oligonucleotide SEQ ID NO 87092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24 BP; 5 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 51;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17.6;
Pred. No. 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           921 AGAGCCTTATTAGAAATGCAGAAT 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; SEQ ID NO 60; 48pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Nassif N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 1.6%;
Local Similarity 83.3%;
Les 20; Conservative (
                                                                                                                                                                                                                                                                    09-DEC-2002; 2002US-00314810.
                                                                                                                                                                                                                                                                                                              15-SEP-2000; 2000US-00663020.
24-APR-2001; 2001US-00841366.
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Calso disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises of at least one or more nucleic acid states and detecting the hybridisation. The nucleic acid probes are and detecting the hybridisation. The nucleic acid probes are altached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, cor family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific or nucleic acids further comprises a tag sequence or specific acid subclones to matations of any gene, in mapping the 5' terminal of mRNA molecules by containing segments of DNA that have been containing segments of DNA that have been containing segments of DNA that have been contained in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence thml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour suppression; tumour reversion; apoptosis; virus resistance; yrtostatic; virucide; neuroprotective; nootropic; neuroleptic; probe; primer; PCR; gene chip; antisense; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
                                                                                                                                                                                                                                 New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human tumour suppression/reversion-related DNA sequence SeqID3789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25 BP; 7 A; 2 C; 4 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.6%; Score 17.6; 183.3%; Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 87092; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    652 CAAATTTAGATTATGTTACTCAAA 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 CAAATTTAAACTATGTCACTGAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADI51286 standard; DNA; 17 BP.
                    15-MAR-2002; 2002US-00098263.
                                                            16-MAR-2001; 2001US-0276759P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 83.3°
Marches 20; Conservative
                                                                                                      (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                           WPI; 2003-567953/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003025177-A2
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                                                                                                                                                Mittmann MP;
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in the phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses. The invention may be useful for the development of compounds with a cytostatic, viruside, neuroprotective, nootropic or neuroleptic activity. The DNA sequences may be useful as probes and primers for detecting, indentifying, quantifying and/or amplifying nucleic acid, for example as one component of a gene chip, in vitro as antisense reagents and for production of recombinant polypeptides. The invention may therefore be useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. The present sequence is that of a nucleic acid sequence of the invention.

Specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                    New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
                                                                                                                                                                                                                                                                         This invention relates to novel isolated nucleic acid sequences involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antilipaemic, Cardiovascular, Analgesic; Antianginal, Antisense therapy; Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL; cardiovascular disorder; metabolic syndrome X; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "This oligonucleotide has a phosphorothioate backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5' and 3' ends, which are 4 nucleotides in length. Also all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human endothelial lipase antisense oligonucleotide, SEQ ID 3493.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.5%; Score 17; DB 1; Length 17; 100.0%; Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 6 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Prea. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/publishedpct_sequences
                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 3789; 30pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                    Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mod base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     981 GATCCAAAGGAGTTGTA 997
                                                                   (MOLE-) MOLECULAR ENGINES LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATCCAAAGGAGTTGTA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ25095 standard; DNA; 20 BP.
17-SEP-2002; 2002WO-IB004523.
                                 17-SEP-2001; 2001FR-00011980.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Conservative
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                                                                                                  Telerman A, Amson R,
                                                                                                                                    WPI; 2003-313354/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ25095;
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Matches
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WPI; 2004-132912/13.

Bhat BG;

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                                                                                                                                                       New antisense oligonucleotide for modulating endothelial lipase expression, for diagnosing, preventing or treating e.g. dyslipidemia, low high density lipoprotein or cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy; Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL; cardiovascular disorder; metabolic syndrome X; ss.
                                                                                                                                                                                                                                                  The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25517), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of EL. The antisense oligonucleotides or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are used for diagnostics, prophylaxis, or as research reagents or kits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human endothelial lipase antisense oligonucleotide, SEQ ID 3648.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 2 A; 6 C; 11 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 65;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.5%; Score 16.8;
90.0%; Pred. No. 65
                                                                                                                                                                                                                           Claim 3; SEQ ID NO 3493; 1007pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 CCCGGGCCGTGGCAGGAGC 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJ25250 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUL-2003; 2003WO-US022410.
                                       19-JUL-2002; 2002US-0397106P.
         18-JUL-2003; 2003WO-US022410
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Best Local Similarity 90.0°
Matches 18; Conservative
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*tag=
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                                                                       (PHAA ) PHARMACIA CORP
                                                                                                                                   WPI; 2004-132912/13.
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modified_base
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Synthetic.
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                                                                                                          Bhat BG;
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New antisense oligonucleotide for modulating endothelial lipase expression, for diagnosing, preventing or treating e.g. dyslipidemia, low high density lipoprotein or cardiovascular disorders.
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                                                                                                                                             The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25517), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of EL. The actisense oligonucleotides or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular discorder or metabolic syndrome X. In addition, the oligonucleotides are used for diagnostics, prophylaxis, or as research reagents or kits.
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seed; development; FIS; endosperm; autonomous embryogenesis;
transgenic plant; seedless fruit; parthenocarpic; citrus fruit;
stone fruit; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                             DB 1; Length 20;
                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                Sequence 20 BP; 2 A; 5 C; 12 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                             5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer 1F used in FIS2 gene identification.
                                                                                                                                                                                                                                                                                                                             1.5%; Score 16.8; D. Local Similarity 90.0%; Pred. No. 65; les 18; Conservative 0; Mismatches
                                                                                                                        Claim 3; SEQ ID NO 3648; 1007pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CSIR ) COMMONWEALTH SCI & IND RES ORG.
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                                                                                                                                                                                                                                                                                                                                                                                            GCCCGGGCCGTGGCAGGAAG 38
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98AU-00006063.
99AU-00001345.
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AAA50752 standard; DNA; 21 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-283392/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
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22-SEP-1998;
22-SEP-1998;
01-JUL-1999;
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Peacock WJ;
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                                                                                                                                                                                                                                                                                                                                                                   Matches
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Sequence 21 BP; 4 A; 5 C; 2 G; 10 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                  PCR primer used for hepatitis C virus genotyping.
                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                       radioimmunoassay or histochemical tests
                                                                                                                                                                                                                                      606 ACTTCATAAGTAGGAGATGA 625
                                                                                                                                                                                                                                              20 ACTTCATAAGGAAGAGATGA 1
                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                     95JP-00035997.
                                                                                                                                                                                                                                                                                                                                                                                         96JP-00038875
                                                                                                                                                                                                                                                                               AAT89716 standard; DNA; 24
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                    Local Similarity 90.0
nes 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                       (SRLS-) SRL KK
                                                                                                                                                                                                                                                                                                                                                                  JP09234072-A.
                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                            30-DEC-1995;
                                                                                                                                                                                                                                                                                                       05-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                              09-SEP-1997
                                                                                                                                                                                                                                                                                                                              Hepatitis
                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                           AAT89716;
                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                   RESULT 48
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Primers used for determining hepatitis C virus genotype - provide a rapid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              into chromosomes of eukaryotes or for obtaining site-specific replacement of nucleic acids in a target construct. The method may also be used to stably integrate a polynucleotide into any eukaryotic cell that can be
                                                                                                                             AAT89689-T89744 are individually claimed oligonucleotides used as PCR (polymerase chain reaction) primers for the discrimination of the genotype of hepatitis C virus (HCV). Classification of the genotype of HCV can be achieved precisely and simply according to the International Standardisation of Classification. The primers can be used to distinguible where HCV genotypes 1a, 1b, 2a, 2b, 3a, 3b, 4, 5a, 6a and 6b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for obtaining specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and stable integration of nucleic acids into chromosomes of eukaryotes, by employing irreversible recombination sites (IRS) and irreversible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR; primer; site-specific gene replacement; irreversible recombinase; irreversible recombination site; IRS; ss.
                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR primer corresponding to the plasmid backbone of pJK148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                         and accurate method of hepatitis C virus genotyping
                                                                                                                                                                                                                                                                                                                            Sequence 24 BP; 3 A; 8 C; 8 G; 4 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                                             1.5%; Score 16.8; L
81.8%; Pred. No. 70;
:ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Obtaining site-specific gene replacement,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.5%; Score 16.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 TGGGCAGGCTGCCCGGGCCGTG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGACAGGCKGCCCGGGCCTTG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 32; 84pp; English.
                                                                               Claim 28; Page 15; 33pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transformed by a polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200208409-A2
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 49
ABA99037
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
##X8X8888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method of inducing the development of seeds in a plant, comprising inhibiting, interrupting or reducing the seeds in a plant, comprising inhibiting, interrupting or reducing the expression of a negative regulator of seed formation in one or more female reproductive cells, tissues, or organs of the plant or a progenitor cell, tissue or organ. The negative regulator is a polypeptide. The FIS family of genes are known to be capable of cregulating autonomous endosperm development and/or autonomous embryogenesis. In the invention the reduced expression of the negative cregulating autonomous endosperm development and/or autonomous embryogenesis. In the invention the reduced expression of the negative cregulator is achieved by the introduced expression of the present a FIS genetic sequence which may inhibit FIS activity. The present cregarded fruit, where the fruit are made parthenocarpic fruit or sequence represents a PCR primer used to identify the FIS2 gene. Plants of sequence for soft seeded fruit, where the fruit are made parthenocarpic fruit or soft seeded fruit at tissue or organ of the fruit. The plant produced soid in the production of an antisense molecule, a gene-silencing molecule and a dominant-negative sense molecule, a gene-silencing molecule and a dominant-negative sense molecule, a gene-silencing concluded for the production of a transformed plant. The transformed plant is appendent to production of a transformed plant. The transformed plant is appeadnes, citrus fruits such as oranges, lemons, grapefruit and chert fruits such as grapes, apples, melons, pears and madarins and other fruits such as grapes, apples, melons, pears and chert sequely in the planted made of detect the peptides of the invention and characteristics stably between generations. Antibodies produced to the call in an enryme linked immunosorbant assay (ELISA),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     patitis C virus; HCV; genotype determination; la; lb; 2a; 2b; 3a; 3b; 5a; 6a; 6b; diagnosis; amplification; PCR; primer; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.5%; Score 16.8; DB 1; Length 21; 90.0%; Pred. No. 66;
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Candida albicans GRACE strain PCR primer SEQ ID NO 4596.
                                                            Candida albicans
                                                                                WO200253728-A2.
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                                                                                                  11-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADK67738;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents a PCR primer used to isolate nucleic acid molecules encoding a platelet-derived growth factor (PDGF) associated protein, PRO. Polypeptides, nucleic acids and antibodies of the invention set used to treat or prevent a pathological state in a mammal, particularly a PDGF-associated disorder in a human. Specifically, these molecules can be used to control myofibroblast development, wound healing or angiogenesis, for example in the treatment of cancer and tumours, or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                  Gaps
                                                                                                                                                                              Rat; platelet-derived growth factor; PDGF; PRO; tumour; cancer; PDGF-associated disorder; myofibroblast development; wound healing; angiogenesis; cancer; tumour; muscle wasting disease; PCR primer; s
                                                                                                                                                                                                                                                                                                                                                                                    Polypeptides related to platelet-derived growth factor-associated proteins, useful for increasing muscle mass and to treat wasting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                   Indels
                                                                                                                                                              Rat PDGF-associated protein, PRO, PCR primer Ag197#1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23 BP; 9 A; 3 C; 6 G; 5 T; 0 U; 0 Other;
                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.6; I
Pred. No. 75;
          Pred. No. 70;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            386 AATGCAGTCATTTTCCTTACAAT 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 75; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTGCATTCGTTTTCCTGACAAT
                                       294 CTGGAATTGTTGTTTCTGCC 313
                                                      CTGAAATTGTTGCTTCTGCC 24
                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.5%;
Local Similarity 82.6%;
Les 19; Conservative
                                                                                                                                                                                                                                                                                                   25-OCT-1999; 99US-0161315P.
24-OCT-2000; 2000US-00695366.
                                                                                                                                                                                                                                                                                25-OCT-2000; 2000WO-US029391.
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ID ABZ30445 standard; DNA; 23
            90.06
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                                                                                                         AAS03279 standard; DNA; 23
                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or angiogenesis, for exe
muscle wasting diseases
                     18; Conservative
                                                                                                                                                                                                                                                                                                                                                  Rastelli L;
                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-308644/32
           Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                             WO200131010-A1.
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                                                                                                                                                                                                                                                                03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                   Burgess C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABZ30445;
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                                                                                                                                                                                                                                                                                                                                                                                                             diseases.
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                                                                                                                                                                                                                            Rattus
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The invention relates to constructing (MI) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by the recombination, of a promoter replacement fragment with a heterologous promoter. (MI) is useful for constructing a strain of diploid fungal promoter. (MI) is useful for constructing a strain of diploid fungal cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus cand for identifying a therapeutic agent for treatment of a mammalian agent, an antifungal agent that inhibits the growth of a diploid fungus compound catabolism, biosynthetic, transporter, transcriptional, compound catabolism, biosynthetic, transporter, transcriptional, compound catabolism, biosynthetic, transporter, transcriptional, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the compound, signal transduction, proferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of a PCR primer used in the method of the invention. Note: The sequence data for this patent is not repersented in the printed appearance is that of a personner of the present sequence is the present of the present sequence is the passed the method of the invention by the printed appearance is the present of the present sequence is the present in the method of the invention by the printed appearance is the present in the present in the present in the present in the present is present.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the Buropean Patent Office
Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 36; SEQ ID NO 4596; 167pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23 BP; 10 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.5%; Score 16.6; E
Best Local Similarity 82.6%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bussey H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           477 TGATTACAGTGCATTGAATTTCT 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-DEC-2000; 2000US-0259128P.
20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-DEC-2001; 2001WO-US049486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADK67738 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roemer T, Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-566694/60.
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Sequences were determined from the ends of chromosome 11-specific cosmids by automated sequencing without intermediate subcloning. A sample of 371 by automated sequencing without intermediate subcloning. A sample of 371 but sequence fragments were determined and of these, 277 were suitable cor STS primer prediction by computer analysis (using the "Primer" program available from E.Lander, MTJ. The STSs and cosmids were mapped by in situ hybridisation, somatic cell hybrid analysis or both. Using complet from were regionally mapped. This procedure illustrates a novel method for sequencing complex genomes, designated "sequence sampled mapping". The sequence sampled mapping method is useful for the completion of high density sequence-based maps, and ultimately, for the complete sequencing of genomic DNA directly from cosmid clones. See AAQ82101-082706 and AAQ91255-Q91358 for STS primers. (Updated on 25-MAR-
                                                                                                                                                                                                                                                                                  Sequencing complex genomes, present as fragments in a cosmid library - k sequencing end-specific nucleotides of each clone then correlating with spatial relationship of cosmid, esp. for mammalian chromosomes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer #2 to amplify repeat sequence marker Mfd90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21 BP; 5 A; 3 C; 4 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16.2; DB
Pred. No. 84;
0; Mismatches
                                                                                                                                                 (SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 89; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Arcrerarararerere 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513 ATCTGTATACATGTGCACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.5%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-00222177.
                                         94WO-US006810
                                                                                   93US-00078471
93US-00117952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89US-00341562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-00754351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT65977 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                               Smith MW;
                                                                                                                                                                                                                                         WPI; 1995-036508/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                   15-JUN-1993;
07-SEP-1993;
                                       15-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
18-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-1989;
22-DEC-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5582979-A.
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                                                                                                                                                                                               Evans GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT65977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to methods for generating cell lines and mammals with site-specific genetic modification. The methods use homologous recombination between an artificial chromosome having the modification and an endogenous chromosome of a cell. The resulting modified cells can be used to generate genetically modified mammals useful in screening methods to identify compounds of therapeutic interest. Cells can also be modified to eliminate a mutation associated with a disease, e.g. cancer, and then transplanted into patients for treatment of the disease. In an example of the method, bacterial artificial chromosomes (BACS) containing mutations in fancg/xrcc9 were used to modify mouse embryonic stem (ES) cells for the generation of fancy/xrcc9 knockout mice. The present primer, designated G34, was used in a nested PCR to screen modified BAC clones for correct targeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence sampled mapping; genomic analysis; complex genome mapping; cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing a genetically modified mammalian cell, useful in producing modified non-human mammal for screening compounds to treat or prevent cancer, by inserting into mammalian cells an artificial chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                         Transgenic; knockout; gene therapy; bacterial artificial chromosome; mouse; fancg/xrcc9 gene; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.5%; Score 16.6; DB 1; Length 23; 82.6%; Pred. No. 75; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23 BP; 3 A; 9 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chromosome 11 (locus D11S870) STS primer 350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 9; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 CCCGGGCCGTGGCAGGAGCCGG 42
                  Murine fancg/xrcc9 gene primer G34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 cccecrcerecreadades
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                                                                                                                                                                                                                                                                                                         02-AUG-2002; 2002US-0400900P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                   (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 82.6
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprising a cassette.
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-157118/15
                                                                                                                                                                                                                                                                                                                                                                                                 Seed B, Yang Y;
                                                                                                                                                                      WO2004013299-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9429486-A1
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14-SEP-1995
                                                                                                                                                                                                                    12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ82600;
                                                                                                                            Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        events.
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Gaps

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DB 1; Length 21; 3; Indels (DNAS-) DNA SCI LAB INC

Hall J;

Guida M,

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WPI; 1997-042299/04.
 Weber JL;
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                                                                                                                                                                                   The invention relates to the isolation of polymorphic repeat sequences having the sequence (dd-da)n.(dd-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones contraining the animal or plant breeding or pedigree analysis. Or or containing the phage libraries with a synthetic poly(dc-da).(dd-dT) probe. Over 100 phage libraries with a synthetic poly(dc-da).(dd-dT) probe. Over 100 repeat blocks were isolated. The primers AAT65798-T66047 were used to PCR sequences. The primers AAT65797-7 were used to emplify the inserts from the isolated clones containing the repeat sequence marker clone Mfd90. (Updated on 25-MAR-2003 to correct PF
Detection of polymorphic genetic markers of the form (dC-dA)\,n\,(dG-dT)\,n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 5 A; 3 C; 4 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5%; Score 16.2; I
Best Local Similarity 85.7%; Pred. No. 84;
Matches 18; Conservative 0: Micmata
                                                                                                                                     Disclosure; Col 11-12; 186pp; English.
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513 ATCTGTATACATGTGCACATG 533
                       1 Arcidiararardidigracid 21
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Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1;

Cytochrome Cytochrom
                                                                                                                                                                                                                                                                       Human multidrug resistance associated protein 3 polymorphic sequence #62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single nucleotide polymorphism
                                                               ABS98440 standard; DNA; 21 BP
                                                                                                                                                                                                                   23-DEC-2002 (first entry)
                                                                                                                                                   ABS98440;
RESULT 55
                                       ABS98440
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21

1 TAGTAGCTGAGTTTGATTCTC

g

ABK86295 standard; DNA; 23

ABK86295/

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28-NOV-2000; 2000US-00724389.
                                                                                                                28-NOV-2001; 2001WO-US044838.
                                      40200257410-A2.
Homo sapiens
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Human; TGR342; primer; ss; G-protein coupled receptor; GPCR; TGR; RT-PCR;

Human TGR342 RT-PCR primer #2.

27-AUG-2002 ABK86295;

XXXXXXXXXX

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This invention relates to the sequence of an isolated nucleic acid

This invention relates to the sequence of an isolated nucleic acid

This invention relates to the sequence of an isolated nucleic acid

This invention relates to the sequence of a known

Molecule comprising at least one base variation from that of a known

Molecule comprising at least one base variation from that of a known

This invention (ARR), aryl Mydrocarbon receptor betal (ADRBA),

CCC

This procedure (TARS), cyclooxgenase 2 (CRX2), diazepam binding

(ARRY), cathepsin S (CTSS), cyclooxgenase 2 (CRX2), diazepam binding

Inhitior (DBI), gputathone-Stransferase 12 (GYS12), histamine-N-methyl

transferase (HWMT), MADPH quinone oxidoreductase 2 (WO22),

(MCT2B4), UDP-qluuronosyl transferase 2B4

(MCT2B4), UDP-qluuronosyl transferase 2B4

(MCT2B4), urckinase receptor (URM), multidug resistance 1

(MRMI), lactotransferant (CRMI12), or acetylcholine muscarinic

(MRMI), lactotransferant (CRMI12), or acetylcholine muscarinic

(MRMI), lactotransferase for locating and characterising the genes transman and eventually

are responsible for specific traits within the genome and eventually

are responsible for specific traits within the genome and eventually

are responsible for teaching middiduals for arterity of disorder-related

traits as a result of their e-g., overexpression, which may be used in diagnosing

conductority and or underexpression, which may be used in diagnosing

and/or reating the disorders. The nucleic acid molecules comprising the

conduction of their e-g., overexpression, which may be used to career individuals for altered cardiovascular function, in CRM2 for altered cusceptibil
                                                                                                          Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.5%; Score 16.2; DB 1; Length 21; 85.7%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 4 A; 3 C; 5 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                      Example 24; Page 153; 714pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated G-protein couple receptor polypeptide, termed TGR, for diagnosis and treatment of diseases such as renal failure, nephritis, hypothyroidism, diabetes insipidus, and disturbances of thirst and sleep.
TGR-associated disorder; signal transduction; renal failure; nephritis; hypothyroidism; hypogonadism; retinitis pigmentosa; growth disorder; diabetes insipidus; hyperprolactinaemia; thirst disturbance; appetite; sleep disturbance; temperature regulation; blood pressure; hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                        Gupte JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKN1-1R; 88; human; DYXC1; dyslexia; neurological disorder; reading disability; phonological processing; rapid naming; verbal short-term memory; primer; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXN1-1R human-specific intronic PCR primer for DYXC1.
                                                                                                                                                                                                                                                                                                                                                                                                                        X,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Match 1.5%; Score 16.2;
Local Similarity 85.7%; Pred. No. 88
Les 18; Conservative 0; Mismatche
                                                                              circadian rhythm; reverse transcriptase
                                                                                                                                                                                                                                                                                                                                                                                                                        Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                        Cutler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 65; 98pp; English
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22-DEC-2000; 2000US-025765FD.
12-JAN-2001; 2001US-0251377P.
28-MAR-2001; 2001US-029554P.
29-MAR-2001; 2001US-0280696P.
                                                                                                                                                                                                                             21-NOV-2001; 2001WO-US043404
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                                                                                                                                                                                                                                                                                                                                                                                                                      Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                 (TULA-) TULARIK INC.
                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao J,
                                                                                                                                                       WO200242458-A2
                                                                                                                   Homo sapiens
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                                                                                                                                                                                          30-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                        Tian H,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory; Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic; Leptin receptor related protein; OB-RGRP; leptin receptor; leptin-related disorders; osteoporossis; calcification; obssity; diabetes; anorexia; sexual maturity disorder; haematopolesis; angiogenesis; thrombus formation; immunity; inflammation; fetal development; cancer;
                                                                                                                                                                                                                                                                                  New isolated, purified DYXC1 nucleic acid for studying brain processes, e.g. reading, phonological processing, rapid naming or verbal short-term memory, or for diagnosing dyslexia or assessing the predisposition to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23 BP; 9 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                                                                                              Kaminen N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 88;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.2;
                                                                                                                                                                                                              Taipale M, Nopola-Hemmi J,
                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 23; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1000 CACATGAAAGTTTGAGAAGCA 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.5%;
                                                                                                        12-FEB-2003; 2003WO-FI000110.
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                                                                                                                                           12-FEB-2002; 2002US-0355782P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; RT-PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                           (LICN ) LICENTIA LTD
                                                                                                                                                                                                                                                  WPI; 2003-646482/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 18; Conserv
                                   WO2003068814-A1.
 Homo sapiens.
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                                                                      21-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADR27674;
                                                                                                                                                                                                                                                                                                                                          dyslexia
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                                                                                                                                                                                                              Kere J,
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Tuijnder M;

Amson R,

relerman A,

(MOLE-) MOLECULAR ENGINES LAB

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The present invention relates to a leptin receptor related protein (OB-RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises CG RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises preditically with and inhibits the expression of ADR27652. The ON promotes expression of leptin receptors on the cell surface and may contain phosphorothioate bonds; 2'-on-methyl nucleotides and/or a contain phosphorothioate bonds; 2'-on-methyl nucleotides and/or a criatethyleneglycol residue at the 3'-end. Also claimed are interfering RNA triatethyleneglycol residue at the 3'-end. Also claimed are interfering RNA (IRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit contains sequences comprising OB-RGRP or MY047 (thought to be a member of coding sequences comprising OB-RGRP or MY047 (thought to be a member of the OB-RGRP family, shares 68% homology with OB-RGRP, and a protein that the observation of energy e.g. luciferase or yellow fluorescent or protein (YPP) for detecting compounds that modify the interaction between continuous for protein (YPP) for detecting compounds that modify the interaction between containing the leptin related disorders. ON, also related interfering RNA, are created for prevention and/or treatment of leptin-related disorders, costeoporosis (or other conditions involving reduced bone density); calcification, obseity; diabetes, anorexia; disorders of sexual maturity, and inflammation, fetal development and cancer. The present sequence is a content of illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour suppression; tumour reversion; apoptosis; virus resistance; cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe; primer; PCR; gene chip; antisense; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
                                                                                                                                                                                             New oligonucleotides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human tumour suppression/reversion-related DNA seguence SegID4573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16; DB 1; Length 16;
Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16 BP; 6 A; 6 C; 4 G; 0 T; 0 U; 0 Other;
                                                    (AVET ) AVENTIS PHARMA SA.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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                                                                                                                                                                                                                                                                                                       Disclosure; Page 23; 104pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.4%; Scor-
100.0%; Pre
0, h
                                                                                                                     Uhlmann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        332 CTIGCICGIGIGGCIG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 CTTGCTCGTGTGGCTG 1
               10-FEB-2003; 2003FR-00001543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                     Couturier C,
                                                                                                                                                          WPI; 2004-595751/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003025177-A2
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                                                                                                                                                                                                                                                                       angiogenesis.
                                                                                                                       Jockers R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI52070;
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in the phenomena of tumour suppression, tumour reversion, apoptosis in the phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses. The invention may be useful for the and/or resistance to viruses. The invention may be useful for the development of compounds with a cytostatic, virucide, neuroprotective, correctly primers for detecting, indentifying, quantifying and/or probes and primers for detecting, indentifying, quantifying and/or correctly for example as one component of a gene chip, in amplifying nucleic acid, for example as one component of a gene chip, in viru as antisense reagents and for production of recombinant correctly preparation of colypeptides. The invention may therefore be useful for preparation of opypeptides. The invention and/or treatment of viral diseases that correctly concern but also Alzheimer's disease and schizophrenia. The specifically cancer but also Alzheimer's disease and schizophrenia. The present sequence data for this patent did not form part of the printed Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO content to the printed of the printed of the printed of the printed of the form part of the printed of the fire wipo.int/pub/publishedpct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, mouse, SACI, carbohydrate, sweetener; ethanol; alcoholism; s8;
obesity, diabetes; transgenic embryo; body tissue; body fluid; pancreas;
blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
                                                                                                             New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
                                                                                                                                                                                                                                   This invention relates to novel isolated nucleic acid sequences involved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Score 16; DB 1; Length 17;
100.0%; Pred. No. 84;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human SAC1 gene-specific oligonucleotide PCR primer #37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 5 A; 2 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA, Beauchamp GK, Chatterjee A,
Reed DR, Ross D, Tordoff MG;
                                                                                                                                                                                                  Disclosure; SEQ ID NO 4573; 30pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (WARN ) WARNER LAMBERT CO.
(MONE-) MONELL CHEM SENSES CENT.
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28-JUL-2000; 2000US-0221419P.
10-NOV-2000; 2000US-0247443P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS97676 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  981 GATCCAAAGGAGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 16; Conservative
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Ohmen JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS97676;
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Gaps

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The invention relates to an isolated polypeptide, comprising a variant form of mouse or human SACI polypeptide. The variant form is associated with altered preference for carbohydrates, other sweeteners or ethanol.

The polypeptide and its associated DNA sequence can be produced by crecombinant techniques and is useful for preventing obesity, diabetes or alcoholism associated with SACI expression. The sequences are useful in screening for drugs and sweeteners. Recombinant cell lines and transgenic cor repress function of SACI. Predisposition to diabetes, obesity or alcoholism can be ascertained by testing any fluid or tissue of a human can be ascertained by testing any fluid or tissue of a human can be ascertained by testing any fluid or tissue of a human can be ascertained by testing any fluid or tissue of a human can be ascertained by testing any fluid or tissue of a human can be ascertained by the SACI locus may indicate a predisposition to diabetes, obesity and/or alcoholism and may provide a diagnostic mark. The polynucleotide can be detected in a biological sample by contacting the DNA with a probe to form a hybridisation complex which is then detected. The sequences represent cDNA encoding human and conservation of the SACI pens specific for the SCAI genes
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                                                 Novel isolated polypeptide comprising variant form of mouse or human SACI polypeptide, and is associated with altered preference for carbohydrates or other sweeteners, useful for preventing obesity, diabetes, alcoholism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; mouse; SAC1; carbohydrate; sweetener; ethanol; alcoholism; ss;
obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ×
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human SAC1 gene-specific oligonucleotide PCR primer #35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
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100.0%; Pred. No. ...
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Tordoff MG;
                                                                                                                            Claim 14; Page 84; 239pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (WARN ) WARNER LAMBERT CO. (MONE-) MONELL CHEM SENSES CENT.
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28-JUL-2000; 2000US-0221419P.
10-NOV-2000; 2000US-0247443P.
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Reed DR, Ross D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-APR-2001; 2001WO-US013387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein replacement therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 GGTGTTACCTGCTCAT 1
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AAS97674 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity 100.'
Matches 16; Conservative
                 WPI; 2002-075162/10.
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Ohmen JD, Re
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The invention relates to an isolated polypeptide, comprising a variant form of mouse or human SAC1 polypeptide. The variant form is associated with altered preference for carbohydrates, other sweeteners or ethanol. The polypeptide and its associated DNA sequence can be produced by recombinant techniques and is useful for preventing obesity, diabetes or alcoholism associated with SAC1 expression. The sequences are useful in screening for drugs and sweeteners. Recombinant cell lines and transgenic embryos may be used in screening for and identifying agents that induce or repress function of SAC1. Predisposition to diabetes, obesity or alcoholism can be ascertained by testing any fluid or tissue of a human (such as blood, pancreas or tongue) for sequence variations of the SAC1 ocus may indicate a predisposition to diabetes, obesity and/or alcoholism and may provide a diagnostic mark. The polymucleotide can be detected in a biological sample by contacting the DNA with a probe to form a hybridisation complex
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Novel isolated polypeptide comprising variant form of mouse or human SAC1 polypeptide, and is associated with altered preference for carbohydrates or other sweeteners, useful for preventing obesity, diabetes, alcoholism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antirheumatic; antiarthritic; antibacterial; antiaeborrheic; dermachogical; antipaoriatic; neuroprotective; noctropic; antiparkinsonian; antidabetic; ophthalmological; antiasthmatic; antidepressant; neuroleptic; hypotensive; tranquilizer; hypertensive; anotectic; metabolic; virucide; osteopathic; antiaspinal; vulnerary; gene therapy; G-protein coupled receptor protein; HGPRBAK30; immune disorder; cardiovascular disorder; inflammatory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppressive; cardiant; antiinflammatory; cytostatic; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which is then detected. The sequences represent cDNA encoding human mouse SAC1 polypeptides and PCR primers specific for the SCA1 genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metabolic disorder; reproductive disorder; testicular cancer; neural disorder; endocrine disorder; gastrointestinal disorder; halzheimer's disease; parkinson's diseases; diabetes; dwarfism, at schizophrenia; obesity; anorexia; osteoporosis; angina pectoris; myocardial infarction; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.4%; Score 16; DB 1; Length 20; 100.0%; Pred. No. 90; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
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                                                                                           Claim 14; Page 84; 239pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Conservative
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Best Local Similarity
Matches 16; Conserv
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E S.
                                                                                                        Homo sapiens.
                                                                                          15-JUL-2004
                                                                                                               29-APR-2004.
                                                                                       ADM16016;
                                                                                                                           (BEAU/)
(LISS/)
                                                                Query Match
                                                                                                     primer.
                                                                  Best Loca
Matches
                                                                                RESULT 63
                                                                                  ADM16016,
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Human; SAC1; PCR; ss; carbohydrate; sweetener; ethanol; obesity;
diabetes; alcoholism; antidiabetic; alcohol; anorectic; antialcoholic;
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TD ADM16014 standard; DNA; 20
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nes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                          The invention relates to an isolated human G-protein coupled receptor, CC HGPBMY30 polypeptide or a sequence having 95% identity to the above HGPBMY30 polypeptide or a sequence having 95% identity to the above condition, selected from an immune disorder; a cardiovascular disorder; an inflammatory disorder in which G-protein coupled receptors are either disorder; a reproductive disorder; a metabolic disorder; a metabolic disorder; a metabolic disorder; a neural disorder; an endocrine disorder; castionteetinal disorder; and (II) are also useful for detecting, proprietic and pulmonary disorders. Alzheimer's, Parkinson's alseases, diabetes, dwarfism, color blindness, retinal pigmentosa, astima, expression, schizophrenia, sleeplessnesses, hypertension, anxiety, stress, renal failure, acute heart failure, hypotension, obesity, anorexia, HIV infections, osteoporosis, angina pectoris, and myocardial infarction. (I) and (II) are useful for modifying the activities of (I).

C food additive or preservative, and for modifying the activities of (I).

C food additive or preservative, and for modifying the activities of tissue, pigmentation, size and shape, to change a mammal's mental state or physical state by influencing biorhythms, caricadia rhythms, caricadia rhythms, caricadia rhythms, caricadia rhythms, caricadia rhythms, creassion, tendency for violence, tolerance for pain, reproductive capabilities, hormonal or endocrine levels, appetite, libido, memory, creass, or other cognitive qualities. This sequence corresponds to a PCR primer for the coding sequence for the novel HGPRBMY30 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                        Novel human G-protein coupled receptor, HGPRBMY30 polypeptide useful for preventing and treating e.g. immune disorders, cardiovascular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; SAC1; PCR; ss; carbohydrate; sweetener; ethanol; obesity;
diabetes; alcoholism; antidiabetic; alcohol; anorectic; antialcoholic;
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100.0%; Pred. No. 90;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
                                                                                                                                   Example 3; SEQ ID NO 21; 343pp; English.
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                                                                                             or inflammatory disorders.
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           WPI; 2003-140445/13
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100.0%; Pred. ...

1092 GGTGTTACCTGCTCAT 1107

GGTGTTACCTGCTCAT

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(first entry)

1.4%; Score 16; DB 1; Length 20; 00.0%; Pred. No. 90;

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The invention relates to SACI polypeptides and the polymucleotides canceling them. The polymucleotides contain a variation associated with encoding them. The polymucleotides contain a variation also sensing carbohydrates, other sweeteners or ethanol. The invention also comprising altering SACI activity in the sample and measuring the comprising altering SACI activity in the sample and measuring the activity, a method for analysing a polymucleotide in a biological sample, comprising contacting a polymucleotide in a biological sample, activity, a method for analysing a polymucleotide in a biological sample, comprising comparing to probe where the probe hybridises to a SACI polymucleotide to form a probe where the probe hybridises to a SACI polymucleotide to form a probe where the probe hybridises of the Nybridisation complex, a method of it is mucleotide sequence of the suspected SACI allele with a wild type condition sequence, and a method of treating or preventing obseity, and the wild-type sequence identifies a sequence variation of the SACI allele sequence, and a method of treating or preventing obseity, and instering to a subject a pharmaccuntical composition and a transgenic comming that carries an altered SACI allele. The methods and compositions and invention are useful for screening drugs for inhibition or consumption therapies and for identifying sweeteners and alcohols. This consumption therapies and for identifying sweeteners and alcohols. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotides for sensing carbohydrates, other sweeteners, or ethanol, useful for screening drugs for inhibition or restoration of gene function as antidiabetic, antiobesity or antialcohol consumption
                                                                                                                                                                                                                                                                           Tordoff MG;
                                                                                                                                                                                                                                                                           Li X, Reed DR,
De Jong PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 12; SEQ ID NO 286; 148pp; English.
                                                                                                                                                                                                                                                                                          Li S,
                                                                                                                                                                                                                                                                                                                            Chatterjee A,
                                                                                                                                                                                                                                                                                              Beauchamp GK,
                                                                                                          ROSS D A.
OHMAN J D.
CHATTERJEE A.
DE JONG P J.
LI X.
REED D R.
TORDOFF M G.
                                                                                                                                                                                                                                                                                                 AA, Beaucl
Ohman JD,
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-340133/31.
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                                                                                                                      (ROSS/)
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Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to SACI polypeptides and the polynucleotides encoding them. The polynucleotides contain a variation associated with sensing carbohydrates, other sweeteners or ethanol. The invention also relates to a method for analysing a biomolecule in a biological sample, comprising altering SACI activity in the sample and measuring the activity, a method for analysing a polynucleotide in a biological sample, comprising contacting a polynucleotide in a biological sample, comprising contacting a polynucleotide in a biological sample, comprising contacting a polynucleotide in a biological sample, comprising comparing the hybridisation complex, a method of identifying susceptibility to obesity or diabetes comprising comparing the nucleotide sequence of the suspected SACI allele with a wild type nucleotide sequence, where the difference between the suspected allele and the wild-type sequence identifies a sequence variation of the SACI nucleotide sequence, and a method of treating or preventing obesity, administering to a subject a pharmaceutical composition and a transgenic animal that carries an altered SACI allele. The methods and compositions of the invention are useful for screening drugs for inhibition or restoration of gene function as antidiabetic, antiobesity or antialcohols. This sequence represents a PCR primer used to amplify human SACI DNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotides for sensing carbohydrates, other sweeteners, or ethanol, useful for screening drugs for inhibition or restoration of gene function as antidiabetic, antiobesity or antialcohol consumption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metabolite; carotene; plant; carotene hydroxylase; lycopene beta-cyclase;
                                                                                                                                                                                                                                                                             Tordoff MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.4%; Score 16; DB 1; Length 20; 100.0%; Pred. No. 90; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endogenous carotenoid gene expression RT-PCR primer #19.
                                                                                                                                                                                                                                                                           Li X, Reed DR,
De Jong PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 12; SEQ ID NO 284; 148pp; English.
                                                                                                                                                                                                                                                                             Li S,
                                                                                                                                                                                                                                                                                             Ohman JD, Chatterjee A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1092 GGTGTTACCTGCTCAT 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADE78595 standard; DNA; 19 BP.
                                                                                                                                                                                                                                                                             Beauchamp GK,
            25-OCT-2002; 2002US-00280183
                                               25-OCT-2002; 2002US-00280183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 GGTGTTACCTGCTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                        CHATTERJEE A.
DE JONG P J.
                                                                                 BEAUCHAMP G
                                                                                                                                                 REED D R.
TORDOFF M G.
                                                                                                                                                                                                                                                                                                                              WPI; 2004-340133/31
                                                                                                                                                                                     ROSS D A.
OHMAN J D.
                                                                                                                                                                                                                                                                           Bachmanov AA,
                                                                                                                  LI S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                       therapies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention
                                                                                                                                                                                                                                                                                               Ковв DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE78595;
                                                                                                                                                                                                                        (CHAT/)
(DJON/)
                                                                                                                                 (LIXX/)
(REED/)
(TORD/)
(ROSS/)
(OHMA/)
                                                                                BACH/)
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**EXEXEXEXE** 

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The invention relates to a novel process for increasing the metabolites of carotene content of a plant. The novel process comprises upregulating at least one gene which encodes carotene hydroxylase activity. The compositions of the novel process have lycopene beta-cyclase or a beta-carotene hydroxylase activity. The process is useful for increasing the metabolites of carotene content of a plant, comprising transforming a plant cell from which viable plants may be recovered, using a plant expression cassette, or a DNA construct, and generating viable plants from the cell. The carotene metabolites are useful for increasing roamantin and beta-carotene, including oxygenated carotenoids. This polymucleotide sequence represents an RT-PCR primer used in the process for the expression of the introduced proteins and endogenous carotenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference; cytostatic; immunosuppressive; virucide; anti-HIV; cancer; autoimmune disease; viral infection; HIV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Increasing the metabolites of carotene content in a plant useful for producing recombinant plants comprises upregulating a gene encoding
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beta-carotene hydroxylase; zeaxanthin; beta-carotene; oxygenated carotenoid; RT-PCR; primer; carotenoid; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pallara P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19 BP; 6 A; 1 C; 8 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human BCL2 siNA upper sequence SEQ ID NO:805.
                                                                                                                                                                                                                                                                                                                                                                                                                                         (CNEN ) ENEA ENTE NUOVE TECNOLOGIE ENERGIA. (BIOJ ) BIOGEN SRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.4%; Score 15.8; Deg. No. 95; Pred. No. 95; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dharmapuri S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 12; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435 GAGGAGATGATTTTAGCTG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGAGAGAGTTTAGCTG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carotene hydroxylase activity.
                                                                                                                                                                                                                                                                                                                                                                         09-NOV-2001; 2001IT-RM000670.
                                                                                                                                                                                                                                                                                                      08-NOV-2002; 2002EP-00425681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Giuliano G, Rosati C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-714401/68.
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                                                                                                   Unidentified
                                                                                                                                                                      EP1323825-A2
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                                                                                                                                                                                                                                      02-JUL-2003.
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09-SEP-2002; 2002US-0409293P.
15-JAN-2003; 2003US-0440129P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9613608-A2
                                                                                                                        BCL2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT36558;
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
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     that downtion relates to a novel short interfering nucleic acid (siNh) that downregulates expression of the BCL2 gene by RNA interference. A siNA of the invention has cytostatic, immunosuppressive, virucide, and anti-HIV activity. The siNA are useful for modulation (inhibition) of expression or activity of BCL2 by RNA interference. siNA are used to modulate expression of BCL2 genes, in cells, tissue explants or organisms, e.g. for treating cancer, autoimmune diseases and viral infections (including by HIV) but also for drug screening, diagnosis, target identification and validation, genetic enginecting, pharmacogenomics, studying gene function and gene mapping (e.g. of single-nuclectide polymorphisms). The sequences shown in ADF49273-ADF50143 represent siNA of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference; cytostatic; immunosuppressive; virucide; anti-HIV; cancer; autoimmune disease; viral infection; HIV.
                                                                                                                                                                     New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer or autoimmune disease, downregulates expression of
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 8 A; 4 C; 3 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human BCL2 siNA upper sequence SEQ ID NO:391.
                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.8; DB
Pred. No. 95;
0; Mismatches
                                                                                                                                                                                                                   Example 3; SEQ ID NO 805; 148pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                 482 ACAGTGCATTGAATTTCTT 500
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0
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11-MAR-2002; 2002US-0363124P.
06-JUN-2002; 2002US-0386782P.
18-JUL-2002; 2002US-0396905P.
29-AUG-2002; 2002US-0406784P.
05-SEP-2002; 2002US-0408378P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acadregarrecarricrr 1
      20-FEB-2002; 2002US-0358580P.
11-MAR-2002; 2002US-0363124P.
06-JUN-2002; 2002US-0386782P.
18-JUL-2002; 2002US-0396905P.
29-AUG-2002; 2002US-0406784P.
05-SEP-2002; 2002US-0408378P.
05-SEP-2002; 2002US-0409378P.
15-JAN-2003; 2003US-040929P.
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                                                                                                                                                                                                                                                                                                                                                                                                         1.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADF49663 standard; RNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-FEB-2004 (first entry)
                                                                                                         (RIBO-) RIBOZYME PHARM INC.
                                                                                                                              Mcswiggen J, Beigelman L;
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 89.5
nes 17; Conservative
                                                                                                                                                    WPI; 2003-712622/67.
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                                                                                                                                                                                                 the BCL2 gene.
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Matches
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c-gtp; guanosine 5'-triphosphatase; GTPase; enzyme; probe;
GTP-binding protein; primer; detection; differentiation; microorganism;
biological sample; thermophilic; veterinary; Campylobacter; jejuni; coli;
lari; upsaliensis; human; pathogen; diarrhoea; infection; fetus;
hyointestinalis; mucosalis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTPase gene family sequences derived from Campylobacter species - for use
                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel short interfering nucleic acid (siNA) that downregulates expression of the BCL2 gene by RNA interference. A siNA of the invention has cytostatic, immunosuppressive, virucide, and anti-HIV activity. The siNA are useful for modulation (inhibition) of expression or activity of BCL2 by RNA interference. siNA are used to modulate expression of BCL2 genes, in cells, tissue explants or organisms, e.g. for treating cancer, autoimmune diseases and viral infections (including by HIV) but also for drug screening, diagnosis, target identification and validation, genetic engineering, pharmacogenomics, studying gene function and gene mapping (e.g. of sing runcleotide polymorphisms). The sequences shown in ADF49273-ADF50143 represent siNA of the invention.
                                                                                                                                                                         New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer or autoimmune disease, downregulates expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19 BP; 4 A; 3 C; 4 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.4%; Score 15.8; E
17.4%; Pred. No. 95;
ive 8; Mismatches
                                                                                                                                                                                                                                                                                                              Example 3; SEQ ID NO 391; 148pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campylobacter fetus specific probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INNO-) INNOGENETICS NV. (DELF-) DELFT DIAGNOSTIC LAB BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         482 ACAGTGCATTGAATTTCTT 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT36558 standard; DNA; 20
(RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                               Mcswiggen J, Beigelman L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-239513/24.
                                                                                                                          WPI; 2003-712622/67.
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2 GTGCATGAAGAGGCAGATA 20

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                                                                                    The present sequence is a Campylobacter fetus c-gtp gene specific probe. The c-gtp gene encodes a guanosine 5'-triphosphatase (GTBase) enzyme, or GTP-binding protein. The gene can be used in the prepn. Of probes and primers, i.e. the present sequence, for the detection and differentiation of microorganisms in biological samples. Thermophilic and veterinary campylobacter sp. can be detected with probes or primers derived from the c-gtp-1 and c-gtp-2 gene families, respectively. Thermophilic campylobacter sp. include C. jejuni, C. coli, C. lari and C. upsaliensis, which are human pathogens involved in diarrhoes causing infections.
                                                                                                                                                                                                                                                       Veterinary Campylobacter sp., encompass sp. which are important in veterinary infections, e.g. C. fetus, C. hyointestinalis and C. mucosalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method of identifying textiles of fur, comprising amplifying DNA fragment specific for each animal fur, and analysing amplified DNA. The method is useful for identifying fur textiles. The method effectively distinguishes the origin of animal fur. The present sequence represents a fox specific PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying fur textiles involves amplifying DNA fragment specific for each animal fur, and analyzing amplified DNA.
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
detection and differentiation of thermophilic and veterinary
                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                               ch 1.4%; Score 15.8; DB 1; Length 20; Il Similarity 89.5%; Pred. No. 97; 17; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fur textile; animal fur; ss; PCR; primer; fox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NIBO-) ZH NIPPON BOSEKI KENSA KYOKAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 2; 9pp; Japanese.
                                                   Claim 21; Page 62; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            931 TAGAAATGCAGAATCTGAA 949
                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TAGCAATGCAGAATCTGCA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG37263 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fox specific PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                   species of Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-819736/77.
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canidae.
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Matches
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The invention relates to an antisense oligonucleotide comprising 8-80 nucleobases in length targeted to the coding region of a nucleic acid molecule encoding PPAR-delta (peroxisome proliferative activated receptor delta), where the antisense compound inhibits the expression of the PPAR-delta delta and has any of the 66 sequences of 20 amino acids fully defined in the specification. Also included are a compound of 8-80 nucleobases in length that specifically hybridises with at least an 8-nucleobase portion of a preferred target region on a nucleic acid molecule encoding PPAR-delta and a composition comprising the antisense oligonucleotide and a carrier. The antisense oligonucleotide comprises at least one modified internucleoside linkage (preferably a phosphorothioate linkage), at least one sugar molety (preferably 2'-O-methoxyethyl molety) and at least one modified nucleobase (which is a 5-methyl cytosins). The antisense compounds are useful for treating cancer, osteoporosis, diabetes or various endocrine disorders. The Human PPAR delta gene is located on chromosome 6p21. The present sequence is an antisense oligonucleotide of the invention targeting human PPAR delta.
                                                                                                                                                                                                                                                                                                               /mod_base= OTHER
/note= "Phosphorothioate linkages and all cytidines are 5
-methylcytidines"
                                                                                                                                                                    Human, 88; PPAR delta; peroxisome proliferative activated receptor delta; antisense gene therapy; cytostatic; osteopathic; antidiabetic; cancer; osteoporosis; diabetes; endocrine disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense oligonucleotides of 8-80 nucleobases, useful for treating cancer, diabetes, osteoporosis or various endocrine disorders.
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                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/mod_base= OTHER
/note= "2'-methoxyethyl residue"
16 .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "2'-methoxyethyl residue"
                                                                                                                                     Human PPAR antisense oligonuclotide ISIS 136891.
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                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mod base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watt AT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAY-2002; 2002US-00160807
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                                ADG86812 standard; DNA; 20
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/*tag= b
                                                                                                   11-MAR-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-022078/02.
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                                                                                                                                                                                                                                                                            Key
modified_base
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                                                                                                                                                                                                                                            Homo sapiens
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                                                                ADG86812;
RESULT 70
                ADG8681
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Ouery Match
1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels

791 GTGCTTGGAGAGGCAGATA 809

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interleukin; IL-4 receptor; IL-5 receptor; lung disease; airway inflammation; allergy; asthma; impeded respiration; cystic fibrosis; acute respiratory distress syndrome; pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
                                                                                                                       Oligonucleotide associated to IL5R-X61176 #222.
                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-2002; 2002US-0399076P.
                                                                                                                                                                                                                                                                                                                                                                        25-JUL-2003; 2003WO-US023509.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENESIS PHARM INC
                         ADJ61530 standard; DNA; 20
                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang L, Sr
                                                                                                                                                                                                                                                                                                     WO2004011613-A2.
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Shahabuddin S,
                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
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                                                                                               06-MAY-2004
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                                                               ADJ61530;
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              ADJ61530,
                                g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an antisense oligomucleotide comprising 8-80 mucleobases in length targeted to the coding region of a nucleic acid mucleobases in length targeted to the coding region of a nucleic acid delta, where the antisense compound inhibits the expression of the PPAR-delta delta and has any of the 66 sequences of 20 amino acids fully defined in the specification. Also included are a compound of 8-80 nucleobases in length that specifically hybridises with at least an 8-nucleobase portion of a preferred target region on a nucleic acid molecule encoding PPAR-colfa and a composition comprising the antisense oligonucleotide and a carrier. The antisense oligonucleotide comprises at least one modified on sugar moiety (preferably a phosphorothioate linkage), at least one sugar moiety (preferably 2.0-methoxyethyl moiety) and at least one compounds are useful for treating cancer, osteoporosis, diabetes or compounds are useful for treating cancer, osteoporosis, diabetes or various endocrine disorders. The Human PPAR delta gene is located on chromosome 6p21. The present sequence is a human PPAR delta cDNA target consequence for the antisense oligonucleotides of the invention.
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                                                                                                                                                                                                                                                                                                                       Human; ss; PPAR delta; peroxisome proliferative activated receptor delta; antisense gene therapy; cytostatic; osteopathic; antidiabetic; cancer; osteoporosis; diabetes; endocrine disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense oligonucleotides of 8-80 nucleobases, useful for treating cancer, diabetes, osteoporosis or various endocrine disorders.
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                                    Gaps
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Length 20;
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                                                                                                                                                                                                                                                                                            Human PPAR antisense oligonucleotoide target sequence #22.
                                      Indels
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                                      5;
     DB 1;
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Pred. No. 97;
 1.4%; Score 15.8; Lilarity 89.5%; Pred. No. 97; Conservative 0; Mismatches
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                                                                          783 TTGGGGATGTGCTTGGAGA 801
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Conservative
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                                                                                                                                                                                              ADG86960 standard; cDNA; 20
                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Freier SM,
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                         Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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          Query Match
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                                                                                                                                                                 RESULT 71
                                                                                                                                                                                 ADG86960/
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Miller S;

Aguilar D,

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The present invention relates to an oligonucleotide anti-sense to e.g., cinitiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-cinitiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-complexity of 11.0-4 receptor. IL-5 receptor or salts of the coligonucleotide and optionally surfactant operatively linked to the oligonucleotide. The method is useful for preventing or treating a ceptional partiactory or lung disease, which involves administering to the alrways of subject an effective amount of an inhibitor. The oligonucleotide is of a subject an effective amount of a medicament for the prevention and/or treatment constructory or lung disease. The respiratory or lung disease. The respiratory or lung disease. The respiratory or lung disease. Consention alrway inflammation, allergy(ies), asthma, impeded chosen from alrway inflammation, allergy(ies), asthma, impeded constructive pulmonary diseases syndrome (CODP), allergic rhinitis (AR), acutte respiratory distress syndrome (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway construction. The present sequence represents an oligonucleotide of the
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                                                                                                                                         Novel single or multiple target oligonucleotide anti-sense to e.g. initiation codons and introns of respiratory disease-relevant genes e.g., CCRI, RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g., asthma.
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89.5%; Pred. No. 97;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                         Claim 2; SEQ ID NO 2386; 85pp; English
Sandrasagra A,
H, Cong H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression, for diagnosing, preventing or treating e.g. dyslipidemia, low high density lipoprotein or cardiovascular disorders.
                                                                                                                                                                                                                 /mod_base= OTHER /note= or phosphorothioate /note= "This oligonucleotide has a phosphorothioate backbone and 2.'methyoxyethyl (2'-MOE) wings at the 5' and 3' ends, which are 4 nucleocides in length. Also all
                                                                    Antilipaemic, Cardiovascular, Analgesic, Antianginal, Antisense therapy, Human, Endothelial Lipase, dyslipidaemia, high density lipoprotein, HDL, cardiovascular disorder, metabolic syndrome X; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25517), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are used for diagnostics, prophylaxis, or as research reagents or kits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
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                                         Human endothelial lipase antisense oligonucleotide, SEQ ID 3287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense oligonucleotide for modulating endothelial lipase
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                                                                                                                                                                                                                                                                            cytidine residues are 5-methylcytidines'
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                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 GCCCGGGCCGTGGCAGGAA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В.
                                                                                                                                                                                                                                                                                                                                                                 18-JUL-2003; 2003WO-US022410
                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2002; 2002US-0397106P
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                                                                                                                                                                                                       ಶ
             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                       . 20
                                                                                                                                                                                                       *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                          (PHAA ) PHARMACIA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-132912/13.
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                                                                                                                                                                        Key
modified_base
                                                                                                                              sapiens
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             20-MAY-2004
                                                                                                                                                                                                                                                                                                                                      29-JAN-2004
                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bhat BG;
                                                                                                                               Ношо
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                                                                                                                                                                                                                                                          /*tag= a //*tag= a //*tag= a //*tag= A //*tag= //*mod_base= OTHER //*mod_base= "This Oligonucleotide has a phosphorothioate backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5' and 3' ends, which are 4 nucleotides in length. Also all cytidine residues are 5-methylcytidines"
Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL; cardiovascular disorder; metabolic syndrome X; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25511), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are used for diagnostics, prophylaxis, or as research reagents or kits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antisense; PPAR-delta; human; hybridisation; inhibitor; phosphorothioate linkage; 2'-O-methoxyethyl sugar; 5-methylcytosine; hyperproliferative disorder; cancer; cytostatic; gene therapy; 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 2 A; 5 C; 12 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.8; I
Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; SEQ ID NO 2262; 1007pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense oligonucleotide ISIS 136891.
                                                                                                                                                                                                  location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccececearecases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PHAA ) PHARMACIA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-132912/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004009541-A2.
                                                                                                                                                                                                      Key
modified_base
                                                                                                        Homo sapiens
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This invention describes novel antisense oligonucleotides targeted to a nucleic acid encoding PPAR-delta, which specifically hybridise to and inhibit expression of PPAR-delta. The oligonucleotide specifically hybridises with at least an 8-nucleobase portion of an active site on the mucleic acid molecule encoding the PPAR-delta and comprises at least one modified internucleoside linkage, which is a phosphorothicate linkage, at least one modified sugar moiety, which is a 2'-O-methoxyethyl sugar moiety or at least one modified nucleobase, which is a 5-methylcytosine. The antisense oligonucleotides are useful for preparing a composition for treating hyperproliferative disorders, e.g., cancer. The oligonucleotides of the invention have cytostatic activity and can be used for gene
                                                                                                                                                                                                                                New antisense oligonucleotide, having a sequence targeted to a nucleic acid encoding PPAR-delta, useful for preparing a composition for treating hyperproliferative disorder, e.g., cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antisense; PPAR-delta; human; hybridisation; inhibitor;
phosphorothioate linkage; 2'-O-methoxyethyl sugar; 5-methylcytosine;
hyperproliferative disorder; cancer; cytostatic; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.8; DB 1; Length 20; Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 5 A; 1 C; 7 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human PPAR-delta target site ID 50011.
                                                                                                                                                                                                                                                                                                Example 15; SEQ ID NO 48; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     783 TTGGGGATGTGCTTGGAGA 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TTGTAGATGTGCTTGGAGA 19
                                                                                                                                                                               Watt AT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-SEP-2003; 2003US-00655847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-2002; 2002US-00160807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.4%;
                                                         05-SEP-2003; 2003US-00655847
                                                                                     31-MAY-2002; 2002US-00160807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL34898 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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nes 17; Conservative
                                                                                                                                                                             Saarde W, Freier SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GAAR/) GAARDE W.
(FREI/) FREIER S M.
(WAIT/) WAIT A T.
                                                                                                                                                                                                          WPI; 2004-282460/26.
                                                                                                                  (GAAR/) GAARDE W.
(FREI/) FREIER S M.
(WATT/) WATT A T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2004063129-A1.
US2004063129-A1
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                              01-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL34898;
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This invention describes novel antisense oligonucleotides targeted to a nucleic acid encoding PPAR-delta, which specifically hybridise to and inhibit expression of PPAR-delta. The oligonucleotide specifically hybridises with at least an 8-nucleobase portion of an active site on the nucleic acid molecule encoding the PPAR-delta and comprises at least one modified internucleoside linkage, which is a phosphorothhoate linkage, at least one modified sugar moiety, which is a 2'-O-methoxyethyl sugar moiety of an at least one dedified nucleobase, which is a 5-methylcytosine. The antisense oligonucleotides are useful for preparing a composition for treating hyperproliferative disorders, e.g., cancer. The oligonucleotides of the invention have cytostatic activity and can be used for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                          New antisense oligonucleotide, having a sequence targeted to a nucleic acid encoding PPAR-delta, useful for preparing a composition for treating hyperproliferative disorder, e.g., cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5; CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a; tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease; tryptase b; PDE5 A; PDE4 B; PDE6 C; PDE5 D; adenosine A receptor; asthma; lung disease; hyper-responsiveness; adenosine; adenosine A receptor; asthma; lung allergy; inflammation; inflammatory disease; airway inflammation; allergy; impeded respirator; disease; chronic obstructive pulmonary disease; COPD; allergic fibrosis; CF; acute respiratory distress syndrome; pulmonary hypertension; lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 7 A; 7 C; 1 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                            Score 15.8; DF
                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 97;
0; Mismatches
                                                                                                                                Example 16; SEQ ID NO 196; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGGGGATGTGCTTGGAGA 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 TTGTAGATGTGCTTGGAGA 2
          Watt AT;
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23-APR-2002; 2002WO-US013143.
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                                                                                                                                                                                                                                                                                                                                                                                                             1.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human oligonucleotide #2286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADO46920 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 89.5
nes 17; Conservative
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AGUILAR D.
MILLER S.
SHAHABUDDIN S.
LU H.
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SANDRASAGRA
          Freier SM,
                                      WPI; 2004-282460/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2004049022-A1.
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          Gaarde W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NYCE/)
(SAND/)
(TANG/)
(AGUI/)
(MILL/)
(SHAH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             783
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                  therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO46920/c
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 77
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The invention relates to oligonucleotides anti-sense to an initiation codon, coding region, 5' or 3' intron-exon junction, intron or region with 2-10 mucleotides of the 5'-end or 3'-end of a mucleotides of the forest of a method of screening a candidate compound that binds to one or more nucleic acid target (8) or expressed product (8), for the prevention and/or treatment of a respiratory or lung disease. The coligonucleotides are useful for reducing or inhibiting expression of a constant of a post a. PDE4 & post B. PDE4 & post B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                          Novel single or multiple target oligonucleotide anti-sense to e.g. initiation codon, intron of respiratory disease-relevant gene e.g. CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arthritic condition; CD21L; lymphotoxin-beta; chemoattractant; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bronchoconstriction. This sequence represents an oligonucleotide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer used to amplify a beta-actin cDNA fragment.
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                                            Aguilar D, Miller
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                               Claim 2; SEQ ID NO 2386; 174pp; English.
                                            \, Tang L,
Cong H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      624 GAGTTTTATTCTCAGCAAA 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 GACTITIATCCTCAGCAAA 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta-actin; PCR; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABV76832 standard; DNA; 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Conservative
                                              Sandrasagra A,
                                                                  Shahabuddin S, Lu H,
                                                                                                              WPI; 2004-293804/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
(CONG/) CONG H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200280010-A1
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                                                Nyce JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                      arthritic condition in a mammal. The method comprises determining whether or not a sample from the mammal contains at least 1 marker (e.g. an elevated level of a LD21L polypeptide, an elevated level of a lymphotoxin-beta polypeptide, or an elevated level of a chemoattractant polypeptide). The presence of the marker indicates that the arthritis condition is severe. The method is useful for diagnosing the severity of an arthritis condition (e.g. rheumacoid arthritis) in a mammal, particularly a human. Control PCR primers ABU76832-33 were used to amplify a beta-actin cDNA fragment from a synovial tissue sample. The primers were used in the method of the invention
                                                                                                 Determining the severity of arthritic conditions, e.g. rheumatoid arthritis, in a mammal or human by detecting whether a sample contains elevated levels of marker(8), e.g. CD21L polypeptides or lymphotoxin-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rheumatoid arthritis condition, RA; cytokine; interleukin-1 beta; IL-1beta; interleukin-4; IL-4; interleukin-10; IL-10; interferon-gamma; IFN-gamma; tumour necrosis factor-alpa; TNF-alpha; transforming growth factor-beta; TGF-beta; diffuse; follicular; granulomatous; human; beta-actin; PCR; primer; ss.
                                                                                                                                                                                                                           specification describes a method for determining the severity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Evaluating rheumatoid arthritis condition in patient, by comparing cytokine levels in sample from patient to reference levels to obtain information about condition, and classifying condition based on the Information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21 BP; 3 A; 8 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primer #1 for DNA encoding human beta-actin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15.8; DB
Pred. No. 99;
0; Mismatches
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(MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
                                                                                                                                                                                        Example 2; Page 12; 27pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 GCCGGAAGCAGCCGCGCC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 deredakáckáckéredece 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 89.5
Matches 17; Conservative
                                  Weyand CM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-687206/65.
                                                                 WPI; 2003-058450/05.
                                                                                                                                                      polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6555320-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-SEP-1998;
                                  Goronzy JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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ADA73990/
8X1X8X244444X8X22222222222
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The present invention relates to novel methods for constructing fungal strains useful for identification and validation of gene products as targets for therapeutic agents, for creating a collection of identified essential genes, and screening assays for the discovery of new drugs. The invention provides the GRACE (gene replacement and conditional expression) method for the construction of mutant organisms referred to as GRACE strains of the organism. The invention can be applied to any Aspergillus fumigatus and Cryptococcus neoformans. The methods are useful to identify agents that may be used in the treatment of fungal infections. AAS23687-AAS23747 represent primers A #1-61 used as probes
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                            The present invention relates to a method for evaluating rheumatoid arthritis (RA) condition in a patient. The method involves determining the level of cytokines (e.g. interleukin-1 (IL-1) beta, interleukin-4 (IL-4), interleukin-4 (IL-4), interleukin-4 (IL-4), interleukin-4 (IL-4), interleukin-10 (IL-10), interferon gamma, tumour necrosis factor-4), interleukin-10 (IL-10), interferon gamma, tumour necrosis factor-4 lapha (TMR-alpha), and transforming growth factor-beta (TGF-beta)) within the sample from a patient, comparing the level to reference levels to condition as batient bout the RA condition, and classifying the RA condition based on information. The method is useful for classifying a RA condition based on information. The method is useful for classifying a RA condition as diffuse, follicular, or granulomatous, and for determining if an individual suffering from a RA condition will develop severe disease. The present sequence represents a PCR primer used in the examples of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   essential gene; GRACE; pathogenic fungus; conditional expression; fungal infection; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer A #15 used as probe for identifying C. albicans GRACE strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying genes essential to fungal metabolisms and identifying potential therapeutic agents that target these genes.
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                                                                                                                                                                                                                                                                                                                                                                                              1.4%; Score 15.8; DB 1; Length 21; 89.5%; Pred. No. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 3 A; 8 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 99;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 303; 324pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 GCCGGAAGCAGCCGCGCC 56
Example 1; Col 9; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GCTGGAAGCAGCCGTGGCC 3
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AAS23701 standard; DNA; 22 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene identification;
gene replacement and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-489080/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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The invention relates to constructing (MI) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by the expression of the second allele is regulated by the promoter. Go that expression of the second allele is regulated by the promoter. (MI) is useful for constructing a strain of diploid fungal promoter. (MI) is useful for pathogenicity of a fungus, a gene that cells having both alleles modified are useful for identifying a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian capen. (MI) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon activity of a gene product, preferably enzymatic activity, carbon activity of a useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon cativity of a gene product, preferably enzymatic activity, carbon activity of a seful for identifying a compound having the activity to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of a primer used in the method of the invention. Note: The sequence data for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 36; SEQ ID NO 4031; 167pp + Sequence Listing; English.
                                                                               Score 15.8; DB 1; Length 22;
Pred. No. 1e+02;
                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Candida albicans GRACE strain PCR primer SEQ ID NO 4031.
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                                                                                                                         5,
                                     Sequence 22 BP; 9 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                           0; Mismatches
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for identifying C. albicans GRACE strains
                                                                                                                                                                     337 TCGTGTGGCTGTGATCAAA 355
                                                                                                                                                                                                          19 rcdrdrddcrdrrcrcaaa 1
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20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
                                                                                                                                                                                                                                                                                                                    BP
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                                                                                     Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                      ABZ29880 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Candida albicans
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                                                                                                                                                                                                                                                                                   RESULT 81
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This invention describes a novel method for the detection and/or typing of Helicobacter pylori strains present in a sample using PCR primers and probes to detect regions of the vacuolating toxin (vacad) gene and other virulence determinant genes (VDG) e.g. the cytotoxin-associated (cagh) gene. The method allows the typing and allele-specific detection of a strain according to the VDG alleles present in that particular H. pylori strain. The virulence determinant genes are the genetic elements involved in enabling, determining, and marking the infectivity and/or pathogenicity of the H. pylori strain. The method provides a way of detecting H. pylori strains in a sample with respect to the development of chronic active gastritis, gastric and duodenal ulcers, gastric adencarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or determining eradication therapy. AAV73508-V73546 represent PCR primers and probes used in the detection of the H. pylori vacA and cagA genes. The primers and probes are used especially to detect the vacA S regions Slabb/c and S2 and the M regions MI and M2 which are represented in
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this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR primer; probe; vacA; cagA; detection; vacuolating toxin; VDG; virulence determinant gene; cytotoxin-associated gene; allele-specific; infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer; adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy; S region; Sla; Slb; Slc; S2; M region; M1; M2; ss.
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Method for detecting and/or typing Helicobacter pylori strains - comprises use of primers and probes based on vacA and cagA gene.
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0
                                                                                             1.4%; Score 15.8; DB 1; Length 22; 89.5%; Pred. No. 1e+02;
                                                                                                                                   2; Indels
                                                     Sequence 22 BP; 9 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
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                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 46; 122pp; English.
                                                                                                                                                                     337 TCGTGTGGCTGTGATCAAA 355
                                                                                                                                                                                               19 TCGTGTGCTGTTCTCAAA 1
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                                                                                                               Local Similarity 89.5
nes 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori
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                                                                                             Query Match
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Matches
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                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                     Novel human nucleic acid NOVX gene probe Ag650 forward primer.
  Length 20;
                                              Indels
Score 15.6; DB 1;
Pred. No. 1.1e+02;
2; Mismatches 1;
                                                                                             CTTCAGTGGGGCTATTGG 120
                                                                                                                                            CTTTAGTRGGGYTATTGG 19
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2002US-0387668P.
2002US-0387696P.
2002US-0387859P.
1.4%;
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2002US-0387610P.
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2002US-0386796P.
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2002US-0387078P.
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                                                 Conservative
                        Best Local Similarity
Matches 15; Conserv
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06-JUN-2002;
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                                                                                             103
                                                                                                                                                                                                                                                                                                            ADH42586;
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    Query Match
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                                                                                                                                                                                                              RESULT 83
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(first entry)

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Preparing a DNA molecule comprises attaching an adaptor having at least one known sequence and a nonblocked 3' end to the ends of the modified DNA fragments to produce adaptor-linked fragments.
                                            DNA molecule preparation method oligonucleotide primer #95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 95; 205pp; English.
                                                                                         ss; primer; DNA preparation; adaptor.
                                                                                                                                                                                                                                                                                                          07-MAR-2003; 2003US-0453071P.
                                                                                                                                                                                                                                                                    08-MAR-2004; 2004WO-US006982
                                                                                                                                                                                                                                                                                                                                                     (RUBI-) RUBICON GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-668947/65.
                                                                                                                                                                                     WO2004081183-A2.
                                                                                                                                                                                                                              23-SEP-2004.
               16-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                    Pinter J, 1
Makarov VL;
                                                                                                                                               Synthetic.
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to 566 new isolated human polypeptides and their encoding genes, sequences that are at least 95% identical to these or sequences comprising one or more conservative substitutions in these. The polypeptide, polymelectide and antibodies against the polypeptides are useful in diagnosing, treating or preventing NOYX-associated disorders, e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, Alzheimer's disease, Rultiple sclerosis, graft-versus-host disease, hand, multiple sclerosis, asthma, or fertility disorders. The nucleic acids are further used as hybridization probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as vaccines. This sequence represents an example of the forward primer used to amplify a probe to isolate the nucleic acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New NOVX polypeptides and nucleic acid molecules useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, in chromosome mapping, tissue typing or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kekuda R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL; Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR; Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Kekuda R, Grosse WM, Gunther E, Guo X, Gusev VY, Herrmann JL, JW, Kekuda R, Khramtsov NV, Larochelle WJ, Li, L, Liang H, Low K, Macdougall JR; Maclachlan T, Malyankar UM, Mcqueeney K, Mezick AJ, Miller CE; Miller T, Radigaru M, Patturajan M, Peyman JA, Qian X, Rastelli L; Rieger DK, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ; Wolenc AR, Zhong M, Zhong H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22 BP; 3 A; 4 C; 3 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.4%; Score 15.6; DB 1;
81.8%; Pred. No. 1.1e+02;
iive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 1139; 1503pp; English.
                                                                   06-AUG-2002; 2002US-0401528P.
09-AUG-2002; 2002US-0401528P.
13-AUG-2002; 2002US-0403458P.
15-AUG-2002; 2002US-0403458P.
15-AUG-2002; 2002US-0403417P.
15-AUG-2002; 2002US-040317P.
15-AUG-2002; 2002US-0403178P.
26-AUG-2002; 2002US-0406182P.
13-SEP-2002; 2002US-0410885P.
13-SEP-2002; 2002US-04105958P.
23-CCT-2002; 2002US-0415958P.
23-CCT-2002; 2002US-0415958P.
23-CCT-2002; 2002US-0415958P.
                                                                                                                                                                                                                                                                                                                                                   2002US-0420852P
                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-2002; 2002US-0423095P
05-NOV-2002; 2002US-0423748P
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-053467/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmacogenomics.
                                                                                                                                                                                                                                                                                                            23-OCT-2002;
23-OCT-2002;
24-OCT-2002;
31-OCT-2002;
01-NOV-2002;
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Kurihara T, Sleptsova I, Bruening E, Ziehler W;

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The invention relates to a method of preparing a DNA molecule by attaching an adaptor having at least one known sequence and a nonblocked attaching an adaptor having at least one known sequence and a nonblocked 3 and to the ends of the modified DNA fragments to produce adaptor.

Combolocked 3, end of the adaptor, leaving a nick site between the combolocked 3, end of the adaptor, leaving a nick site between the comprises: (a) obtaining at least one DNA molecule; (b) randomly comprises: (a) obtaining at least one DNA fragments; (c) modifying the chase of the DNA fragments to produce DNA fragments; (d) attaching an adaptor having at least one known sequence and a nonblocked 3 end to adaptor having at least one known sequence and a nonblocked 3 end to fragments, where the 5 end of the modified DNA is attached to the comblocked 3 end of the adaptor, leaving a nick site between the comblocked 3 end of the modified DNA is adaptor; (e) extending the adaptor-linked fragments. This sequence corresponds to an of the adaptor-linked fragments. This sequence corresponds to an of the modified DNA from the nick site; and (f) amplifying the coligonucleotide used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 1.4%; Score 15.6; DB 1; Length 22; 1 Similarity 81.8%; Pred. No. 1.1e+02; 18; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22 BP; 2 A; 2 C; 6 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 GAATTGTTGTTTCTGCCTTTGG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAATTTGGTTTCTTGCTTTGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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Best Local S
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Gaps ;

4; Indels

GATTACAGTGCATTGAATTTCT 499 Griricariccarriccarricr 22

478

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18; Conservative

Matches

ADS75784 standard; DNA; 22 BP.

RESULT 84 ADS75784 ADS75784;

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Jarvis T,
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                                                                                                                                                                                 and amplifying a genome or a transcriptome comprises subjecting
                                                                                                                                                                                                                                          The present invention relates to a method for preparing and amplifying a
                                                                                                                                                                                                                                                       genome, a transcriptome, or both, or a nucleic acid, e.g. DNA or RNA molecule or a DNA molecule generated from at least one mRNA molecule. The method comprises subjecting the DNA molecule/primer mixture or the RNA molecule/primer mixture to a polymerase, under conditions where the subjecting steps generate molecules including all or part of the constant region at each end. The present sequence was used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour and; ogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; kippel-Trenannay-Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
                                                                                                                          Kurihara T;
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ERG hammerhead ribozyme target sequence, Seq ID No 1048
                                                                                                                                                                                                                                                                                                                                                                                 1.4%; Score 15.6; DB 1; Length 22;
81.8%; Pred. No. 1.1e+02;
                                                                                                                       Sleptsova I,
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                          Sequence 22 BP; 2 A; 2 C; 6 G; 12 T; 0 U; 0 Other;
                                                                                                                       Pinter J,
                                                                                                                                                                                            molecule/primer mixture to a polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                   Example 25; SEQ ID NO 93; 208pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                 297 GAATTGTTGTTTCTGCCTTTGG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                        22
                                                                                                                       Bruening E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAATTTTGGTTTCTTGCTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK18401 standard; RNA; 17 BP
                                                08-MAR-2004; 2004WO-US006983
                                                                       07-MAR-2003; 2003US-0453060P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                               (RUBI-) RUBICON GENOMICS
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 81.8
nes 18; Conservative
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                                                                                                                       Sun T,
                                                                                                                                                           WPI; 2004-677550/66.
WO2004081225-A2
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                                                                                                                      Kamberov E,
Makarov VL;
                         23-SEP-2004
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                                                                                                                                                                                  Preparing
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, the conditions selected from cancer, lymphoma, arthritis, psoriasis, vertuca neovascular glaucoma, myopic degeneration, arthritis, psoriasis, vertuca conditionme, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu (Weber syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more therapies under conditions suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (I) to the patient in conjunction with one or more of other therapies such as radiation or chemotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting the cell with (I). (I) is useful for cleaving RNA of SEG gene, by contacting the cell with (I). (I) is useful for cleaving RNA of cation such as Mg2+. (I) is useful for reducing ERG activity in a cell, by contacting the expression of ERG, and as diagnostic tool to cation such as Mg2+. (I) is useful for diagnostic fool to cation such as Mg2+. (I) is useful for diagnostic tool to cation such as man especifically cation genes that share homology with ERG gene or ERG fusion genes.

CRANINGSA-ABKZ1919 represent nucleic acids, including antisense and carried acides acides including antisense and construction or cation and cation or cation or cation cation or cation or cation or cation cation cation or cation 
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                                                                                                                                                                                                                               Novel polynucleotide which down regulates expression of Ets-related genuseful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABKI7354 ABK22719 represent nucleic acids, including antisense and enzymatic nucleic acid molecules which regulate expression of ERG, and related PCR primers of the invention
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Randi AM
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Pred. No. 1.1e+02;
4; Mismatches 1; Indels
      Mclaughlin F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 4 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
            Mcswiggen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 78; 149pp; English.
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ABT38549 standard; DNA; 17 BP.
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      Von Carlowitz I,
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                                                                                                            WPI; 2002-082995/11.
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New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.

Tuijnder M;

Telerman A, Amson R, WPI; 2003-441574/41. Disclosure; Page 406; 771pp; French.

Fri Aug 19 11:00:00 2005

Tuijnder M;

Amson R,

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WPI; 2003-313353/30.
Telerman A,
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The invention relates to a novel isolated 17 mer nucleic acid sequence, a given in the specification, a sequence containing at least 15 consecutive given in the specification, a sequence with, after optimal anceled alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of hybridizes to them under highly stringent conditions, or the complement of acids of the invention are useful as probes and primers for detecting, identifying and/or amplifying a nucleic acid, e.g. as one identifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti) sense reagents, and for component of a gene chip, in vitro as (anti) sense reagents, and for component of a gene chip, in vitro as (anti) sense reagents, or and for component of the mortalic acids, cells containing the nucleic acids for prevention and/or treatment of viral components of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell components. Analysis of the expression of the 17 mer nucleic acids in degeneration, specifically cancer but also Alzheimer's disease and diseases. The polypeptides can also be used to generate antibodies, and chips. The nucleic acid sequences of the invention can be used in gene chips. The nucleic acid sequences of the invention can be used in gene chips. The nucleic acid sequence represents a tumour suppression contacted human fukutin oligonuclectide of the invention
New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
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44.1%; Pred. No. 1.1e+02;
ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 3 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                  Disclosure, Page 523; 720pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          838 GAAGGCCGGGGTGGATC 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity 94.1%;
16; Conservative
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The invention relates to the isolation of 6327 nucleotide sequences, c fragments of at least 15 consecutive nucleotides of these nucleotides, a consecutive nucleotides of these nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides, a sequence that hybridizes under stringent conditions with nucleotides, a sequence that hybridizes under stringent conditions with nucleotides, or the complement, or corresponding RNA, of the nucleotides are used as probes or primers for detecting, nucleotides. The nucleotides are used as probes or primers for detecting, identifying and/or amplifying nucleic acids, as in vitro sepse and antisense sequences, of nucleotides involved in tumour c suppression or reversion, apptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as compained in the polypeptides (also vectors containing them and complements). The nucleotides (also vectors containing the vectors), the encoded polypeptides and antibodies colving the vectors), the encoded polypeptides and antibodies or viral infections or diseases characterized by development of tumours or eall degeneration (e.g. Alzheimer's disease or schizophrenia).

Con cell degeneration (e.g. Alzheimer's disease or schizophrenia).

Con and/or prognosis of these diseases characterides can be used to screen for their specific interactive molecules, other their specific interactive molecules, other entially useful for treating diseases associated with abnormal expression of the nucleotides associated with abnormal

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Human biallelic marker downstream amplification primer SEQ ID NO:11660.
                                                         Gaps
                                                                                                                                                                                                                                                                                                 Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
                                                         .;
0
                           1.4%; Score 15.4; DB 1; Length 17;
14.1%; Pred. No. 1.1e+02;
[ve 0; Mismatches 1; Indels
Sequence 17 BP; 3 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
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                                                                                        838 GAAGGCCGGGGTGGATC 854
                                                                                                                                                                                          BP.
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98US-0109732P.
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                                                94.18;
                                                                                                                                                                                         AAZ77304 standard; DNA; 18
                                                                                                                     17 GAAGGCCTGGGTGGATC
                                                                                                                                                                                                                                                  (first entry)
                                           Best Local Similarity 94.1
Matches 16, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                   diagnosis; ss.
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23-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                        AAZ77304;
                                    Query Match
                                                                                                                                                                    RESULT 89
                                                                                                                                                                                   AAZ77304
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                                                                                                                                                                                                                                                                                                                                                                    cytostatic, antiviral; neuroprotective; nootropic; neuroleptic; ss;
primer; probe; tumour suppression; tumour reversion; apoptosis;
virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
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Tumour suppression/reversion associated nucleotide #3203.

(first entry) (revised)

18-DEC-2003 04-DEC-2003

ADB42880;

ADB42880 standard; DNA; 17 BP.

ADB42880/ RESULT

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ð g (MOLE-) MOLECULAR ENGINES LAB

17-SEP-2001; 2001FR-00011981. 17-SEP-2002; 2002WO-IB004219

WO2003040369-A2. ношо варіепв

virus resi diagnosis.

15-MAY-2003

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                                                                                                    AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ7440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyphing studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the pharmaceutical agents are agents and sisease states. When the secting on a disease as well as other treatment.

N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3056, 3157, 3227, 3297 and 3357, are not actually given a sequence in the Sequence Listing from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel diagnostic kit for determining tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnostic; pharmaceutical tolerance; side effect; drug; human; allelic variability; polymorphism; phase I; phase II; detoxification mechanism; PCR; primer; probe; NAT2; CYP2D6; CYP1A2; CYP3A4; mEH; TPMT; MTHFR; paraoxonase; CYP2C9; CYP2C19; CYP2E1; DPD; ss.
                              Novel biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnostic kit, useful for assessing a subject's tolerance of drugs, comprises reagents for determining alleles of genes encoding
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Pred. No. 1.1e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                          Sequence 18 BP; 4 A; 2 C; 6 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human CYP2D6 C100T mutant probe H154.
                                                                           Claim 9; Page 2716; 2745pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 13; 156pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waschuetza S, Schnakenberg E,
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30-APR-2002; 2002DE-01019373.
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.4%;
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 TTCAGTGGGGCTATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD24780 standard; DNA; 18
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                                             map of the human genome.
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 WPI; 2000-013267/01
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                                                                                                                                                                                                                                                                                                                             present invention
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CC of pharmaceuticals in humans by determining allelic variability of at least two polymorphisms of a human enzyme involved in phase I and/or II CC for the detoxification mechanism in a blood, tissue or other human sample, where tolerance is determined from presence or absence of alleles. The cxit comprises two pairs of oligonucleotide primers, in which each pair of a gene for a human detoxification mechanism—associated enzyme. The kit may also contain two further pairs of oligonucleotides, serving as probes for detection of amplified DNA segments, especially where the probes are complementary to a single trand of one allele of the target gene. The probes are labelled with the fluorophores (LC-Red040 or LC-Red056 for 5'-labelling or fluorescein for 3'-labelling) which generate a different signal in the hybridized and non thypridized condition. The enzymes detected include NAT2, CYP2B1 or DPD. CYP3A4, mEH, TPWT, MTHFR, parcoxonase, CYP2C9, CYP2C19, CYP2B1 or DPD. CYP3A4, mEH, TPWT, MTHFR, parcoxonase, CYP2C9, CYP2C19, CYP2B1 or DPD. CYP3A4, mEH, TPWT, MTHFR, parcoxonase, CYP2C9, CYP2C19, CYP2B1 or DPD. CYP3A4, mEH, is used to determine an individual's tolerance of a particular drug, to establish a suitable dose and/or to predict if a subject will condition of the metabolic capacity of phase I and/or II enzymes at the molecular level. This sequence represents a probe used in the kit of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Target site; ribozyme; hammerhead; hairpin; hepatitis delta virus; group 1 intron; RNaseP RNA motif; transforming growth factor-beta; GFE-beta; Fibroue; connective; tissue disease; TGF-alpha; inhibin; epidermal growth factor; EGF; activin; amphiregulin; insulin; bone morphogenic protein; fibroblast growth factor; relaxin; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribozyme target sequence in TGF-beta mRNA (bases 2447-2465).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.4%; Score 15.4; DB 1; Length 18; Best Local Similarity 94.1%; Pred. No. 1.1e+02; Matches 16; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ81302;
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AAQ81302/0
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Cyclin B1 ribozyme binding site SEQ ID NO:3309.

(first entry)

10-SEP-2001

AAH60885;

BP

AAH60885 standard; DNA; 19

AAH60885,

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motif) cleaves the mRNA of the transforming growth factor-beta (TGF-beta) gene. This sequence corresponds to bases 2447-2465 of the TGF-beta mRNA. The ribozymes can also target the mRNAs of genes associated with the development or maintenance of fibrous or connective tissue disease in order to prevent or treat these diseases. Such genes include TGF-alpha or beta, epidermal growth factor, inhibins, activins, amphiregulin, bone morphogenic proteins, fibroblast growth factors a and b, insulin growth factor 1 or 2, insulin or relaxin. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.

Representative examples of ribozyme recognition sites are given in AAA8215 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.
                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                         Score 15.4; DB 1; Length 19; Pred. No. 1.1e+02; 0; Mismatches 1; Indel8
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                                                                                                                                                                                        Sequence 19 BP; 6 A; 3 C; 8 G; 0 T; 2 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robbins JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 96; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyclin B1 ribozyme binding site #52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barber JR,
                                                                                                                                                                                                                                                                                                    1077 CACTTAACCTCTGGG 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US028772.
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                                                                                                                                                                                                                               Query Match 1.4%;
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                           cccrraaccrcrcrgg
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA85723 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tritz R, Welch PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMU-) IMMUSOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-412314/35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA85723
                                                                                                                                                             field.)
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 92
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The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a skin or eye disease and scarring. The method involves administering a ribozyme [1] which cleaves RNA encoding a cytokine irrolved in confinemation, matrix metalloproteinase (WMP), cyclin, cell-cycle inflammation, matrix metalloproteinase (WMP), cyclin, cell-cycle candenate kinase, growth factor or a reductase, or administering a dependent kinase, growth factor or a reductase, or administering a dependent kinase, growth factor or a reductase, or administering a cholic acid molecule [1]) comprising a promoter operably linked to a nucleic acid molecule [1]). (1) can have antipsoriatic, antibication ophthalmological, cytostatic, antiseborrheic, antidiabetic, antidiabetic, antidiabetic, antidiametion. (1) can be used classases such as propriasis, atopic dermatitis, actinic keratosis, diseases such as postiasis, atopic dermatitis, actinic keratosis, calso be used for treating proliferative eye diseases such as diabetic content and etachment, and for treating and preventing correctinopathy, vitreortinopathy, sickle cell retinopathy, retinopathy of creating such as keloid, adhesion and hypertrophic or hypertrophic burn content and content and for treating and preventing content. The content of the content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.
                                                                                                                                                  Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnerary; proliferative disease; skin disease; psoriasis; diabetic retinopathy; cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP; matrix metalloproteinase; growth factor; reductase; scarring; cytostatic; antipiosoriatic; dermatological; antiseborrheic; antidiabetic; virucide; antisickling; ophthalmological; keratolytic; gene therapy; viral wart; acopic dermatitis; actinic keratosis; squamous cell carcinoma; actinic keratosis; squamous cell carcinoma; sickle cell carcinopathy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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44.1%; Pred. No. 1.1e+02;
ve 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 312; 408pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.4%;
Best Local Similarity 94.1%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMU-) IMMUSOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robbins JM, Tritz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200130362-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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790 TGTGCTTGGAGAGGCAG 806

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Gaps

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1; Indels

0; Mismatches

1.4%;

790 TGTGCTTGGAGAGGCAG 806

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Conservative

Best Local Similarity Matches 16; Conserva

Query Match

0

18 resecrissasasacas

Score 15.4; DB 1; Length 19; Pred. No. 1.1e+02;

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AAT50887-T50904 represent oligonucleotides of the invention. These sequences are all probes for interleukin-6 receptor (IL-6R) mRNA. IL-6 is one of the most well characterised of the cytokines. It functions through interacting with at least two transmembrane glycoprotein receptor. Come of the signal transduction by IL-6 involves the angenal transduction by IL-6 involves the concerted action of both IL-6R and gpl30. IL-6 overproduction is implicated in many different disease states, particularly in cellular proliferation associated with these diseases. These sequences bind to the IL-6R coding sequence, thereby inhibiting IL-6R production. The sequences therefore inhibit the functioning of IL-6. These sequences can be used for inhibiting disease-associated cellular proliferation. The oligonucleotides are especially useful for treating cancer (e.g. renal cell carcinoma), autoimmune diseases or viral infections. They can also be used as probes for detecting IL-6 receptor mRNA, especially for contacting the effectiveness of drugs in reducing IL-6 receptor mRNA
                                                                                                                                                                                                                        Probe; interleukin-6 receptor; IL-6R; cytokine; cellular proliferation; transmembrane glycoprotein receptor; signal transducer; gpl30; inhibitor; IL-6; cancer; renal cell carcinoma; autoimmune disease; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligo:nucleotide(s) complementary to interleukin-6 receptor mRNA - for treating proliferative diseases, e.g. cancer, auto-immune diseases or
                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "optionally phosphorothioated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 1 A; 8 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                         Probe #13 for interleukin-6 receptor
                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Naidu YM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 16; 18pp; English.
                                                                                    AAT50899 standard; DNA; 20 BP
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95US-00486408.
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18 resecrrecaeaceae
                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dattagupta N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENP-) GEN-PROBE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-023093/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    viral infections.
                                                                                                                                                       26-AUG-1997
                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-DEC-1996.
                                                                                                                                                                                                                                                                              therapy; ss
                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brown SJ,
                                                                                                                     AAT50899;
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The intention describes a movel antibody which receptor one crosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor of activity to a cell expressing DRS in vivo. It is also useful for preparing a therapeutic for selective apoptosis of abnormal or disregulated cells, and for inhibiting cell proliferation in a cell, preferably a human breast, ovary, colon, haematopoietic, prostate, lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may also be administered e.g. pacitizes, taxol or cycloheximide. The antibody is used to treat an autoimmune disease, systemic lupus crythematosus. Hashimoto's disease, rheumatoid arthritis, graft-versus-host disease, Sjogram's syndrome, controlmented addison disease, scleroderma, Goodpasture's syndrome, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, seterility, myasthenia gravis, multiple sclerosis, mephritis, hypoplastic anaemia, rejection after organ transplantation, and numerous malignancies of lung, prostate, liver, ovary, lymphatic or breast tissue. This primer was used to isolate the mouse TRAIL TRA-8, a ligand of the DRS receptor and the TRAIL on which the humanised antibodies of the invention are based
                                                                                                                                                                                                                                                               Tumour necrosis factor-related apoptosis-inducing ligand receptor; TRAIL;
                                                                                                                                                                                                                                                                          TRAIL receptor DR5; cytoetatic; apoptosis; cell proliferation; autoimmune disease; systemic lupus erythematosus; Hashimoto's disease; rheumatoid arthritis; Sigoren's syndrome; Crohn's disease; anaemia; Addison disease; solaroderma; Goodpasture's syndrome; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes; allergy; arteriosclerosis; myocarditis; cardiomyopathy; TRA-8; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel antibody specific for tumor necrosis factor-related apoptosis-
inducing ligand, useful for inhibiting cell proliferation in cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention describes a novel antibody which recognizes a tumour
                                                                                                                                                                                                                       TRA-8 heavy and light chain RT-PCR primer H5SS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kimberly RP, Koopman WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 16; Page 72; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAY-2000; 2000US-0201344P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAY-2001; 2001WO-US014151.
18 CAGGAAGCCGGCAGCAG 2
                                                                                               AAS97050 standard; DNA; 20
                                                                                                                                                                               26-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UABR-) UAB RES FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-049338/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                         AAS97050;
                                                           RESULT 95
                                                                                  AAS97050
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Sequence 20 BP; 5 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

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Gaps

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Gaps

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Indels

1.4%; Score 15.4; DB 1; Length 20; 94.1%; Pred. No. 1.1e+02;

0; Mismatches

48

32 CAGGAAGCCGGAAGCAG

Best Local Similarity 94.1 Matches 16; Conservative

Query Match

992 GTTGTATGCACATGAAA 1008

human; single nucleotide polymorphism; microarray; side effect; ss;

Single nucleotide polymorphism detection primer, SEQ ID No 1170.

26-FEB-2004 (first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an antibody that specifically binds a tumour necrosis factor (TNF) related apoptosis-inducing ligand (TRAIL) receptor DR4 or DR5. Antibodies of the invention are useful for selectively inducing apoptosis in target cells expressing DR4, for inhibiting proliferation of target cells expressing DR4 or for treating cancer, inflammatory disease or autoimmune disease in a subject e.g. systemic lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-host disease, Goodpasture's syndrome, Crohn's disease, multiple sclerosis, diabetes mellitus, allergy, asthma, arteriosclerosis or glomerular nephritis. The present sequence is a PCR primer used to clone mouse anti-human DR5 antibody (TRA-8) CDNA
                                                                                                                                                                                                                                             Tumour necrosis factor; TNF-related apoptosis-inducing ligand; allergy; inflammatory disease; TRAIL receptor; systemic lupus erythematosus; DR4; Hashimoto's disease; rheumatoid arthxitis; inflammatory; disease; cancer; multiple sclerosis; graft-versus-host disease; arteriosclerosis; asthma Goodpasture's syndrome; autofimmune disease; glomerular nephritis; DR5; crohn's disease; diabetes mellitus; TRA-8 antibody; mouse; PCR; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New purified antibody that specifically binds a TNF-related apoptosis-
inducing ligand receptor DR4 or DR5, useful for treating cancer,
inflammatory disease or autoimmune disease in a subject, e.g. asthma or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                Mouse anti-human DRS antibody (TRA-8) cDNA cloning PCR primer, H5SS2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buchsbaum DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15.4; DB 1; Length 20; Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lobuglio AF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 16; Page 77; 251pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Koopman WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.4%;
94.1%;
                                                                                                                BP
                             13
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            AAL60465 standard; DNA; 20
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                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UABR-) UAB RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rheumatoid arthritis
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                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003037913-A2
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Local Sir.
16;
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                                                                                                                                                                                      27-AUG-2003
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                                                                                                                                                       AAL60465;
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                                                                                                                                                                                                                                                                                                                                                                                                        Mus sp.
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Matches
                                                                                    RESULT 96
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Novel polynucleotide useful for detecting single nucleotide polymorphisms

(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

WPI; 2003-820454/77.

in human gene

12-FEB-2002; 2002JP-00034717.

12-FEB-2002; 2002JP-00034717

JP2003235571-A.

26-AUG-2003

Homo sapiens

Synthetic.

primer; PCR

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The invention relates to a novel polynucleotide isolated and purified from a human gene having any one of 935 fully defined sequences as given in specification, or a sequence having a base substitution. The invention further relates to: an oligonucleotide containing single nucleotide further relates to: an oligonucleotide containing single nucleotide fragments from any one of 1220 fully defined sequences as given in fragments from any one of 1220 fully defined sequences as given in a specification; a labelling probe containing oligo. The isolated human gene. The isolated human gene is also useful for detecting the single nucleotide containing oligo. The isolated human gene is also effective in detecting single nucleotide polymorphisms in a human gene. This polymucleotide sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ss; primer; nephrotropic; antiarteriosclerotic; cardiant; antiasthmatic; antiallergic; antiinflammatory; antidiabetic; haemostatic; neuroprotective; antiinfertility; immunosuppressive; dermatological; antianaemic; antirheumatic; antiarthritic; thyromimetic; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proliferation; tumor related apoptosis-inducing ligand receptor; TNF; tumor necrosis factor-related apoptosis-inducing ligand receptor; TNF; TRAIL; symovial cell; lymphocyte; neutrophil; systemic lupus erythematosus; Hashimoto's disease; rheumatoid arthritis;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 2 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15.4; DB 1;
Pred. No. 1.1e+02;
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SEQ ID NO 1170; 704pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                            of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity 94.1%;
16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               detection method
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          Claim 2;
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ADJ79773
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GTTGTATGCACATGAAA 1008

992

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7587/c ADF87587 standard; DNA; 20 BP.

RESULT 97 ADF87587 ADF87587;

20-MAY-2004 (first entry)

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The invention relates to a method of selectively inducing apoptosis in and inhibiting (M1) proliferation of target cells expressing DRS, comprising contacting the cell with an antibody that specifically binds tumor necrosis factor (TMP)-related apoptosis-inducing ligand (TMALL) receptor DRS, where the antibody, in its soluble form, has in vivo and in vitro apoptosis-inducing activity in the cell expressing DRS, and contacting the cell with one or more therapeutic agents. M1 is useful for inducing apoptosis in target cell and inhibiting proliferation of target cell expressing DRS, where the target cell is an abnormally proliferating synovial cells (e.g. rheumatoid arthritis synovial cell), activated immune cell (e.g. activated lymphocyte), neutrophil, or virally infected immune cell (e.g. activated lymphocyte), neutrophil, or virally infected cell. maximated lighamatory or autoimmune diseases. The inflammatory or autoimmune disease are selected from systemic lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-host disease, Sjogren's syndrome, Crohn's carchitis, graft-versus-host disease, Sjogren's syndrome, Crohn's carchitises, allergy, carchitals apprintis, and hypoplastic anemia, Addison disease, arteriosclerosis, myocarditis, cardiomyopathy, continual applitis, and hypoplastic anemia. This sequence represents a privare and an arteriosclerosis, myocarditis, cardiomyopathy, continual and propersis and hypoplastic anemia. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inducing apoptosis and inhibiting proliferation of target cells expressing DRS, by contacting the target cell with an antibody that binds TNF-related apoptosis-inducing ligand receptor DRS and with therapeutic
                   Addison disease; scleroderma; Goodpasture's syndrome; Crohn's disease; autoimmune hemolytic anemia; sterility; myasthenia gravis; multiple scleroais; Basedow's disease; thrombotic; thrombocytopenia; thrombopenia purpura; insulin dependent diabetes mellitus; allergy; asthma; atopic disease; arterioscleroais; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anemia.
graft-versus-host disease; Sjogren's syndrome; pernicious anemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ichikawa K, Kimberly RP, Koopman WJ, Oshumi J;
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                                                                                                                                                                                                                                                                                                                                    25-OCT-2002; 2002WO-US034420
                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-2001; 2001US-0346402P.
24-JUN-2002; 2002US-0391478P.
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Best Local Si
Matches 16
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; 0 19 GCCCGGGCCGTGGCAGG 35 20 ADJ24880 standard; DNA; 20 BP 4 GCCCGGGCGGTGGCAGG 20-MAY-2004 (first entry) 16; Conservative Local Similarity ADJ24880; Query Match RESULT 100 ઠે 셤 ö Gaps ; 0 1.4%; Score 15.4; DB 1; Length 20; 94.1%; Pred. No. 1.1e+02; Indels 0; Mismatches 992 GTTGTATGCACATGAAA 1008 ВР. 13 ADJ25296 standard; DNA; 20 Local Similarity 94.1 hes 16; Conservative

ADJ25296

RESULT 99 ADJ25296

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New antisense oligonucleotide for modulating endothelial lipase expression, for diagnosing, preventing or treating e.g. dyslipidemia, low high density lipoprotein or cardiovascular disorders.
                                                                                                                                                                                                                                                                                     /note= "This oligonucleotide has a phosphorothioate backbone and 2-'methyoxyethyl (2. MDB) wings at the 5' and 3' ends, which are 4 nucleotides in length. Also all cytidine residues are 5-methylcytidines"
                                                                       Antilipaemic, Cardiovascular, Analgesic, Antianginal, Antisense therapy, Human, Endothelial Lipase, dyslipidaemia, high density lipoprotein, HDL; cardiovascular disorder, metabolic syndrome X, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25517), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotetin (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are used for diagnostics, prophylaxis, or as research reagents or kits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                 Human endothelial lipase antisense oligonucleotide, SEQ ID 3694.
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Pred. No. 1.1e+02;
0; Mismatches 1;
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                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                             Key
modified_base
                                                                                                                                                   Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense oligonucleotide for modulating endothelial lipase expression, for diagnosing, preventing or treating e.g. dyslipidemia, low high density lipoprotein or cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to antisense oligonuclectides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25517), where the antisense oligonuclectide specifically hybridises with and inhibits the expression of EL. The antisense oligonuclectides are useful for modulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are used for diagnostics, prophylaxis, or as research reagents or kits.
                                                                                                                                                                                                                                                   /mod_base= OTHER
/mote= "This oligonucleotide has a phosphorothioate
/note= "This oligonucleotide (2'-MOE) wings at the 5'
backbone and 2'-methyoxyethyl (2'-MOE) wings at the 5'
backbone and 3'-methy witch are 4 nucleotides in length. Also all
aridine residues are 5-methyloytidines"
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Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 1.1e+02;
0; Mismatches 1; Indels
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      cardiovascular disorder; metabolic syndrome X; ss.
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1. .4
                                                                                                                                                              Location/Qualifiers
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Local Similarity 94.1%;
Les 16; Conservative
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modified_base
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modified_base
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                                                                               Homo sapiens.
Synthetic.
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Best Local Si
Matches 16;
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The present invention relates to a compound which specifically hybridizes with a nucleic acid molecule encoding GFAT, and inhibits the expression of GFAT. Specifically claimed are antisense oligonuclectides capable of modulating the expression of GFAT, and which comprise any of the 3063 sequences of 20 base pairs, given in the specification. The compound, composition and methods are useful for treating a disease or condition associated with GFAT, such as a disease or condition, eardiovascular or neurological disorder, ischemia/repertusion injury. They are also useful in research and diagnostics for modulating the expression of GFAT. The present sequence represents a chimeric phosphorothioate oligonuclectide with 2'-MOE wings and a deoxy gap, these diagnostics in the research and man are also services of the second se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New compounds, particularly antisense oligomucleotides targeted to a nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase (GFAI), for treating diabetes, a cardiovascular or neurologic disorder, ischemia/reperfusion injury.
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Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
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                                                                                                                                             /*tag= b
/mod_base= other
/note= "2-methoxyethyl wing"
                                               "2-methoxyethyl wing"
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/mod_base= other
/mod_base= other
/note= "2-methoxy
17. .20
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Best Local Similarity 94.1%;
Matches 16; Conservative (
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The present invention relates to a compound which specifically hybridizes with a nucleic acid molecule encoding GFAT, and inhibits the expression of GFAT. Specifically claimed are antisense oligonucleotides capable of modulating the expression of GFAT, and which comprise any of the 3063 sequences of 20 base pairs, given in the specification. The compound, composition and methods are useful for treating a disease or condition associated with GFAT, such as a disease or condition. They are also useful in research and disgnostics for modulating the expression of GFAT. The present sequence represents a chimeric phosphorothicate oligonucleotide with 2' MOE wings and a deoxy gap, these oligonucleotides inhibit human GFAT expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase (GPAT), for treating diabetes, a cardiovascular or neurologic disorder, ischemia/reperfusion injury.
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Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
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94.1%; Pred. No. 1.1e+02;
iive 0; Mismatches 1;
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/note= "2-methoxyethyl wing"
17. .20
                                            /mod_base= other
/note= "2-methoxyethyl wing"
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nes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New compounds, particularly antisense oligonucleotides targeted to a nuclaic acid encoding glutamine-fructose-6-phosphate amidotransferase (NGRI), for treating diabetes, a cardiovascular or neurologic disorder, ischemia/reperfusion injury.
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Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
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/*tag= a
/mod_base= other
/note= "2-methoxyethyl wing"
17. .20
/note= "2-methoxyethyl wing"
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   /note= "2-methoxyethyl wing"
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nes 16; Conservative
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                                                                                                             (PHAA ) PHARMACIA CORP.
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AAX91991-X97517 represent PCR primers used to amplify open reading frames and other nucleic acid sequences from the genome of Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory disease such as
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                                                                                                                                                                                                                                                                 The invention relates to a recombinant dimethyl sulphide (DMS):acceptor oxidoreductase (I) or its subunit selected from recombinant alpha, beta, delta and gamma subunits. (I) is useful for oxidising prochiral organic sulphides to form sulphoxide enantiomers for chiral drug synthesis. (I) is expressed in a transformed bacterium. The enantiomer formed is useful for producing a chiral drug. (I) is useful for synthesis of optically-active functional groups of drug. DNA encoding (I) is useful for producing a strain of DMS:acceptor oxidoreductase-deficient Rhodovulum sulfidophilum, which is useful in whole-cell reaction, where DMS:acceptor oxidoreductase activity is unwanted. ABK53751-ABK53805 represent R. sulfidophilum DMS:acceptor oxidoreductase subunit coding sequences and PCR primers of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
                                                                                                 New recombinant dimethyl sulfide:acceptor oxidoreductase or its subunits, useful for oxidizing prochiral organic sulfides to form sulfoxide enantiomers for chiral drug synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.4%; Score 15.4; DB 1; Length 21; 94.1%; Pred. No. 1.2e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer used to amplify an ORF of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21 BP; 3 A; 9 C; 8 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 1849; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                     Claim 15; Page 46; 66pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
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98US-0107078P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydophila pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Conservative
Mcdevitt CA, Mcewan AG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-357842/30.
                                                        WPI; 2002-280922/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
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pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see ANY14584- AAV15879) can be used in immunogenic compositions as voccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antiinflammatory; cytostatic; antibacterial; methionine aminopeptidase 2; inhibitor; metAE2; eukaryotic initiation factor associated profein; p67; eIF-2; protein synthesis; antisense oligonuclectide; infection; human; inflammation; tumour; phosphorothioate; 2-methoxyethyl wing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense compounds which specifically hybridize with and inhibit human methionine aminopeptidase 2 expression, useful for treating methionine aminopeptidase 2 related disorders and preventing inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methionine aminopeptidase 2 (also known as MetAP2 and eukaryotic initiation factor [eIF-2] associated protein, p67) is a cellular glycopyrotein that promotes protein synthesis in the presence of active eIF-2 kinases by protecting the eIF-2 alpha subunit from phosphorylation. The present invention relates to antisense oligonucleotides (AACG7690-C67767) which inhibit human methionine aminopeptidase 2 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression (see AAC67683). The present sequence is one such antisense oligonucleotide. The present sequence may be used for treating a patient suspected of having or being prone to a disease or condition associated with expression of MetAP2. In addition, the present sequence can also be used as research reagents, diagnostics and to distinguish between functions of various members of a biological pathway. The antisense oligonucleotide may further be used prophylactically, e.g. to prevent or delay infection, inflammation or tumour formation. Note: the present sequence may have a phosphorothioate backbone and 2-methoxyethyl (2'-MOE)
                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                            Score 15.2; DB 1; Length 20;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                        Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                             459 AGTGGTAGCACTTTATTCTG 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide #2 ISIS #116870.
                                                                                                                                                                                                                                                                                                                                    20 AGCGGTAGCAGTTTCTTCTG 1
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                                                                                                                                                                                                                                1.4%;
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                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.0°
Matchee 17; Conservative
                                                                                                                                                epitope of C. pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-030942/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monia BP, Wyatt J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumor formation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel oligonucleotide sequences of internal transcribing spacer region of non-tuberculosis mycobacteria (NTM) used as probes or primers for detecting and identifying mycobacteria and distinguish TB complex from
                                                                                                                                                                                                                                                                                                                                                                                                          ITS; internal transcribed spacer region; Mycobacterium fortuitum; Mycobacterium chelonae; Mycobacterium abscessus; Mycobacterium vaccae; Mycobacterium flavescens; Mycobacterium asiaticum; tuberculosis; Mycobacterium asiaticum; tuberculosis; Mycobacterium porcinum; Mycobacterium acapulcensis; identification; Mycobacterium diernhoferi; PCR primer; probe; detection; ss.
                                                                                                    Gaps
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                                                                 Length 20;
                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide for detection of Mycobacterium diernhoferi.
                                                                                                  3; Indels
                               Sequence 20 BP; 4 A; 9 C; 4 G; 3 T; 0 U; 0 Other;
                                                             Score 15.2; DB 1;
Pred. No. 1.2e+02;
0; Mismatches 3;
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                                                                                                                                                                         20 rceeccaacareeceeerer 1
                                                                                                                                       TCGGGAGACATGGCGGGCGT
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07-APR-2000; 2000KR-00018189
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                                                                   1.4%;
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                                                                                                                                                                                                                                                                AAF23345 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                       19-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium diernhoferi.
                                                                                 Local Similaricy
hes 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PARK/) PARK H K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KIM C M.
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                                                                 Query Match
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Matches
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AAF92365 standard; DNA; 20 BP.
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                                                                                                                                        Homo sapiens
                                                                                                                                                                                        22-FEB-2001
                                                   16-MAY-2001
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                                                                                                                                                                                                                                                                                      Ishida I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABV73091;
                           AAF92365;
                                                                                                     Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to compounds and methods for inhibiting histone deacetylase (HDAC) enzymatic activity. Compounds of the invention are used for the treatment of cell proliferative diseases and conditions such as cancer, restencists or psoriasis. They are also used for treating or preventing protozoal or fungal disease or infections. The present sequence is antisense oligonucleotide, HDAC8 AS2 which is targetted to the 3' untranslated region (UTR) of human HDAC8 to inhibit its enzymatic
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                                                                                                                                                                                                                                                                                                               Human; cytostatic; vasotropic; fungicide; histone deacetylase; inhibitor; HDAC; therapy; cell proliferative disease; cancer; restenosis; psoriasis; protozoal disease; fungal disease; infection; ss.
   from ITS of mycobacteria, it is possible to detect mycobacteria, distinguish tuberculosis (TB) complex from non-tuberculosis mycobacteria (NTM), and to identify mycobacteria species accurately and effectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An inhibitor of histone deacetylase for the treatment of cell proliferation diseases and conditions such as cancer, restenosis or psoriasis or preventing protozoal or fungal disease or infections.
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                                                                                                                                                                                                                                                                                         Human histone deacetylase antisense oligonucleotide, HDAC8 AS2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 20;
                                                                           Query Match
1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15.2; DB 1;
Pred. No. 1.2e+02;
0; Mismatches 3;
                                                      Sequence 20 BP; 9 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 54; 241pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                743 AGGCAGCTGCCACCTTATGC 762
                                                                                                                                 998 TGCACATGAAAGTTTGAGAA 1017
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                                                                                                                                                                                                                      BP
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Best Local Similarity 85.0%;
Matches 17; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2001; 2001WO-IB000683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAR-2000; 2000US-0192151P
                                                                                                                                                                                                                      AAD20131 standard; DNA; 20
                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (METH-) METHYLGENE INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-639108/73
                                                                                                                                                                                                                                                                                                                                                                                              MO200170675-A2
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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RESULT 110 AAF92365

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This invention relates to a mouse containing the human cytochrome P450 gene (from the CYP3A family). PCR primers AAF92356 - AAF9241 are used in examples illustrating the construction of vectors used in the production of the transgenic mouse of the invention. The mouse can be used for studying human drug efficacy, metabolism and toxicity, including the application of immortalised cell and tissue cultures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Histone deacetylase; HDAC-4; cytostatic; neoplastic; cell proliferation; HDAC-8; human; cancer; antisense; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse having completely humanized human cytochrome P450 gene for use in studying drug efficacy, metabolism and toxicity with ease.
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0
                                                                    cytochrome P450; Cyp3A; PCR primer; transgenic mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 20;
                                                                                                                                                                                                                                                                                                                                                             Suzuki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human HDAC-8 mRNA inhibiting antisense oligo HDAC8 AS2.
                              PCR primer specific for human CYP3A4 DNA SEQ ID 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 3 A; 2 C; 8 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Score 15.2; DB 1;
85.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                             Ohshima T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Page 43; 137pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                               Kuroiwa Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 TCAGTGGGGCTATTGGACTG 124
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                                                                                                                                                                                                                                                11-AUG-2000; 2000WO-JP005424.
                                                                                                                                                                                                                                                                                        99JP-00229094
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Best Local Similarity 85.0
Matches 17; Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                 Tomizuka K,
                                                                                                immortalised cell; ss.
                                                                                                                                                                                                                                                                                                                          (KIRI ) KIRIN BEER KK
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-202806/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200269947-A2.
                                                                                                                                                                         WO200111951-A1.
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24-MAR-2000; 2000US-0192157P
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                                                                                                                                                                                                                                                                                                                       167
                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                       ABK87739;
                                                                                                                                                                                                                                                                                                                                                                             RESULT 113
                                                                                                                                                                                                                                                                                                                                                                                         ABK87739
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                                                                                             Inhibition of HDAC-4 activity in a cell useful for treating e.g. cancer involves contacting the cell with an antisense oligonucleotide or a small molecule inhibitor of HDAC-4.
                                                                                                                                                            The invention relates to inhibition of histone deacetylase (HDAC)-4 activity in a cell that involves contacting the cell with an antisense oligonucleotide complementary to a region of RNA encoding a portion of HDAC-4 or a small molecule inhibitor of HDAC-4. The method is useful for inhibiting neoplastic cell proliferation in an animal (preferably human) and for treating cancer. Sequences ABV73073-3091 represent HDAC isotype-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, K-ras, PCR primer; probe; capture probe; mutation detection; ligase detection reaction, LDR; p53; BRCA1; BRCA2; infectious disease; infection; 21 hydroxylase deficiency; Turner Syndrome, obesity; cancer; oncogene; tumour suppressor; human pabillomavirus; forensic; environmental monitoring; food industry; feed industry; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Designing capture oligonucleotide probes for use on a support to which complementary oligonucleotides hybridize with little mismatch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method (M1) for designing capture oligonucleotide probes (1) for use on a support to which complementary
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                           Score 15.2; DB 1; Length 20; Pred. No. 1.2e+02;
                                           Delorme D;
                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kliman R;
                                                                                                                                                                                                                                                     Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                               specific antisense and mismatch oligonucleotides
                                           Vaisburg A,
                                                                                                                                                                                                                                                                    1.4%; Scor.
85.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Capture oligonucleptide Zip ID#140 oligo #9.
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                                                                                                                                         Disclosure; Page 33; 124pp; English.
                                         Woo SH,
Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Fig 29; 300pp; English.
                                                                                                                                                                                                                                                                                                                      743 AGGCAGCTGCCACCTTATGC 762
                                                                                                                                                                                                                                                                                                                                           1 Acccaecreccaerrearec 20
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                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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12-JAN-2001; 2001US-0261674P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-APR-2001; 2001WO-US010958.
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                                                                                                                                                                                                                                                                                                                                                                                                  AB193053 standard; DNA; 20
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                                           E.C
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.0
Matches 17; Conservative
                                          Besterman JM, Bonfils
Fournel M, Lavoie R,
                     (METH-) METHYLGENE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-034366/04.
                                                                         WPI; 2002-750436/81.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200179548-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                           15-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                     AB193053;
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Confecting infectious diseases caused by bacterial infectious agents e.g. Salmonellar, Listeria emonocytogenes and Haemophilus influenza, fungal infectious agents e.g. Cryptococcus and Haemophilus influenza, fungal infectious agents e.g. Cryptococcus neoformans, Candida abbicans and infectious agents e.g. Cryptococcus neoformans, Candida abbicans and Case infectious agents e.g. Cryptococcus neoformans, Candida abbicans and Descriptions of Special Darr virus and pollo virus, and parasitic infectious agents selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus medinesis. The method is also useful for detecting genetic diseases such case 21 hydroxylase deficiency, Turner Syndrome and obesity defects.

Detecting cancer involving oncogenes, tumour suppressor genes, or genes involved in DNA amplification, replication, recombination or repair, the cancer is specifically associated with a gene selected from BRCA1 gene, p53 gene, human papillomavirus types 16 and 18 and liver cancers. The method is also used for environmental monitoring, forensics and the food and feed industry, detecting comprises scanning (using e.g. a scanning electron microscope and infrared microscope) the support at the particular sites and identifying if ligation of the oligonucleotide probe gressence or absence of the target nucleotide sequences. AB195074 to
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oligonucleotide probes (II) will hybridise with little mismatch, where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; 88; histone deacetylase; HDAC-8; cancer; cytostatic; antisense;
tumour suppressor; cell proliferation; tumour; programmed cell death;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human histone deacetylase isoform 8 antisense oligonucleotide AS2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.2; DB 1; Length 20;
Pred. No. 1.2e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mod base= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.4%;
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Best Local Similarity 85.0
Matches 17; Conservative
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/*tag=
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30-MAR-2001; 2001FR-00004404.

(GENO-) GENODYSSEE SA.

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The invention relates to an agent that inhibits an isoform of histone deacetylase (HDAC-1 to HDAC-8) but not all isoforms, e.g. an antisense deacetylase (HDAC-1 to HDAC-8) but not all isoforms, e.g. an antisense oligonucleotide. Also included are inhibiting an HDAC isoform in a cell for induction of cell proliferation or differentiation and inhibiting for induction of cell proliferation or differentiation and inhibiting cell proliferation by treatment with two antisense oligonucleotides or small molecules that inhibit a specific HDAC isoform, or antisense oligonucleotide or small molecules that inhibit DNA methyltransferase. The agent therefore acts as a tumour suppressor. The agents are used to treat diseases of cell proliferation and differentiation (e.g cancer and tumours), by inducing growth retardation, growth arrest or tumours), by inducing growth retardation, growth arrest or programmed/necrotic cell death, specifically neoplastic cell proliferation in humans. The agents are selective for particular isoforms, compared to known inhibitors which are not selective. The present sequence is an antisense oligonucleotide of the invention targeting the polynucleotide which encodes the HDAC-8 isoform
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                                                                                                                                                                                                                                                                                         Agent that specifically inhibits an isoform of histone deacetylase, useful for treating cancer and other cell proliferative diseases, preferably comprises an antisense oligonuclectide.
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Similarity 85.0%; Pred. No. 1.2e+02;
17; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; Page 6; 60pp; English.
                                                                                                                                                     Bonfils C, Besterman J;
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(LIZZ/) LI Z.
(BONF/) BONFILS C.
(BEST/) BESTERMAN J.
                                                                                                                                                                                                                                   WPI; 2002-507650/54.
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The present invention relates to human alphainterferon-21. The coding sequence (see ABV/4504) for this protein can contain at least one of the collowing single nucleotide polymorphisms (SNP): C9734, G1011C, T10494, C1011c, T10494, G1011c, G1041c, G1041c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; histone deacetylase; isoform; HDAC-1; HDAC-2; HDAC-3; HDAC-4;
HDAC-5; HDAC-6; HDAC-7; HDAC-8; antisense gene therapy;
cell proliferation; programmed cell death; necrotic cell death;
neoplastic cell proliferation; cell differentiation; neoplasm; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                             New nucleic acid, useful for treatment or diagnosis of e.g. cancer, encodes mutant forms of human interferon-alpha21, also derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.4%; Score 15.2; DB 1; Length 20; 85.0%; Pred. No. 1.2e+02; ative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is a PCR primer, used in an example from the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
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/mod_base= OTHER
/note= "2'-0-methyl residues"
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17. .20
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                                                                                                                                                                                                                                                                                                 Example 2; Page 45; 100pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    608 TTCATAAGTAGGAGATGAGT 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mod_base= OTHER
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                                                                                                                                                                                                                                                    polypeptides and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC21719 standard; DNA; 20
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Best Local Similarity 85.09
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*tag=
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modified_base
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                                                                                                                   Escary JL;
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ADC21719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an antisense oligonucleotide comprising a nucleotide sequence of 13 to 15 nucleotides that inhibits one or more nucleotide sequence of 13 to 15 nucleotides that inhibits one or more specific histone deacetylase isoforms (HDA-1 to HDAC-8), where the oligonucleotide is useful in inhibiting one or more histone deacetylases isoforms in a cell comprising contacting the cell with the oligonucleotide. Cell proliferation is inhibited in the contacted cell which undergoes programmed and necrotic cell death. The oligonucleotide is also useful in inhibiting neoplastic cell proliferation in an animal, to preferably a human. The oligonucleotide is also useful in identifying a histone deacetylase isoform that is required for the induction of cell proliferation. The above method is also applicable to identifying indicates that the isoform is required for the induction of cell conditions to indicate that the isoform is required for the induction of cell in identifying an isoform required for the induction of cell in identifying an isoform required for the induction of cell in identifying an isoform required for the induction of cell in identifying an isoform required for the induction of cell conditions. Where an induction of cell differentiation indicates that the isoform is required for the induction of cell conditions. The present sequence condition is required for differentiation indicates that the isoform is required for differentiation indicates containing an an antisense oligonucleotide directed against an HDAC isoform containing
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                                                                                                                                                                                                                                                                                                                                                                                                            New antisense oligonucleotide that inhibits one or more specific histone deacetylase isoforms, is useful in modulating cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5'-RACE primer for amplifying fluorescent protein cDNA #SEQ ID 18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                               Bonfils C, Besterman JM;
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                                                                                            26-MAR-2001; 2001US-00817538
                                                                                                                                            24-MAR-2000; 2000US-0192157P.
                                                                                                                                                                     12-JAN-2001; 2001US-0261522P.
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Matches 17; Conservative
                                                                                                                                                                                                                (LIZZ/) LI Z.
(BONF/) BONFILS C.
(BEST/) BESTERMAN J M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           especially neoplasia
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US2002137162-A1
                                             26-SEP-2002
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                                                                                                                                                                                                                                                                                                               Li 2,
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The invention relates to 4 fluorescent proteins originating from Fungia species. Also disclosed are DNA sequences encoding the novel fluorescent proteins, expression vectors containing this DNA, hosts transformed by this vector, fluorescent fusion proteins containing the novel fluorescent proteins fused to another protein, and a method for analysis of function and distribution of another protein using the fluorescent fusion protein. Novel proteins of the invention are useful for analysis of the intracellular activity, function and localisation of proteins of biological interest, using the fluorescent protein as a fluorescence properties and a low sensitivity to pH. The current sequence represents a 5'-RACE (rapid amplification of cDNA ends) primer used to recover fungal fluorescent protein terminal sequence from extracted cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                     Fluorescent proteins from Fungia species and DNA encoding them for analysis of function and distribution of proteins in living systems.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human HDAC8 mRNA targeting antisense oligo HDAC8 AS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 20 BP; 5 A; 6 C; 1 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15.2; DB 1;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Woo SH, Vaisburg A, Moradel O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                           (RIKE ) RIKEN KK.
(MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 21; 59pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                497 TCTTAGAACTCATACTATCT 516
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26-JUN-2002; 2002US-0391728P.
                                                           20-DEC-2002; 2002WO-JP013363
                                                                                                                   20-DEC-2001; 2001JP-00387510
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                                                                                                                                                                                                                                                                     Miyawaki A, Karasawa S;
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                                                                                                                                                                                                                                                                                                                                WPI; 2003-541818/51
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03-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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ADH50625;
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                                                 New histone deacetylase inhibitors, useful for treatment of proliferative diseases or conditions e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New compound having a sequence targeted to a nucleic acid encoding IL-1 receptor-associated kinase-1, useful for preparing a composition for treating hyperproliferative or autoimmune disorder or inflammation.
                                                                                                                            Hormine and their salts. The compounds inhibit histone deactvlase (HDAC) enzymatic activity. They can be used for treating cell proliferative diseases or condition (e.g. cancer, restenosis and psoriasis). Sequences AB276476-492 represent antisense and mismatch oligonucleotides targeting the 5'- UTR (untranslated region) and 3'-UTRs of the human HDAC1-8 genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense therapy; human; interleukin-1 receptor-associated kinase-1; IL-1 receptor-associated kinase-1; IRAK-1; hyperproliferative disorder e.g.; cancer; autoimmune disorder; alterative disorder inflammation; cytostatic; immunosuppressive; osteopathic; antiinflammatory; ds.
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                 specified
                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                             1.4%; Score 15.2; DB 1; Length 20; 85.0%; Pred. No. 1.2e+02;
                                                                                                                 invention relates to histone deacetylase inhibitors of
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                     Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human IRAK-1 DNA target sequence #18.
                                                                                             Disclosure; Page 72; 347pp; English
                                                                                                                                                                                                                                                                                                743 AGGCAGCTGCCACCTTATGC 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dobie KW;
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                                                                                                                                                                                                                                                                                                                                                                                         ADH50696 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.0
Matches 17; Conservative
        Bouchain G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS PHARM INC.
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                                WPI; 2003-342612/32
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        Frechette S,
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It also comprises at least one modified sugar moiety, preferably a 2'-0-methoxyethyl (2'-MOB) sugar moiety. The antisense oligonucleotide further comprises at least one modified nucleobase, preferably a 5-methylcytosine. The antisense oligonucleotides are useful for the treatment of diseases such as hyperproliferative disorders, e.g. cancer, autoimmune disorders, altered bone metabolism, and inflammation. The present sequence represents a human IRAK-1 DNA target sequence for an
                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to antisense compounds targeted to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated kinase-1 (IRAK-1). The antisense compound comprises an antisense oligonucleotide that specifically hybridises with the nucleic acid and inhibits the expression of IRAK-1. The antisense oligonucleotide is a chimeric oligonucleotide. The antisense oligonucleotide comprises at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense therapy; human; interleukin-1 receptor-associated kinase-1; IL-1 receptor-associated kinase-1; IRAK-1; hyperproliferative disorder e.g.; cancer; autoimmune disorder; altered bone metabolism or inflammation; cytostatic; immunosuppressive; osteopathic; antiinflammatory; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mod_base= OTHER
/mod_base= This oligonucleotide has a phosphorothioate
/note= This oligonucleotide has a the 5'
backbone and 2'-methyoxyethyl (2'-MOE) wings at the 5'
and 3' ends, which are 5 nucleotides in length at each
end. All cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New compound having a sequence targeted to a nucleic acid encoding II receptor-associated kinase-1, useful for preparing a composition for treating hyperproliferative or autoimmune disorder or inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                             Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                             1.4%; Score 15.2; DB 1;
85.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human IRAK-1 DNA, antisense oligonucleotide #19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 15; SEQ ID NO 32; 66pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AGGAGGCCTCCTATGACCCA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JUN-2002; 2002US-00167034.
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                                                                                                                                                                                                                                                                  antisense oligonucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-052028/05.
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2003228690-A1
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modified_base
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Fri Aug 19 11:00:00 2005

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modified internucleoside linkage, preferably a phosphorothioate linkage. It also comprises at least one modified sugar moiety, preferably a 2'-0-methoyathyl (2'-MOE) sugar moiety. The antisense oligonucleotide further comprises at least one modified nucleobase, preferably a 5-methylcytosine. The antisense oligonucleotides are useful for the treatment of diseases such as hyperproliferative disorders, e.g. cancer, autoimmune disorders, altered bone metabolism, and inflammation. The present sequence represents an antisense oligonucleotide used in the examples of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; endocrine; hepatoma-derived growth factor inhibitor; hepatoma-derived growth factor; metabolic disorder; hyperproliferative; human; ss; antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mod_base= OTHER
/note= "OTHER= Phosphorothioate backbone. All cytidines
are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mod_base= OTHER
/note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleotides
                                                                                                                                                                                                          Gaps
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                                                                                                                                                                         1.4%; Score 15.2; DB 1; Length 20; 85.0%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "OTHER= 2'-0-Methoxyethyl (2'-MOE) 15. .20
                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatoma-derived growth factor antisense oligo segid 24.
                                                                                                                                                  Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                         0; Mismatches
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/*tag= a
/mod_base= OTHER
                                                                                                                                                                                                                                                    20 AGGAGGCCTCCTATGACCCA 1
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                                                                                                                                                                                       Best Local Similarity 85.0
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-142660/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2004023379-A1
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modified_base
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                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                          RESULT 120
ADJ45254/c
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The invention describes a compound 8-80 nucleobases in length targeted to, and which specifically hybridises with a nucleic acid molecule encoding hepatoma-derived growth factor, and inhibits the expression of hepatoma-derived growth factor. The compound, composition and methods are useful for treating a disease or condition associated with hepatoma-derived growth factor, such as a metabolic disorder, or hyperproliferative disorder, e.g. cancer, which is selected from hepatoma, leiomyoma, esophageal cancer or ovarian cancer. They are also useful in research and diagnostics for modulating the expression of hepatoma-derived growth factor. This sequence represents a human hepatoma-derived growth factor antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; endocrine; hepatoma-derived growth factor inhibitor; hepatoma-derived growth factor; metabolic disorder; hyperproliferative; human; ss; antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorothioate backbone. All cytidines
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/note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
15. .20
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                                                                                                                                                                                                                                                    Gape
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                                                                                                                                                                                                                    Length 20;
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                                                                                                                                                                                       Sequence 20 BP; 1 A; 6 C; 4 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                  Score 15.2; DB 1;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                801 AGGCAGATAACGCTGAAGCA 820
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/*tag= b
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                                                                                                                                                                                                                                                  17; Conservative
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                                                                                                                                                                                                                                  Local Similarity
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modified_base
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                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting neoplastic cell proliferation in animals by administering an antisense oligonuclectide complementary to region of RNA encoding portion of histone deacetylase-7 (HDAC-7) or HDAC-8, or small molecule inhibitor of HDAC-7 or HDAC-8.
                                                                                                                                                                                                                                                                                                                                                                                ö
                                   The invention describes a compound 8-80 nucleobases in length targeted to, and which specifically hybridises with a nucleic acid molecule encoding hepatoma-derived growth factor, and inhibits the expression of useful for treating a disease or condition associated with hepatoma-derived growth factor. The compound, composition and methods are hyperproliferative disease or condition associated with hepatoma-hyperproliferative disorder, e.g. cancer, which is selected from hyperproliferative disorders, e.g. cancer, which is selected from useful in research and diagnostics for modulating the expression of hepatoma-derived growth factor. This sequence represents a human hepatoma-derived growth factor. This sequence represents a human hepatoma-derived growth factor antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
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                                                                                                                                                                                                                                                                                                                                    Query Match
1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                             Sequence 20 BP; 9 A; 4 C; 6 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonfils C;
      Example 15; SEQ ID NO 95; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human HDAC8-specific oligo HDAC8AS2.
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                                                                                                                                                                                                                                                                                                                                                                                                                            801 AGGCAGATAACGCTGAAGCA 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGCAGAAACCCTGAAGGA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADI34745 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-099393/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Phosphorothioate backbone where all cytidines are 5'- methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense oligonucleotide compounds, useful for diagnosing, preventing and/or treating conditions with aberrant activity of breast cancer-1, such as breast, ovary, prostate and/or peritoneum cancers.
                                                                                                                                                                                                             Gaps
portion of HDAC-1, preferably chimeric or hybrid HDAC-1 antisense oligonucleotide. Sequences ADI34722-ADI34746 represent HDAC isotypespecific antisense and mismatch oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Breast cancer-1; diagnosis; hyperproliferative disorder; cancer; antisense therapy; human; antisense; ss.
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//mod_base= OTHER
16..20 nucleotides"
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                                                                                                                                                       Score 15.2; DB 1; Length 20;
Pred. No. 1.2e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human breast cancer-1 antisense oligonucleotide #159144.
                                                                                                         Sequence 20 BP; 4 A; 7 C; 5 G; 3 T; 1 U; 0 Other;
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                                                                                                                                                                                                                                                                   743 AGGCAGCTGCCACCTTATGC 762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
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                                                                                                                                                                       Query Match
Best Local Similarity 80.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-121557/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brown-Driver VL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2004014051-A1
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ96374;
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ96374
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65

antisense oligonucleotide.

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06-MAY-2004

ADJ96440;

RESULT 124 ADJ96440/c

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8

22-JAN-2004

(ISIS-)

ADJ23397;

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New antisense oligonuclectide for modulating endothelial lipase expression, for diagnosing, preventing or treating e.g. dyslipidemia, low high density lipoprotein or cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                     /note= "This oligonucleotide has a phosphorothioate backbone and 2- methyoxyethyl (2. +MS) wings at the 5' and 3' ends, which are 4 nucleotides in length. Also all cytidine residues are 5-methylcytidines"
                                                                                                               Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy; Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL; cardiovascular disorder; metabolic syndrome X; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25517), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotrion (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are used for diagnostics, prophylaxis, or as research reagents or kits.
                                                                          Human endothelial lipase antisense oligonucleotide, SEQ ID 1795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human endothelial lipase antisense oligonucleotide, SEQ ID 2362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.2; DB 1;
Pred. No. 1.2e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; SEQ ID NO 1795; 1007pp; English.
                                                                                                                                                                                                                                                        location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGIAGICCATGCIATIAAA 884
                                                                                                                                                                                                                                                                                                                /mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rreradceariecrarraca 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUL-2003; 2003WO-US022410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-2002; 2002US-0397106P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 85.0
nes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADJ23964 standard; DNA;
                                                                                                                                                                                                                                                                                                *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PHAA ) PHARMACIA CORP
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                                                                                                                                                                                                                                                          Key
modified base
                                                                                                                                                                                                Homo sapiens
                                       20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-2004
                                                                                                                                                                                                                     Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Note: This sequence given in example 15 of the that given in the sequence listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to breast cancer-1 proteins and their encoding nucleic acids. The invention is useful for the diagnosis, prevention and/or treatment of diseases and conditions associated with aberrant expression and activity of breast cancer-1 such as a hyperprollicrative disorder in particular breast, ovary, prostate and peritoneum cancers. The invention is also used in antisense therapy. The present sequence is human breast cancer-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention is directed to novel antisense compounds targetted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense oligonucleotide compounds, useful for diagnosing, preventing and/or treating conditions with aberrant activity of breast cancer-1, such as breast, ovary, prostate and/or peritoneum cancers.
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Breast cancer-1; diagnosis; hyperproliferative disorder; cancer;
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                                                                                               20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                    3; Indels
                                                                                             Score 15.2; DB 1; Length
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 4 A; 6 C; 3 G; 7 T; 0 U; 0 Other;
                                                     Sequence 20 BP; 7 A; 3 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human breast cancer-1 target, oligonucleotide #25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 15; Page 32; 175pp; English
                                                                                                                                                                         224 GCCAAAAGAGTCACCTATGA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 GCCAAAAGAGTCACCTATGA 243
                                                                                                                                                                                                             1 GGCAGAAGAGTCACTTATGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 GGCAGAAGAGTCACTTATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                  ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antisense therapy; human; ss.
                                                                                               1.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUL-2002; 2002US-00199676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUL-2002; 2002US-00199676
                specification differs from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dobie KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ23397 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                  ADJ96440 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                         Query Match
Best Local Similarity 85.0°
Matches 17; Conservative
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Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brown-Driver VL,
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Gaps

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Query Match

RESULT 125

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ADJ23397 ID ADJ2. XX

Length 20; 3; Indels

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New antisense oligonucleotide for modulating endothelial lipase expression, for diagnosing, preventing or treating e.g. dyslipidemia, low high density lipoprotein or cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25517), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are used for diagnostics, prophylaxis, or as research reagents or kits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human histone deacetylase coding sequence antisense oligonucleotide #17.
                                                                                                                                                                                 /mcve="This oligonucleotide has a phosphorothioate /note="This oligonucleotide" (2'-MOE) wings at the 5' backbone and 2-methyoxyethyl (2'-MOE) wings at the 5' and 3' ends, which are 4 nucleotides in length. Also all cytidine residues are 5-methylcytidines"
Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy; Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL; cardiovascular disorder; metabolic syndrome X; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          histone deacetylase; HDAC; enzyme; benzamide derivative;
cell proliferation; antisense; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; SEQ ID NO 2362; 1007pp; English.
                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             866 TGTAGTCCATGCTATTAAAA 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TGTAGCCAATGCTATTACAA 20
                                                                                                                                                                      base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
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                                                                                                                                                                                                                                                                                                                                         18-JUL-2003; 2003WO-US022410
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                                                                                                                                                                                                                                                                                                                                                                                                            (PHAA ) PHARMACIA CORP
                                                                                                                                                          *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-132912/13.
                                                                                                                                                                                                                                                                              WO2004009541-A2
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                                                                                                                                          modified_base
                                                                           sapiens
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                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bhat BG;
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                                                                             Homo
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WO2004035525-A1

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histone deacetylase inhibitor; HDAC inhibitor; antisense oligonucleotide; proliferative disease; proliferative condition; ss; HDAC8.
                                                                                                                                                                                                                            The present invention relates to benzamide derivatives capable of inhibiting histone deacetylase (HDAC) enzymes. These are useful in the treatment of a cell proliferative disease or condition in a mammal (preferably human). The present sequence is an antisense oligonucleotide for use against a human histone deacetylase gene.
                                                                                                                                                           New benzamide derivatives, useful to treat cell proliferative disease or conditions, are histone deacetylase inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention comprises histone deacetylase (HDAC) inhibitors of the formula: N-(2-Amino-phenyl)-4-[(4-pyridin-3-yl-pyrimidin-2-ylamino)-methyl]-benzamide. The invention also comprises a method of inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New N-(2-Aminophenyl)-4-((4-pyridin-3-yl-pyrimidin-2-ylamino)-methyl)-benzamideis histone deacetylase inhibitor useful to treat cell proliferative diseases.
                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                            Delorme
                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                            Vaisburg A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 77; 335pp; English.
                                                                                                              Paquin I,
                                                                                                                                                                                                          Disclosure; Page 27; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               743 AGGCAGCTGCCACCTTATGC 762
                                                                                                                                                                                                                                                                                                                                                                                                                       AGCCAGCTGCCACTTGATGC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
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                                 16-OCT-2003; 2003WO-CA001557
                                                            17-OCT-2002; 2002US-0419688P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR20736 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.0'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (METH-) METHYLGENE INC
                                                                                                                 Gaudette F,
                                                                                      (METH-) METHYLGENE INC
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                                                                                                                                          WPI; 2004-365141/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-AUG-2004.
         29-APR-2004
                                                                                                                 Raeppel S,
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Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism; pulmonary embolism; paternity test; ds.
                                                                                                                         Human gene single nucleotide polymorphism #686.
     AAF95925 standard; DNA; 21
                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                  sapiens
                                                                      18-NOV-2004
06-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lander ES,
                                                                                                                                                                                                                                                                                                   Key
variation
                                    AAF95925;
                                                                                                                                                                                                                                                  Ношо
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer F1.5 (AAT66953) corresponds to nucleotides 164-184 of a cDNA clone (see AAT66950) coding for human asialoglycoprotein receptor (AGPR) H1 (AAW15245). It was used with other primers (see AAT66952 and AAT6694-55) to amplify AGPR H1 cDNA from human liver cDNA. The isolated clone can be used to produce soluble AGPR H1 derivatives (see AAW15249-50) useful in a claimed method for detecting or measuring anti-AGPR antibody. The appearance of autoantibodies against AGPR is an indicator of autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asialoglycoprotein receptor H1; AGPR; autoimmune hepatitis; autoantibody; liver; diagnosis; human; primer; PCR; polymerase chain reaction; ss.
HDAC in a cell. The HDAC inhibitors of the invention are useful for treating cell proliferative diseases and conditions. The present DNA sequence represents a human HDAC gene-specific antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asialo:glyco:protein receptor H1 and L-H2 soluble derivatives - comprise extracellular domains, optionally also with cytoplasmic domains, useful for autoimmune hepatitis diagnosis.
                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yano A;
                                                                                                                     Query Match
1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Score 15.2; DB 1; Length 21; 85.0%; Pred. No. 1.3e+02;
                                                      that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yagi S, Hasegawa A, Kiyosawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21 BP; 7 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                     Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                         Asialoglycoprotein receptor H1 PCR primer F1.5.
                                                                                                                                                         0; Mismatches
                                                                                                                                                                                          743 AGGCAGCTGCCACCTTATGC 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 6; 40pp; English.
                                                                                                                                                                                                                             1 AGCCAGCTGCCACTTGATGC 20
                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96EP-00113349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95JP-00212118
                                                                                                                                                                                                                                                                                                                  AAT66953 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-261316/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TOFU ) TONEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tanida E, Ohue C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                     23-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP773289-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAY-1997
                                                                                                                                                                                                                                                                                                                                                  AAT66953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thrombosmbolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also correlations to diseases. The present sequence is an example of one of the human gene SNPS shown in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mccarthy JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Revised record issued on 18-NOV-2004 : The variantion feature was
                                                             /*tag= a
/standard_name= "Single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.4%; Score 15.2; DB 1; Length 21; 85.0%; Pred. No. 1.38+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Daley GQ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 4 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bolk S,
                                                                                                                                                                                                                                                                                                                                                                                                                           BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ireland JS,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     733 GCAGTCTTGTAGGCAGCTGC 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Page 95; 242pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          incorrectly given a captial V
                                                                                                                                                                                                                                                     07-SEP-2000; 2000WO-US024503.
                                                                                                                                                                                                                                                                                                            10-SEP-1999; 99US-0153357P-
26-JUL-2000; 2000US-0220947P-
16-AUG-2000; 2000US-0225724P.
                                                                                                                                                                                                                                                                                                                                                                                                                           (WHED ) WHITEHEAD INST BIOME (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gargill M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-226749/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                            WO200118250-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
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Matches
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RESULT 131

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Gaps

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Indels

0; Mismatches

Matches 17; Conservative

820 AGGCCTCTCATGACCCAGGA 839

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1 AGCCCTATCATGACCAAGGA 20

RESULT 130 AAF95925/c

cassette transporter; ABC transporter; oug development; biochemical kinetic; anthelmintic;

(first entry)

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Probes for determination of human ATP-binding cassette (ABC) transporters capable of hybridization with 33 regions of genes.
                                                                                                                              Human ATP-binding cassette (ABC) transporter probe #86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Page 29; 36pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                         (SAKA ) OTSUKA SEIYAKU KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-2000; 2000JP-00303404.
                                                                                                                                                                                                                                                                                                                                                 03-OCT-2000; 2000JP-00303404.
                          ABK82248 standard; DNA; 21
                                                                                                                                                                      Human; ATP-binding cas
expression rate; drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-458864/49.
                                                                                                                                                                                                                                                                               JP2002112775-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention
                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                 16-APR-2002.
                                                                                                  27-AUG-2002
                                                                                                                                                                                                         probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABS98518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                ABK82248;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABS98518,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various oblymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also correlations to diseases. The present sequence is an example of one of the human gene SNPS shown in the specification
                                                                                                                                                                                          polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism; pulmonary embolism; paternity test; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mccarthy JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                record issued on 18-NOV-2004 : The variantion feature was
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/standard_name= "Single_nucleotide_polymorphism"
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                                                                                                                                                                             variant thrombospondin 1; variant thrombospondin 4; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.2; DB 1; Lengtn A. Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Daley GQ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 0 Other;
                                                                                                                                       Human gene single nucleotide polymorphism #1729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bolk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (WHED ) WHITEHEAD INST BIOMEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ireland JS,
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Page 163; 242pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   incorrectly given a captial V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-SEP-1999; 99US-0153357P.
26-JUL-2000; 2000US-0220947P.
16-AUG-2000; 2000US-0225724P.
                    踞
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-SEP-2000; 2000WO-US024503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC
                AAF96968 standard; DNA; 21
                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 85.0
les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gargill M,
                                                                                          (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-226749/23.
                                                                                                                                                                                                                                                                                                                                                                                                                   WO200118250-A2
                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ES,
                                                                                        18-NOV-2004
06-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAR-2001
                                                                                                                                                                                                                                                                                                                                             variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                        AAF96968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Revised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lander
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Matches
AAF96968/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; cytochrome P450 A2; CYP4501A2; cytochrome P450 02B; CYP45002E1; LTF; cytochrome P450 02B; CYP45002E1; LTF; adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MR13; NR13; aryl hydrocarbon; ARNT; cathepsin S; CTSS; cyclooxgenase 2; COX2; diazepam binding inhibitor; DB1; haematological; epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP; eputathone-S-transferase 12; GST12; histamine-N-methyl transferase; HAP; HADP; HADPH quinone oxidoreductase 2; NGO2; sulfortansferase thermolabile; STM; UGT2B7; UDP-glucuronosyl transferase 2B7; UGT2B7; UDP-glucuronosyl transferase 2B7; UGT2B7; UDP-glucuronosyl transferase 2B7; multidrug resistance 1; lactotransferrin; orphan nuclear receptor; uPA;
                                              18
                 binding cassette (ABC) transporters capable of hybridisation with 33 binding cassette (ABC) transporters capable of hybridisation with 33 useful for development of drugs and their biochemical kinetics. This sequence represents a probe used to detect human ATP-binding casette
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human acetyl choline muscarinic receptor 2 polymorphic sequence #1.
describes new probes for identification of human ATP-
                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                           Length 21;
                                                                                                                                                                                                         Score 15.2; DB 1; Length 2
Pred. No. 1.3e+02;
0; Mismatches 3; Indels
                                                                                                                                                             Sequence 21 BP; 2 A; 4 C; 6 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                      295 TGGAATTGTTGTTTCTGCCT 314
                                                                                                                                                                                                                                                                                                                                   1 TGGAGTTCTTGTTGCTGCCT 20
                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                1.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABS98518 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                      Local Similarity 85.0
les 17; Conservative
                                                                                                                          (ABC) transporters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-2002
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CTGGCTTGGGCAGGCTGCCC 22

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21 creccrececciócicarec 2

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This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 Al (CY44501A1), cytochrome P450 Al (CY44501A1), cytochrome P450 Al (CY44501A1), argued by the cytochrome P450 O2EI (CY4501A1), argued by the cytochrome P450 O2EI (CY58), cytochrome P450 Al (CY44501A1), argued by the cytochrome P450 O2EI (CY58), cytochrome Cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for
multidrug resistance associated protein 3; cancer; prostate; acetylcholine muscarinic receptor; CHWR1; CHWR2; CHWR3; CHWR5; altered drug metabolism; cardiovascular function; colorectal tumour; central nervous system; pulmonary; immunological; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polymorphic DNA sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 27; Page 158; 714pp; English
                                                                                       single nucleotide polymorphism
                                                                                                                                                                                                                                                                         28-NOV-2001; 2001WO-US044838
                                                                                                                                                                                                                                                                                                                      28-NOV-2000; 2000US-00724389.
                                                                                                                                                                                                                                                                                                                                                                (DNAS-) DNA SCI LAB INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorder-related traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-698522/75
                                                                                                                                                                                                                                                                                                                                                                                                             Hall J;
                                                                                                                                                                                 WO200257410-A2
                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                            25-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                             Guida M,
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Sequence 21 BP; 4 A; 4 C; 4 G; 9 T; 0 U; 0 Other;
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oligonucleotides from rose microsatellite markers, useful for genomic
                                                                                                            mıcrosatellite marker; rose genome; PCR; hypervariable region;
genetic mapping; relatedness analysis; hybrid identification; plant;
breeding; primer; ss.
                                                                                                                                                                                                                                                                                                                       This invention describes novel oligonucleotides derived from
                                                                                                   Rosa sp forward PCR primer for microsatellite marker RMS009.
                                                                                                                                                                                                                                                                                         analysis, including identification of varieties and hybrids
934 AAATGCAGAATCTGAAGCCC 953
               Н
                                                                                                                                                                                                                                                                                                        Claim 1; Page 5; 52pp; German.
             AATTGTAGAATCAGAAGCCC
                                                     ADH68383 standard; DNA; 21 BP.
                                                                                                                                                                                                   16-MAY-2003; 2003WO-DE001572.
                                                                                                                                                                                                                  17-MAY-2002; 2002DE-01022632
                                                                                    25-MAR-2004 (first entry)
                                                                                                                                                                                                                                  (CONC-) CON CIPIO GMBH
                                                                                                                                                                                                                                                                 WPI; 2004-012541/01.
                                                                                                                                                                   WO2003097869-A2.
                                                                                                                                                                                   27-NOV-2003.
                                                                     ADH68383;
               20
                                                                                                                                                                                                                                                  Suess K;
                                                                                                                                                     Кова вр.
                                      RESULT 134
                                                                                                                                                                                                                                                                                 New
                                              ADH68383
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              셤
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The invention describes movel origonacectaes derived from microsatellite markers and used for the amplification of the rose genome.

The invention also describes a test kit for genetic analysis of cultured or wild forms of the genus Rosa sp. that contains at least one of the new oilgonucleotide primers and preparing microsatellite markers of Rosa sp. by PCR amplification of hypervariable genomic regions, using at least one of the new oilgonucleotide primers and preparing microsatellite markers of Rosa sp. by PCR amplification of hypervariable genomic regions, using at least one of the primer pairs flank the microsatellite locus being amplified. The amplified markers are separated by electrophoresis, complicied. The amplified markers are separated by electrophoresis, complicied are detected by staining (ethidium bromide or silver), candioactive labelling and autoradiography, automated or silver), candioactive labelling and autoradiography, automated or silver), complicied and the cells tested against a high-demsity array of synthetic microsatellites. Inserts in plasmids that hybridised were sequenced and coli and the cells tested against a high-demsity array of synthetic microsatellites. Inserts in plasmids that hybridised were sequenced and constanting and labelling of mono- or poly-genic traits, selection, analysis of cultivated and wild types of roses, particularly for genetic mapping and labelling of mono- or poly-genic traits, selection, analysis of contrive detection of hybrids and plant breeding. The purity, identification of hybrids and plant breeding. The commercial rose varieties. Abless74 represent the PCR primers commercial rose varieties. Abless74 represent the PCR primers commercial commercial rose varieties. Abless74 represent the PCR primers commercial rose warieties. Abless74 represent the PCR primers commercial rose warieties. of the invention.

Sequence 21 BP; 7 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Query Match

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Gaps

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3; Indels

Pred. No. 1.3e+02; 0; Mismatches 3

82.08;

17; Conservative

Best Local Similarity Matches 17; Conserv

Query Match

Score 15.2; DB 1; Length 21;

DB 1; Length 21; Score 15.2; 1.48;

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The present invention relates to a method for determining predisposition to developing cancer in subject, particularly for a subject having anticone to developing cancer in Subject, particularly for a subject having anticoners and the subject that the subject having anticoners are subject to the later and the subject and subject to the later of developing cancer. Also claimed are small interfering RNA (sIRNA) according an end of the later of development of a cancer in a subject. The invention is also useful for treating or preventing diseases such as systemic anaphylaxis or treating to preventing diseases such as systemic anaphylaxis or treating to preventing diseases fund allergies, inflammatory dermaticis), of dermatitis, allergic contact dermatitis), cephalosporins), insect sting allergies, inflammatory dermatitis), cephalosporins, allergic dermatitis, allergic contact dermatitis), cephalosporins allergic dermatitis, allergic contact dermatitis), cephalosporins allergic dermatitis, allergic contact dermatitis), content dermatitis, allergic respiratory allergic dermatitis, allergic rhintis, content of allergic manner of a cancer contact dermatitis), content dermatitis, content dermatitis, content dermatitis, content of a cancer content dermatitis, content dermatitis, content dermatitis, content of a cancer content dermatitis, content of a cancer c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining cancer cell or predisposition to developing cancer in subject candidate for anti-tumor necrosis factor therapy, by determining level of expression of B cell activation factor gene in sample of subject.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antilnflammatory, Antipsoriatic; Gastrointestinal; Antiallergic; Dermatological; Antiulcer; Vasotropic; Antiasthmatic; Immunosuppressive; Antidiabetic; cancer; B cell activation factor; BAFF; small interfering RNA; siRNA; systemic anaphylaxis; hypersensitivity response; allergy; multiple sclerosis; systemic lupus erythematosus; diabetes; graft rejection; ds.
                         Gaps
                         ö
85.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antiarthritic; Antirheumatic; Muscular; Neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21 BP; 6 A; 3 C; 8 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erythematosus, diabetes, graft rejection, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 66; SEQ ID NO 101; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         BAFF siRNA sense strand DNA, SEQ ID 101.
                                                                                   221 ATTGCCAAAAGAGTCACCTA 240
                                                                                                                     1 ATTGGCAAAGATTCTCCTA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GARV-) GARVAN INST MEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Batten M;
                                                                                                                                                                                                                                                                              Bb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-2003; 2003US-0449037P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-2004; 2004WO-AU000215.
                                                                                                                                                                                                                                                                              ADR68090 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                               17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mackay F, Mackay C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-652968/63.
        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004074511-A1
                                                                                                                                                                                                                                                                                                                                                                                              18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                          ADR68090;
                                                                                                                                                                                                                                   RESULT 135
                                        Matches
                                                                                                                                                                                                                                                       ADR68090
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This sequence represents a PCR primer that can be used in the method of the invention. The method is for genetic diagnosis using human mitochondrial DNA where there is at least one base replacement from among the following five replacements: the 3010th base is changed from guanine to adenine; the 4883rd base from cytosine to thymine; the 5178th base from cytosine to thymine; the 14668th base from cytosine to thymine. The method can be used for diagnosing the probability of contracting adult diseases. A confirmation of base replacement can give a diagnosis of the level of probability of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAR; leukocyte antigen related protein; LAR inhibitor;
antisense oligonuclectide; cytostatic; gene therapy; metabolic disorder;
hyperproliferative disorder; cancer; human; phosphorothioate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetic diagnosis using human mitochondrial DNA - comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human LAR chimeric phosphorothioate oligonucleotide SEQ ID NO:82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.3%; Score 15; DB 1; Length 20;
100.0%; Pred. No. 1.3e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                    PCR primer; human; mitochondrial DNA; genetic diagnosis; adult disease contraction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 3 A; 3 C; 6 G; B T; 0 U; 0 Other;
                                                                                                                                                                            PCR primer H5528 for mitochondrial DNA analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 5; 15pp; Japanese.
139 GGGATGTGCCTTAGAGGATT 158
                          21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contraction of adult diseases
                2 GGGAAGTGCCCTAGAAGATT
                                                                                              AAX79744 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         895 ACAGACCAAGAGCCT 909
                                                                                                                                                                                                                                                                                                                                                    97JP-00279127
                                                                                                                                                                                                                                                                                                                                                                               97JP-00279127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ33553 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
nes 15; Conservative
                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-320841/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               base replacements.
                                                                                                                                                                                                                                                                                                                                                                                                           (TANA/) TANAKA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                      13-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                  13-OCT-1997;
                                                                                                                                                                                                                                                                                                 JP11113597-A.
                                                                                                                                                         17-AUG-1999
                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                             27-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ33553;
                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                              AAX79744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
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                                                                         RESULT
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Gaps

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1.4%; Score 15.2; DB 1; Length 21; 15.0%; Pred. No. 1.3e+02; ve 0; Mismatches 3; Indels

85.0%;

Query Match
Best Local Similarity 85.0
Matches 17; Conservative

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short interfering nucleic acid; siNh; downregulation; inhibition; mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference; cytostatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic; immunosuppressive; antibacterial; antirheumatic; antiarthritic; antipsoriatic; gastrointestinal; obesity; diabetes; tumour; inflammatory disease; asthma; septic shock; rheumatoid arthritis; psoriasis; inflammatory bowel disease; drug screening; genetic engineering; pharmacogenomic; gene mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitogen activated protein kinase sinA oligonucleotide SEQ ID NO:274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADE29652 standard; RNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAATGCACAATCTAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-2004 (first entry)
                                                                                                                                                             27-DEC-1999;
                                                                                                                 05-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE29652;
                                                                     Mus sp.
                                                                                                                                                                                                           Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
            PCR
 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a compound (I) comprising a sequence comprising 8-80 base pairs (bp) targeted to a nucleic acid encoding LAR (leukocyte antigen related protein), where (I) specifically hybridises with the nucleic acid and inhibits expression of LAR. Also described: (1) a composition comprising the expression of LAR in cells or tissues; (3) treating an animal having or suspected of having a disease or condition associated with LAR; and (4) screening for an antisense compound. (I) has cytostatic activity, and can be used in gene therapy. The antisense oligonucleotide ecompound (I) can be used for preparing a composition for treating metabolic or hyperproliferative disorders, particularly cancer. The present sequence represents a human LAR chimeric phosphorothioate
                                                                                                                                                                                                                                                                                                                                                                                   New compound comprises a sequence targeted to a nucleic acid encoding Leukocyte Antigen Related protein (LAR), useful for preparing a composition for treating metabolic or hyperproliferative disorders, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.3%; Score 15; DB 1; Length 20; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels
                                                                                        /mod_base= OTHER
/note= "phosphorothioate linkages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 7 A; 3 C; 8 G; 2 T; 0 U; 0 Other;
                                                                                                                          Freier SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 15; SEQ ID NO 82; 197pp; English.
                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        Dobie KW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1079 CTTAACCTCTCTGGG 1093
                                                                                                                                                                                                                                                                   31-JUL-2003; 2003WO-US023994.
                                                                                                                                                                                                                                                                                          31-JUL-2002; 2002US-00210838
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                                                                             Д
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 CTTAACCTCTCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                     . 20
                                                                                                                                                                                                                                                                                                                 (ISIS-) ISIS PHARM INC
2'-O-methoxyethyl; ss
                                                                                                                                                                                                                                                                                                                                        Bhanot S,
                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-143728/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 15; Conserv
                                                                                                                                                                                                                      WO2004010956-A2
                                                        Key
modified_base
                                                                                                               modified_base
                                                                                                                                                             modified base
                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-2001
                                                                                                                                                                                                                                             05-FEB-2004
                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                        Monia BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH73748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 138
                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH73748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BXXXE
8XCCCCCCCCCCCCCX8X44445X3X3X3X4X4X444414141414X8X8X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
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                                                                    Sex determination; ratio; offspring; transgenic animal; PCR primer; tspy; testis specific protein Y-linked; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing transgenic animals, involves creating transgene whose expression interfere with sperm's ability to undergo fertilization, and placing it under post-meiotic spermatogenesis-specific promoter control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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primer used to amplify murine Tspy pseudogene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14.8; DB 1; Length 1
Pred. No. 1.4e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 9 A; 4 C; 2 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the sex ratio of the offspring of the animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 8; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          951
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0
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                                                                                                                                                                                                                                                                                                                                                                                                 27-DEC-2000; 2000WO-US035275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0173096P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Costantini F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-425551/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                       WO200147353-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LIUC/) LIU C.
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The present invention describes a short interfering nucleic acid (siNA) chat downregulates expression of a mitogen-activated protein kinase that downregulates expression of a mitogen-activated protein kinase codulating expression of MAPK genes in cells, tissue explants or coganisms by introduction of MAPK genes in cells, tissue explants or crystaling expression of MAPK genes in cells, tissue explants or organisms by introduction of siNA; (2) kits for in vitro or in vivo corganisms by introduction of siNA; (2) kits for in vitro or in vivo corganisms by introduction and cells containing these vectors. MAPK siNAs contasthmatic, annoractic, antiplacteria, antiminammatory, antischmatic, antiplacteria, antiminammatory, antischmatic, antischmatic and gastrointestinal activities. The MAPK contained contained the expression of MAPK genes, in cells, siNAs can be used to modulate the expression of MAPK genes, in cells, cissue explants or organisms, e.g. for treating obseity; diabetes types I tissue explants or organisms, e.g. for treating obseity; diabetes types I compute shock, rheumatoid arthritis, psoriasis and inflammatory bowel containing sene function and sene mapping (e.g. of single-nucleotide cutomic represents a MAPK siNA which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer, downregulates expression of mitogen-activated protein kinase genes.
inflammatory disease; asthma; septic shock; rheumatoid arthritis; psoriasis; inflammatory bowel disease; drug screening; genetic engineering; pharmacogenomic; gene mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.3%; Score 14.8; DB 1; Length 19; Best Local Similarity 55.6%; Pred. No. 1.4e+02; Matches 10; Conservative 6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19 BP; 7 A; 2 C; 3 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haeberli P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; SEQ ID NO 111; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA interference target sequence #185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mcswiggen J, Beigelman L, Usman N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382 AGGCAATGCAGTCATTT 399
                                                                                                                                                                                                                                                                                                        11-MAR. 2002; 2002US-0363124P.
06-JUN-2002; 2002US-0386782P.
29-AUG-2002; 2002US-0406784P.
05-SEP-2002; 2002US-0408378P.
09-SEP-2002; 2002US-0409293P.
15-JAN-2003; 2003US-0440129P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SIRN-) SIRNA THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AGAAAAUGCAGUCAUUUU
                                                                                                                                                                                                                                           28-JAN-2003; 2003WO-US002510
                                                                                                                                                                                                                                                                                       2002US-0358580P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADQ27277 standard; DNA; 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-689980/65.
                                                                                                                                                    WO2003072590-A1.
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                                                                                                                                                                                                                                                                                            20-FEB-2002;
                                                                                                                                                                                                    04-SEP-2003
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                                                                                                             Synthetic.
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                     g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a short interfering nucleic acid (siNA) that downregulates expression of a mitogen-activated protein kinase that downregulates expression of a material to a method for modulating expression of MAPK genes in cells, tissue explants or corganisms by introduction of siNA; (2) kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or complexes of siNA; and (4) evertors that express siNA and cells containing these vectors. MAPK siNAs vectors that express siNA and cells containing these vectors. MAPK siNAs antiasthmatic, annuosuppressive, antibacterial activities. The MAPK antisachmatic, antipsoriatic and gastrointestinal activities. The MAPK alsa can be used to modulate the expression of MAPK genes, in cells, siNAs can be used to modulate the expression of MAPK genes, in cells, and II; a wide range of tumours, and inflammatory disabetes types I septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel disease). They can also be used for drug screening; diagnosis; target disease). They can also be used for drug screening; diagnosis; target disease). They can also be used for drug screening; pharmacogenomics; incomplement of the contained of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                studying gene function and gene mapping (e.g. of single-nuclectide polymorphisms). The present sequence represents a MAPK siNA which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          short interfering nucleic acid; siNA; downregulation; inhibition; mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference; cytostatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic; immunosuppressive; antibacterial; antirheumatic; antiarthritic; antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer, downregulates expression of mitogen-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                Usman N, Haeberli P, Chowrira B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14.8; DB 1; Length 19;
Pred. No. 1.4e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19 BP; 7 A; 3 C; 2 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; SEQ ID NO 274; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 AGGCAATGCAGTCATTTT 399
                                                                                                                                                                                                            11-MAR-2002; 2002US-0363124P.
06-JUN-2002; 2002US-0386782P.
25-AUG-2002; 2002US-0406784P.
05-SEP-2002; 2002US-0409378P.
09-SEP-2002; 2002US-0409293P.
15-JAN-2003; 2003US-0440129P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADE29489 standard; RNA; 19 BP.
                                                                                                                                                                                                                                                                                                                                                                         (SIRN-) SIRNA THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 AGAAATGCAGTCATTT
                                                                                                                                            28-JAN-2003; 2003WO-US002510
                                                                                                                                                                                               2002US-0358580P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          Mcswiggen J, Beigelman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis of cancer, d
protein kinase genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-689980/65.
                                                          WO2003072590-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2004
                                                                                                                                                                                               20-FEB-2002;
                                                                                                      04-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADE29489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE29489
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Chowrira B;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                               The invention relates to a method of detecting the base sequence for RNA interference by detecting the regions in the DNA sequence fulfilling the following requirements such as: (i) the base at 3 'terminal is adenine, thymine or uracil; (ii) the base at 5' terminal is guanine or cytosine; (iii) the seven base sequence at 3' terminal is rich in adenine, thymine and uracil, and; (iv) there are bases in a such a number that it causes RNA interference without showing cytotoxicity. The method is used for designing and synchesizing siRNA causing RNA interference. This sequence corresponds to an RNA interference target sequence of the invention.
                                                                                                                                                                                                                                                   ecting sequence of RNA interference useful for synthesizing siRNA, by secting regions in sequence fulfilling specific criteria such as base 3' terminal is adenine, thymine or uracil, base at 5' terminal is
detection; RNA interference; siRNA; gene silencing; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ss; primer; single nucleotide polymorphism; SNP; diagnosis; disease association; linkage analysis; autodimune disease; rheumatoid arthritis; diabetes; multiple sclerosis; systemic lupus erythematosus; inflammatory bowel disease; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thyroiditis, celiac disease, pernicious anaemia, asthma, vitiligo, glomerulonephritis, Graves' disease, myocarditis, Sjogren disease, primary systemic vasculitis, genotyping, gene therapy, PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.3%; Score 14.8; DB 1; Length 19; 88.9%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human single nucleotide polymorphism detection primer #618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 199; 325pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      744 GGCAGCTGCCACCTTATG 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACAGCTGCGACCTTATG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADR27528 standard; DNA; 19 BP.
                                                                                                    21-NOV-2003; 2003WO-JP014893
                                                                                                                         22-NOV-2002; 2002JP-00340053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.9%;
                                                                                                                                                                                                        Tei K, Naito Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 88.9
nes 16; Conservative
                                                                                                                                                                                                                                                                                        guanine or cytosine.
                                                                                                                                                                                                                               WPI; 2004-487423/46.
                                                                                                                                             (NATO/) NATORI Y.
(SAIG/) SAIGO K.
(TEIK/) TEI K.
(NAIT/) NAITO Y.
                                                        WO2004048566-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004067779-A2
                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
           cytotoxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-NOV-2004
                                                                             10-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-AUG-2004
                                                                                                                                                                                                                                                    Detecting detecting a
                                                                                                                                                                                                        Saigo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR27528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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The invention relates to an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotide is a single nucleotide polyworphism (SNP) selected from any one of the nucleotide content of the relation (SNP) selected from any one of the nucleotide content of the properties (SNP) selected from any one of the nucleotide content of the species of SNP of SNP of diagnostic reagents and the Gevelopment of the rappeutic agents, as well as for disease association and individual who is at an increased or decreased risk for developing an individual who is at an increased or decreased risk for developing an autoimmune disease such as rheumatoid arthritis, type 1 diabetes, as the primary systemic lupus erythematosus, inflammatory bowel disease, psystemic lupus erythematosus, inflammatory bowel disease, or primary systemic vasculitis, Methods associated with the SNPs are useful for early detection of the disease, myocarditis, cthe surchamna diseases particularly rheumatoid arthritis, and for the autoimmune diseases particularly rheumatoid arthritis, and for screening and selecting therapeutic agents. The SNPs are useful for treating the diseases defined above. The nucleic acid molecules are useful for constructing the disease defined above. The nucleic acid molecules are useful for constructing host cells expressing a part or all of the cucleic acid molecules and variant peptides, for constructing transgenic condens. The nucleic acid molecules are useful for constructing host cells expressing a part or all of the capted as and variant peptides, for constructing transgenic confinence acid molecules and variant peptides, for constructing transgenic confinence acid molecules and variant peptides, for constructing transmission, or for gene therapy in patients whose cells have aberrant constructing region. This sequence corresponds to a PCR primar which containing region. However these sequence are not provided in the specification, however these sequence are not provided in the specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New single nucleotide polymorphisms (SNPs) associated with rheumatoid arthritis (RA), useful in identification of individuals at risk of developing RA or other autoimmune disease, and in development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           Alexander HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primer for detecting mutations in human Int6 gene homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Schrodi SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19 BP; 5 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.46+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 21; SEQ ID NO 50200; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   provided in the printed specification).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                       Carlton VE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1064 CCAGTGGCTAAACCACTT 1081
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                                                                                                             18-WAR-2003; 2003US-045544P.
25-APR-2003; 2003US-0465241P.
15-AUG-2003; 2003US-0495115P.
13-NOV-2003; 2003US-0519270P.
30-JAN-2004; 2004WO-US002652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           Cargill M, Begovich AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Conservative
                                                                                                                                                                                                                                                                                                                           (APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-594223/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapeutic agents.
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                                                                                    30-JAN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT36153;
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AAT36153/c
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AAT36149-T36174 are PCR primers derived from intronic sequences of human homologue of the murine Int6 gene located at chromosome 15 of a mouse genome. The primers are used for detecting mutations within the human Int6 gene. The Int6 gene is associated with MMTV (mouse mammary tumour virus) integration into a host genome during tumourigenesis. Primers and probes can be used in assays to diagnose MMTV infection, or any other int6 gene integration. Antibodies against the Int6 protein can be used in
                                                                                                                                                                                                                                                                           DNA encoding Int6 tumour associated protein - and use of reagents derived from them in cancer gene therapy, vaccines, diagnosis and immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse mammary tumour virus; MMTV; cancer; immunotherapy; gene therapy; prenatal screening; foetus; vaccine; primer; polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          murine; human; Int6; integration site; deregulation; neoplasia;
  MMTV; mouse mammary tumour virus; Int6; breast cancer; neoplasia; diagnosis; treatment; immunotherapy; vaccine; probe; primer; polymerase chain reaction; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14.8; DB 1; Length 20;
Pred. No. 1.4e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 4 A; 3 C; 2 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                         Marchetti A, Buttitta F, Smith GH, Callahan R;
                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                       Claim 16; Page 22; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTATTAGAAATGCAGAA 943
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97US-00875847.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-00385998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Int6 exon 3 primer #1.
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                                                                                                                                               96WO-US001884
                                                                                                                                                                         95US-00385998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.3
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                       WPI; 1996-384444/38.
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09-FEB-1996;
25-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amplify; BB.
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                                                                                           WO9624672-A1
                                                                                                                                                 09-FEB-1996;
                                                                                                                                                                           09-FEB-1995;
                                                                                                                    15-AUG-1996.
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                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            926
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AAI72504/C
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Gaps

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The sequences given in AA172500-23 are primers which were used to amplify the human Int6 coding sequence. The primers were derived from the intromic sequences which border the 5' and 3' ends of each excon of the intromic sequences which border the 5' and 3' ends of each excon of the human Int6 gene. Human Int6 is organised into 13 exons as is the murine line gene, and contains a CA-repeal in the 7th intron. Human Int6 has been localised to chromosome 8, more specifically to 8022-q4. Int6 is an integration site for mouse mammary tumnour virus (MMTV), which causes integration in mammary tumnours. The Int6 protein has been found to be integration in mammary tumnors. The Int6 protein has been found to be integration in mammary tumnors that Int6 is earving a basic life control. The method of the invention comprises assaying a sample to function. The method of the invention comprises assaying a sample to detect a human Int6 nucleic acid sequence, or its fragment, by contacting contession or loss of expression of the variant is associated with expression or loss of expression of the variant is associated with expression or loss of expression of the variant is associated with expression in the Int6 gene can provide diagnostic and prognostic conformation. The method is useful for prenatal screening of a foetus or to mothations in the Int6 gene can provide diagnostic and prognostic conformation. The method for the variant of preventing cancer. The conformation in the Int6 gene can provide diagnostic and prognostic conformation. The method for the tracting of preventing cancer. The conformations in the Int6 gene can provide diagnostic and prognoses of Int6 gene conformations in the Int6 gene can provide diagnostic and prognoses of Int6 gene conformations in the Int6 gene can provide diagnostic and prognoses of Int6 gene conformations in the Int6 gene preventing concer. The method of the formations in the Int6 gene preventing concer. The method of the formations in the Int6 gene preventing concer. The method of the formati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
                                                                                                                               DNA encoding Int6 tumour associated protein - and use of reagents derived from them in cancer gene therapy, vaccines, diagnosis and immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer used to amplify an ORF of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.3%; Score 14.8; DB 1; Length 20; 88.9%; Pred. No. 1.4e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 4 A; 3 C; 2 G; 11 T; 0 U; 0 Other;
                                                 Callahan
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                 Smith GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               926 CTTATTAGAAATGCAGAA 943
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97FR-00016034.
98US-0107077P.
                                                                                                                                                                                                                Claim 11; Col 14; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 CTAATTAAAATGCAGAA 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-OCT-1999 (first entry)
                                                 Marchetti A, Buttitta F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 16; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-NOV-1997;
17-DEC-1997;
04-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 145
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                                                                                                            PCR primers AAZ01426-Z06209 were used to amplify open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs encode polypeptides (see AAY36754-Y37949) which can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases unch as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, cervicitis, calpingitis, participatitis, bartholinitis; peneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; interleukin-5; IL-5; signal transduction; antisense oligonucleotide; antiasthmatic; immunosuppressive; cytostatic; IL-5 receptor-alpha; asthma; eosinophilic syndrome; infection; inflammation; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense oligonucleotide compound used to treat asthma and eosinophilic syndrome in humans modulates interleukin-5 signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is an oligonucleotide used for antisense modulation
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                        1.3%; Score 14.8; DB 1; Length 20;
88.9%; Pred. No. 1.4e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse IL-5R antisense oligonucleotide ISIS #23238.
                                                                                                                                                                                                                                                     Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
                                                                        sequence of Chlamydia trachomatis.
                                                                                          Disclosure; Page 1577; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 25; Page 77; 156pp; English
                                                                                                                                                                                                                                                                                                                   230 AGAGTCACCTATGACTCA 247
                                                                                                                                                                                                                                                                                                                               AGAGGTACCTATGACTCA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mckay R;
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                                                                                                                                                                                                                                                                                                                                                                                          AAC73799 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                              16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Karras JG,
                                                   WPI; 1999-371125/31
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                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 16; Conserv
         (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                    02-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-OCT-2000
                             Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dean NM,
                                                                                                                                                                                                                                                                                                                                                                                                              AAC73799;
                                                                                                                                                                                                                                                                         Query Match
                                                                        Genome
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of interleukin-5 (IL-5) signal transduction. Oligonucleotides were designed to target nucleic acids encoding IL-5 and IL-5 receptor-alpha. The artisense oligonucleotides may be used for the treatment of diseases associated with IL-5 signal transduction, IL-5 expression or IL-5 receptor-alpha expression. Such diseases include asthma and eosinophilic syndrome. The oligonucleotides are also useful for research uses and to prevent or delay infection, inflammation or tumour formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to controlling cell behaviour by modulating the processing of a selected wild-type mRNA target in the cell, is new. The mRNA is bound to a specific-binding antisense compound that does not cleave bound mRNA. The antisense oligonuclectides are useful as research reagents, diagnostic agents (in hybridisation assays), and for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         methoxyethoxy residues. All cytosines in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monia BP;
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse, antisense oligonucleotide; IL-5R; interleukin-5 receptor; ss; antiinfection; antiinflamatory; cytostatic; inflammation; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse interleukin-5 receptor antisense oligonucleotide ISIS 23238.
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baker BF,
                                                                                                                                                                                                                                                                                  Length 20;
                                                                                                                                                                                                                                                                                                                                      Indels
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1. .20
/*tag= b
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/note= "2' methoxyethoxy residues.
region are also 5-methyl-cytosine"
                                                                                                                                                                                                                           Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                            Score 14.8; DB 1;
Pred. No. 1.4e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Crooke ST, Manoharan M, Ackay R, Karras JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                             1050 ACTTCCTTATCTTTCCAG 1067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                  1.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTICCTIACCTITCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour; ISIS 23238; probe.
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                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ISIS-) ISIS PHARM INC
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modified_base
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Synthetic.
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ABL45391
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/note= "all nuclectides are 2'-methoxyethoxy (2'MOE); all
C nuclectides are 5-methyl-cytosines; all linkages are
phosphorothicate"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to the control of cell behaviour by modulating the processing of a wild-type mRNA target, comprising binding to the target an antisense compound which specifically hybridises to the target and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Controlling cell behavior by modulating mRNA modification, useful in therapeutics and as research tool, comprises using antisense oligonuclectide which hybridize to mRNA and block modification regions
or prevention of diseases, e.g. to prevent or delay infections, inflammation and tumours. The present sequence is an antisense oligonuclectide which targets exon 9 of mouse interleukin-5 receptor, with mismatched bases
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monia
                                                                                                                                                                                                                                                                                                                                  Antisense therapy; antisense oligonucleotide; apoptosis; mitosis; differentiation; stress; hormone; cytokine; signalling molecule; mRNA modulation; mRNA cleavage; therapeutic; mouse; IL-5R; interleukin 5 receptor; s8.
                                                                                                                                                                                                                                                                                                          Mouse IL-5R antisense oligonucleotide uniform 2'MOB #SEQ ID 16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baker BF,
                                                                                         Length 20;
                                                                                                                   2; Indels
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                                                                                       1.3%; Score 14.8; DB 1;
ilarity 88.9%; Pred. No. 1.46+02;
Conservative 0; Mismatches 2:
                                                               Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 8; Page 23; 50pp; English.
                                                                                                                                               1050 ACTICCTIATCTTICCAG 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      such as splice acceptor sites.
                                                                                                                                                                       13
                                                                                                                                                                                                                                       ABV73625 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-DEC-2000; 2000US-00734847.
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                                                                                                                                                                      Acriccriaccririccre
                                                                                                                                                                                                                                                                                        (first entry)
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*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-415043/44.
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MANOHARAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WYATT J.
BAKER B F.
MONIA B P.
MCKAY R.
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KARRAS J G.
                                                                                                           Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002049173-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-APR-2002.
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(CROO/)
(MANO/)
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(MONI/)
(MCKA/)
(KARR/)
                                                                                                                                                                         N
                                                                                                                                                                                                                                                                 ABV73625;
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                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp.
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The present invention describes a method of arraying genome clones. The method comprises: (a) clones of the genomic libraries contained in multiwell plates numbered for discrimination are mixed in each of the multiwell plates (b) a primer designed based on the chromosome marker comultiwell plates; (b) a primer designed based on the chromosome marker complished product to specify the discrimination Nos. of the multiwell plates containing the clones having said marker sequence; (d) the order cof the markers is changed so that the same discrimination Nos. succeed to of the markers is changed so that the same discrimination Nos. succeed to che maximum in the specified discrimination Nos. to array the multiwell plates; (e) the clones in the multiwell plates of the specified discrimination Nos. are mixed respectively in each wells of longitudinal compliance in the multiwell plates of the specified configurations of incertions; (f) the mixed clones are cultured and the constituted are ampolified products; (h) the clones in the multiwell cresultant cultures are specified from the detected from the amplified products; (h) the clones are reconstituted as the positions on the chromosome and arrayed. The microarray is useful for gene analysis. ABL42977 to ABL45222 represent creconstituted as the man analysis. BNN, and ABL45323 to ABL45534
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does not elicit cleavage of the mRNA upon binding. The method of the invention can be used in therapeutics (i.e antisense therapy), including prophylaxis, and as a research tool. It is used for controlling the behaviour of a cell (especially responses such as apoptosis, mitosis, differentiation and quiescence to stimuli such as stress, hormones, cytokines and other signalling molecules), tissue or organism through antisense modulation of mRNA processing. The current sequence represents a mouse IL-5R (interleukin-5 receptor) antisense oligonucleotide uniform bround account of the season of the seas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.8; DB 1; Length 20;
pred. No. 1.4e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human chromosome 21q22.1 PCR primer SEQ ID NO:2435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 53; 528pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.3%;
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(GENO-) GENOTEX YG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL45391 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-2002 (first entry)
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arraying genome clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-144136/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense nucleic acid against alpha V integrin for use in pharmaceutical compositions for the specific inhibition of the expression of alpha integrins in mammalian cells useful.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense nucleic acid; ss; alpha-V integrin chain; antisense inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell adhesion modulation; platelet aggregation; immune function; tissue repair; cell proliferation; tumour invasion; cancer; gingivitis; chronic inflammatory disease; Chron's disease; rheumatoid arthritis; cular neovascular disease; diabetic retinopathy; osteoporosis; excessive bone resorption; inflammatory skin disorder; psoriasis.
                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha-V integrin-specific inhibitory antisense nucleic acid 2.
represent PCR primers for human chromosome 21q22.1, which are
                                                                                                                                                                                     Length 20;
                                                                                                                                                                                                                                                       Indels
                                  specifically claimed for use in the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 10 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                        Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                          Score 14.8; DB 1;
Pred. No. 1.4e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                 1010 TTTGAGAAGCATCATCAT 1027
                                                                                                                                                                                                                                                                                                                                                                           1 TTTGAAAGCATCAGCAT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                  1.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2000; 2000EP-00121394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAL42513 standard; DNA; 20
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                                                                                                                                                                                                                                                       16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-364499/40.
                                                                                                                                                                                                                    Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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                                                                                                                                                                                     Query Match
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1.3%; Score 14.8; DB 1; Length 20; 88.9%; Pred. No. 1.4e+02;

Best Local Similarity

Query Match

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The invention relates to an isolated intracellular signaling polypeptide, termed Nod2, comprising a sequence of 1007 or 1040 amino acids, given in the specification. The nucleic acid encoding the isolated procein is useful for identifying subjects at risk of developing Crohn's disease by providing a nucleic acid from the subject, where the nucleic acid comprises a Nod2 gene, and detecting the presence or absence of one or more variations in the Nod2 gene. Detecting comprises comparing the acid. Detection is accomplished by hybridisation analysis. The method further comprises determining if the subject is at risk of developing crohn's disease based on the presence or absence of the variations, and cturther comprises determining if the subject is at risk of developing crohn's disease based on the presence or absence of the variation, and cturther comprises agnorype relative risk or a population attributable risk for the subject. The variation is a polymorphism or a mutation causes a preferably a cytosine residue insertion, where the mutation causes a confinence of the Nod2 gene. The isolated protein is useful as a target for screening drugs that can alter, for example, RICK signaling, and thus the physiological effects of NF-kappa B. The Nod2 gene is useful for producing the isolated protein by recombinant techniques, as starting for producing the isolated protein by recombinant tissues or plant calls as compared to wild-type plants, plant tissues or plant cells as compared to wild-type plants, plant tissues or plant the invariant or manna or the plants of the prepagator of the plants, plant tissues or plant the invariant or manna plants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated intracellular signaling polypeptide, termed Nod2, useful for producing an antibody that recognizes Nod2, and as a target for screening
                                                                                                                                                                                                                                                                                                                              Intracellular signaling polypeptide, Nod2; Crohn's disease; mutation; cytosine residue insertion; nuclear factor; NF-B activation; NF-kappa B; RICK signaling; gene therapy; transgenic plant; plant; ds.
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  Indels
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2
  Mismatches
                                                                                                                                                                                                                                                                                            Nod2 related oliognucleotide SEQ ID No 52.
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                                                                                                                                                                         BP.
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25-APR-2001; 2001US-0286316P.
26-OCT-2001; 2001US-00286316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-2001; 2001WO-US051068
                                      TTTTCCTTATATTTGGAA
                                                                         rrrrccrrararrrccaa
                                                                                                                                                                         ABT05772 standard; DNA; 20
                                                                                                                                                                                                                                                     16-OCT-2002 (first entry)
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UNMI ) UNIV MICHIGAN (UYCH-) UNIV CHICAGO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-547704/58.
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                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
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  16;
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                                                                                                                                                                                                              ABT05772;
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  Matches
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The invention relates to an antisense compound of 8-30 nucleobases in length, which modulates interleukin (IL)-5 signal transduction. Also include are a pharmaceutical composition comprising the antisense to adjagonucleotide and a pharmaceutically acceptable carrier or diluent, and a diagnostic kit for detecting the expression level of the membrane form versus soluble form of IL-5 receptor a. The antisense compound is useful mammalian IL-5 or modulating the expression of mammalian IL-5 or modulating the expression of mammalian in cells or tissues, for altering the ratio of the isoforms of mammalian IL-5 receptor a in mammalian cells or tissues, treating a mammalian having a disease or condition associated with IL-5 signal transduction, IL-5 expression or IL-5 receptor a expression, where the disease or IL-5 receptor a expression, where the disease or condition include eosinophilic syndrome or asthma. An antisense compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     which alters splicing of an RNA encoding IL-5 receptor a is also useful for treating a mammal having a disease or condition. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel antisense compound for treating disease/condition e.g. eosinophilic syndrome or asthma associated with interleukin-5 or IL-5 receptor expression or IL-5 signal transduction, modulates IL-5 signal
                                    6
                                                                                                                                                                                                                                                                                                                                                Mouse; ss; antisense; interleukin 5; IL-5; IL-5 receptor; antiasthmatic; immunosuppressant; eosinophilic syndrome; asthma.
                                        Gaps
                                                                                                                                                                                                                                                                                                                Mouse Interleukin 5 receptor antisense oligonucleotide ISIS 23238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is an antisense oligonucleotide targetting mouse IL-5 receptor
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Score 14.8; DB 1; Length 20;
Pred. No. 1.4e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 25; Page 24; 77pp; English.
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                                                                           784 TGGGGATGTGCTTGGAGA 801
                                                                                                                18 resesarerestreadea 1
                                                                                                                                                                                                           ABX04453 standard; DNA; 20 BP.
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17-MAR-2000; 2000WO-US007318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-2001; 2001US-00800629.
       1.3%;
                                                                                                                                                                                                                                                                                    (first entry)
         Query Match
Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-039602/03.
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(MANO/) MANOHARAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DEAN/) DEAN N M.
(KARR/) KARRAS J G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002128216-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                                                                                    13-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                  ABX04453;
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                                                                                                                                                                            RESULT 152
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The present invention relates to novel antisense oligonucleotides (ABZ81522-ABZ81593) which are targeted to human protein kinase A (PKA) regulatory subunit RII beta nucleotide sequence (ABZ81513), and which specifically hybridise with and inhibit the expression of the PKA regulatory subunit RII beta (PKA is also known as CAMP-dependent protein kinase). The antisense oligonucleotides are useful for modulating the expression of PKA regulatory subunit RII beta and for treating diseases or conditions associated with aberrant expression of PKA regulatory subunit RII beta, e.g. diabetes or cancer. The antisense compounds are also useful for diagnostics, therapeutics, prophylaxis, e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits, and in distinguishing between functions of various members of a biological pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Oligonucleotide has phosphorothicate backbone and all cytidine uncleotides are 5-methylcytidine. Optionally some nucleotides with 2'-methoxyethyl (2'-MOE wings) modification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense oligonucleotides targeted to nucleic acid encoding protein kinase A regulatory subunit RII beta, useful in treating diseases e.g. cancer associated with the aberrant expression of the protein kinase.
                                                                                                                                                                                                                       PKA regulatory subunit RII beta antisense oligonucleotide ISIS #114487.
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                                                                                                                                                                                                                                                         Human, cytostatic, antidiabetic, antisense therapy; phosphorothioate; protein kinase inhibitor; protein kinase A; PKA; regulatory subunit RII beta; cAMP-dependent protein kinase; diabetes; cancer; infection; inflammation; tumour; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 5 A; 2 C; 4 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                              base= OTHER
1050 ACTICCTIATCTTTCCAG 1067
                                 13
                                                                                                                       ABZ81557 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUL-2001; 2001US-00915485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-2002; 2002WO-US022629
                  2 ACTICCTIACCTITCCTG
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                                                                                                                                                                                             26-AUG-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  [ pow/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monia BP, Wyatt JR;
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                                                                                                                                                                                                                                                                                                                                                                                                               modified base
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                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                               ABZ81557;
                                                                                             RESULT 153
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663 TATGTTACTCAAATTATG 680

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0.0ery Match Best Local Similarity 88.9 Matches 16; Conservative

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29-JAN-2004
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                                                                                                                                                                                                                   Synthetic
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                                                                                           ADE25541;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel antisense compounds targetted to a nucleic acid encoding human phospholipid scramblase 4 (also known as PLSCR4, HUPLSCR4, MUPLSCR4 and LOC57088) to inhibit its expression. Antisense compounds of the invention are useful for preparing compositions for treating neurodegenerative diseases, e.g. hyperproliferative or autoimmune disorders. The invention is also useful in gene therapy. The present sequence is an antisense oligo targetted to human PLSCR4 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New compound, useful for preparing a composition for treating hyperproliferative or autoimmune disorders, comprises a sequence targeted to a nucleic acid encoding human phospholipid scramblase 4.
                                                                                                                                                                                                                                                                                                                                                                          note = "Phosphorothioate backbone; All cytidine residues
ire 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                Human, phospholipid scramblase 4; autoimmune disorder; gene therapy;
neurodegenerative disease; hyperproliferative disorder; HuPLSCR4;
MuPLSCR4; PLSCR4; LOC57088; antisense; phosphorothioate; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mod_base= OTHER
note= "2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note = "2'-methoxyethyl (2'-MOE) nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.8; DB 1; Length 20;
Pred. No. 1.4e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                  Human PLSCR4 antisense oligonucleotide, ISIS #196336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 8 A; 3 C; 2 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 15; Page 78; 166pp; English.
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         mod base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                    mod_base= OTHER
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||||||||||| | |||||| TATGTTACTGACATTATG 20
                                                                                           BP
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                                                                                           AAD57723 standard; DNA; 20
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nes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                     modified_base
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                                                                                                                                                      20-NOV-2003
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                                                                                                                                                                                                                                                                                             Synthetic
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Matches
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The invention relates to the treatment and prevention of cancer comprising a compound that inhibits the activity of protein or peptide fragment of a fully defined amino acid sequence TLR1 given as SEQ ID NO 1. TLR1 is useful in the treatment and prevention of cancers of the large intestine, mammary glands, lung, prostate, digestive tract, stomach and present sequence is that of a human TLR1 related for the result of a human TLR1 related PCR primer used in examples of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treatment and prevention for cancer of the e.g. digestive system, liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14.8; DB 1;
Pred. No. 1.4e+02;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nishizawa S;
                                                                                                                                                                                     Human; TLR1; cancer; cytostatic; primer; ss
                                                                                                                                        Human TLR1 related PCR primer SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kakoi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 89; 98pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                        26-DEC-2002; 2002WO-JP013642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-DEC-2001; 2001JP-00398165.
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ADE25541 standard; DNA; 20
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                                                                                            entry)
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les 16; Conservative
                                                                                            (first
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                                                                                                                                                                                                                                                                                                            WO2003061697-A1.
                                                                                                                                                                                                                                                                Homo sapiens.
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18 TIGCCITATATITICAAAG 1

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, conse in antisense gene therapy. The composition may have a immunosuppressive, and cytostatic activity. The composition may have a conse in antisense gene therapy. The composition may have a conse in antisense gene therapy. The composition may have a conse in antisense gene therapy. The composition may have a consent an autisense gene therapy. The composition may have a consent of or enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine or receptor, producing bronchodilation, increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition. Unug allergies, or a respiratory disease or condition. Note: The sequence date for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrom; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
                                                                                                                                                                                                                                                                                                                                                     Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                 Aguilar D;
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                                                                                                                                                                                                                                                      Pabalan J,
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Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 8905; 872pp; English.
                                                                                                                                                                                                                                                    Katz E,
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Tang L, Shahabuddin
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80.0%;
                                                                                                                          23-APR-2002; 2002WO-US013135.
                                                                                                                                                                    24-APR-2001; 2001US-0286137P.
                                                                                                                                                                                                             (EPIG-) EPIGENESIS PHARM INC.
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nes 16; Conservative
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                                        WO200285308-A2.
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  Homo sapiens.
                                                                                   31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                               ubiquinone.
                                                                                                                                                                                                                                                                            Miller S,
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Gaps

This invention describes a novel composition (a) a first active agent, comprising oligonuclectides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and bronchoconstriction respiratory tract inflammation, allergies and bronchoconstriction or hyposecretion, when administered to a mammal. The oligonuclectides are derived from a gene encoding or regulating cyptuction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery construction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery considered in separate containers, (b) the oligonuclectides, (c) instructions for adding a carrier and for use of the kit. The composition of instructions for adding a carrier and for use of the kit. The composition of instructions and antialergic, antiinflammatory, antiasthmatic, or composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition or availability, or to increase the degradation of the target mRNA or to composition, and/or bronchoconstriction and/or lung or availability, or to increase the degradation of the target mRNA or to creduce the amount of target polypeptide present in the lungs. The undantion, allergies and/or bronchoconstriction and/or lung inflammation, allergies asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructions be prevent the breakdown of thymidines present in the target RNA serves to prevent the breakdown of thymidines present in the target RNA serves to prevent the breakdown of thymidines present in the target RNA serves to prevent the breakdown of thymidines present in the target encounted encounted to the objection emphysema. Gaps Pharmaceutical composition for treating asthma, has antisense oligonuclectide containing less percentage of adenosine, targeted to nucleic acids associated with lung airway or lung dysfunction, and bronchodilating agent. Pabalan J, Aguilar D; ö Length 20; 4; Indels Sequence 20 BP; 8 A; 6 C; 2 G; 2 T; 0 U; 2 Other; Score 14.8; DB 1; Pred. No. 1.4e+02; pulmonary transplantation rejection; ss; primer. 80.0%; Pred. w... Katz E, Claim 15; SEQ ID NO 8905; 763pp; English. e.g., lūng, brain, heart, kidney, etc, prevent any unwanted effects due to it Li Y, Sandrasagra A, Ka Tang L, Shahabuddin S; 936 ATGCAGAATCTGAAGCCCCA 955 Archagaarchaaaccccca 20 1.3%; 23-APR-2002; 2002WO-US013143. 24-APR-2001; 2001US-0286036P. (EPIG-) EPIGENESIS PHARM INC. Local Similarity 80.0 nes 16; Conservative WPI; 2003-093058/08. WO200285309-A2. Homo sapiens. 31-OCT-2002 Nyce JW, L Miller S, Query Match RESULT 158 ADJ86050 ID ADJ8 XX AC ADJ8 Š g

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ADJ86050 standard; DNA; 20

ADJ86050;

22-JAN-2004

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The invention relates to a method for treating airway hyperresponsiveness or pulmonary inflammation in an individual comprising administering an antisense compound targeted to a nucleic acid molecule encoding a human B7 protein. The invention also relates to a method of inhibiting a human expression of a nucleic acid molecule encoding B7-1 or B7-2. The antisense compound is an antisense oligonucleotide which has a modified sugar molety and nucleobase. The human B7 protein is human B7-1 or B7-2 protein or both. The compound is useful for treating airway propensionaiveness or pulmonary inflammation, which is associated with asthma, by inhibiting expression of human B7 protein. This sequence represents an antisense oligonucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antilipaemic, Cardiovascular, Analgesic, Antianginal, Antisense therapy;
Human, Endothelial Lipase, dyslipidaemia, high density lipoprotein; HDL;
cardiovascular disorder; metabolic syndrome X; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "This oligonucleotide has a phosphorothioate backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5' and 3' ends, which are 4 nucleotides in length. Also all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating airway hyperresponsiveness or pulmonary inflammation comprises administering an antisense compound targeted to a nucleic acid molecule encoding a human B7 protein to the individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human endothelial lipase antisense oligonucleotide, SEQ ID 2222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.3%; Score 14.8; DB 1; Length 20;
88.9%; Pred. No. 1.4e+02;
ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 7 A; 1 C; 5 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 27; SEQ ID NO 314; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                               Karras JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                          31-DEC-1996; 96US-00777266.
04-JUN-1999; 99US-00326186.
25-MAY-2000; 2000WO-US014471.
09-MAY-2001; 2001US-00851871.
                                                                                                                23-MAY-2003; 2003US-00444206
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                                                                                                                                                                                                                                                                                                                                                                               Bennett CF, Vickers TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.3
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag=
                                                                                                                                                                                                                                                                               BENNETT C F.
VICKERS T A.
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-132608/13.
                                                                                                                                                                                                                                                                                                                              (KARR/) KARRAS J G.
                      US2004023917-A1.
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modified_base
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                                                                    05-FEB-2004
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                                                                                                                                                                                                                                                                                  (BENN/)
                                                                                                                                                                                                                                                                                                          VICK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 160
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ID ADJ2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a novel DNA molecule which comprises a DNA molecule made up of the following elements in a 5' to 3' direction: a first restriction endonuclease site; a T3 promoters site; at least on Tag gene comprising at least 5 20mer Tag sequences; a Poly A site having at least 21 consecutive A residues; a second restriction endonuclease site which may be the same or different than the first restriction endonuclease site; or a T7 Promoter on the opposite strand as the T3 promoter. The invention may be useful as assay controls, in assay development, product development and validation and for quality control. The present sequence is that of a Tag oligonucleotide probe which may be used during the creation of the novel DNA molecule of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New DNA molecules made by annealing and extending overlapping 60mer oligonucleotides, useful in producing synthetic Tag genes useful as assay controls, in assay development, product development and for quality
                                                                                                           restriction endonuclease site; T3 promoter site; Tag gene; Poly A site; T7 Promoter; nucleic acid analysis; synthetic Tag gene; assay control; assay development; product development; product development; product validation; quality control; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 1.3%; Score 14.8; DB 1; Length 20; Local Similarity 88.9%; Pred. No. 1.4e+02; les 16; Conservative 0; Mismatches 2; Indels
                                                               Nucleic acid analysis-related Tag probe SegID1118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human B7-2 DNA antisense oligonucleotide #109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 1118; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            697 TCATGTAGTCACGGTGCT 714
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                   06-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AFFY-) AFFYMETRIX INC
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                                                                                                                                                                                                                              Synthetic.
Unidentified
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06-MAY-2004

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RESULT 159

ADJ54494/

Query Match

Matches

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expression, for diagnosing, preventing or treating e.g. dyslipidemia, low high density lipoprotein or cardiovascular disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy; Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL; cardiovascular disorder; metabolic syndrome X; ss.
                                                                                                                                                                                                                                                                                                                                                             The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25517), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are used for diagnostics, prophylaxis, or as research reagents or kits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human endothelial lipase antisense oligonucleotide, SEQ ID 1168.
                                                                                                                                                                                                                                                                   New antisense oligonucleotide for modulating endothelial lipase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.3%; Score 14.8; DB 1; Length 20; 88.9%; Pred. No. 1.4e+02; ve 0; Mismatches 2; Indels
cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 20 BP; 3 A; 4 C; 12 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                       Claim 3; SEQ ID NO 2222; 1007pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 CGGGCCGTGGCAGGAAGC 39
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                                                                                                    18-JUL-2003; 2003WO-US022410
                                                                                                                                    19-JUL-2002; 2002US-0397106P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.9%;
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                                                                                                                                                                     (PHAA ) PHARMACIA CORP
                                                                                                                                                                                                                                     WPI; 2004-132912/13.
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Best Local Similarity
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                                  WO2004009541-A2
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                                                                                                                                                                                                        Bhat BG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 161
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                                                                                                                                                          New antisense oligonucleotide for modulating endothelial lipase expression, for diagnosing, preventing or treating e.g. dyslipidemia, low high density lipoprotein or cardiovascular disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy; Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; {\rm HDL}_1; cardiovascular disorder; metabolic syndrome X_1; ss.
                                                                                                                                                                                                                                                          The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25517), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are used for diagnostics, prophylaxis, or as research reagents or kits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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88.9%; Pred. No. 1.4e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                  Claim 3; SEQ ID NO 1168; 1007pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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18-JUL-2003; 2003WO-US022410.
                                 19-JUL-2002; 2002US-0397106P.
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                                                                (PHAA ) PHARMACIA CORP
                                                                                                                                  WPI; 2004-132912/13.
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modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                    Bhat BG;
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ADJ23294
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                                                                        New antisense oligonucleotide for modulating endothelial lipase expression, for diagnosing, preventing or treating e.g. dyslipidemia, low high density lipoprotein or cardiovascular disorders.
                                                                                                                                                                                 The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25517), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are used for diagnostics, prophylaxis, or as research reagents or kits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; ss; PCR; cancer; prostate cancer; neuroblastoma; leukaemia; inflammation; arthritis; inflammatory skin disorder; insulin dependent diabetes; adult respiratory distress syndrome; cell death-related disorder; Alzheimer's disease; Parkinson's disease; multiple sclerosis; AIDS; septic shock; stroke; osteoporosis; ischaemia; reperfusion injury; myocardial infarction; appetite; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polymucleotides encoding short polypeptides, for preventing and treating disease conditions associated with the activity of the polypeptide, e.g. inflammation, cancer, arthritis, insulin-dependent diabetes or osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antigen; anaphylaxis; primer; RT-PCR; reverse transcriptase PCR
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.3%; Score 14.8; DB 1; Length 20; Best Local Similarity 88.9%; Pred. No. 1.4e+02; Matches 16; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse cDNA clone C630041L24 RT-PCR primer #2.
                                                                                                                                                Claim 3; SEQ ID NO 1692; 1007pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; SEQ ID NO 67; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         865 TIGTAGTCCATGCTATTA 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 TIGTAGCCAATGCTATTA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HAYA/) HAYASHIZAKI Y.
(KAMI/) KAMIYA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-247724/23.
                                   WPI; 2004-132912/13.
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Bhat BG;
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The invention relates to an isolated mouse polymucleotide having a nucleotide sequence of a clone consisting of 1110005117, 1700007F22, 1700101122, 1700056N9, 2310014H11, 2310031021, 4930651801, 9130004105, 9320110A19, 9230111007, A030004E11, A430045L05, A530065117, A630010816, E2310114010, E2303152020, C230071E12, C630041L24 or D630020916, is new. The CC clones 1110005117, 1700007F22, 1700011022, 1700056N99, 2310014H11, C331004102, A330045L05, A530065117, A830010816, B230114010, B230352020, C230074H11, C3310041C01, 493055B01, 913004105, 9230114007, A030004B11, A330045L05, A530065117, A330010816, B230114010, B230352020, C230071B12, CC C30041L24 and D630020916, appearing as ADK19702-ADK19720. The polymucleotides and proteining applications, and prevention and treatment of disease conditions applications, and prevention and treatment of disease conditions applications, architis, chronic inflammatory conditions of the skin, insulin-dependent diabetes, adult respiratory distress syndrome, or disease, septic shock, stroke, osteoporosis, ischaemia, repertuaion injury, ADS or myocardial infarction. The polypeptides are also useful cincreasing antibody production in response to an antigen, inhibiting anaphylaxis, and reducing inflammation. The present sequence is a reverse cranscriptase PCR (RT)-PCR primer used to isolate a mouse polymucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding cyclin-dependent kinase 6, useful for treating cancer, bacterial/viral infection or conditions involving aberrant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14.8; DB 1; Length 20;
Pred. No. 1.4e+02;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyclin-dependent kinase 6, antisense oligonucleotide #231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antisense therapy; cyclin-dependent kinase 6; hyperproliferative disorder; cancer; bacterial infection; viral infection; apoptosis; ss; probe; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 15; Page 34; 68pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 CCCAGTTCGGGAGACATG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 CCCAGTTTGGGAGACAGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADO56167 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JUL-2002; 2002US-00210802
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-356241/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                           of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2004087523-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AD056167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADO56167
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Example 15; Page 32; 68pp; English

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The invention relates to antisense oligonucleotides targeted to cyclindependent kinase 6, and which inhibit the expression of cyclin-dependent kinase 6. The antisense oligonucleotides are useful for treating a disease or condition associated with cyclin-dependent kinase 6, such as a hyperproliferative disorder (e.g. cancer), or conditions arising from bacterial or viral infections, or involving aberrant apoptosis. They are also useful in research and diagnostics for modulating the expression of cyclin-dependent kinase 6. The present sequence represents a cyclindependent kinase 6 antisense oligonucleotide. Note: Seqid 15-134 are also used in the sequence listing but these sequences do not match seqid 15-134 displayed in Tables 1 and 2 (page 30-34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mod_base= OTHER
/note= "Phosphorothioate backbone. All cytidines are 5-
methylcytidines."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding cyclin-dependent kinase 6, useful for treating cancer, bacterial/viral infection or conditions involving aberrant apoptosis.
                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "note= "2'-methoxyethyl (2'-MOE) nucleotides"
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/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                         1.3%; Score 14.8; DB 1; Length 20; 88.9%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyclin-dependent kinase 6, antisense oligonucleotide #172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antisense therapy; cyclin-dependent kinase 6; hyperproliferative disorder; cancer; bacterial infection; viral infection; apoptosis; ss; probe; human.
                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                             Sequence 20 BP; 4 A; 4 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                             0; Mismatches
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/mod_base= OTHER
                                                                                                                                                                                                                                                                                           602 AAAGACTTCATAAGTAGG 619
                                                                                                                                                                                                                                                                                                                         18 AAACACTTCAGAAGTAGG 1
                                                                                                                                                                                                                                                                                                                                                                                                      BP
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                                                                                                                                                                                                                                              Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-356241/33.
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                                                                                                                                                                                                                                   Query Match
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             The invention relates to antisense oligonucleotides targeted to cyclindependent kinase 6, and which inhibit the expression of cyclin-dependent kinase 6. The antisense oligonucleotides are useful for treating a disease or condition associated with cyclin-dependent kinase 6, such as a hyperproliferative disorder (e.g. cancer), or conditions arising from bacterial or viral infections, or involving aberrant apoptosis. They are also useful in research and diagnostics for modulating the expression of cyclin-dependent kinase 6. The present sequence represents a cyclindependent kinase 6 antisense oligonucleotide. Note: Seqid 15-134 are also used in the sequence listing but these sequences do not match seqid 15-134 displayed in Tables 1 and 2 (page 30-34).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; Int6; PCR; ss; mammary epithelial cellular growth; cancer;
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                                                                                                                                                                                                                                         1.3%; Score 14.8; DB 1; Length 20; 88.9%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 4 A; 3 C; 2 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                          Sequence 20 BP; 8 A; 4 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marchetti A, Buttitta F, Smith GH, Callahan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cellular growth, useful for treating cancer.
                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                          602 AAAGACTTCATAAGTAGG 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-00385998.
96US-00875847.
96WO-US001884.
                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Int6 cDNA PCR primer #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-2001; 2001US-00858152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-00378842
                                                                                                                                                                                                                                                                                                                            3 AAACACTTCAGAAGTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                    ADN31001 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-2004 (first entry)
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Matches 16; Conservative
                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; primer.
                                                                                                                                                                                                                                                        Local Similarity
nes 16; Conserv
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09-FEB-1996;
09-FEB-1996;
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                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 166
                                                                                                                                                                                                                                                                    Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New oligonucleotide compound that inhibits expression of Interleukin 18, useful for preparing a composition for treating hyperproliferative disorder e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mod_base= OTHER
/note= "OTHER= Phosphorothioate backbone. All cytidines
are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; gene therapy; interleukin 18; IL-18; hyperproliferative disorder; cancer; human; antisense oligonucleotide; antisense technology; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .5
/*tag
/*mod_base= OTHER
/note= "OTHER= 2'-0-Methoxyethyl (2'-MOE) nucleotides"
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/note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                Human interleukin-18 antisense oligonucleotide segid 40.
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943
                                                    20 CTAATTAAAATGCAGAA 3
                                                                                                                                                                                                       BP.
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modified_base
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926
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1.3%; Score 14.8; DB 1; Length 20;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New oligonucleotide compound that inhibits expression of Interleukin 18, useful for preparing a composition for treating hyperproliferative disorder e.g. cancer.
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/*tag= b
/mod_base= OTHER
/note= "OTHER= Phosphorothioate backbone. All cytidines
are 5-methylcytidines"
1. .5
                                                                                                                                                                                                                                                                            cytostatic; gene therapy; interleukin 18; IL-18; hyperproliferative disorder; cancer; human; antisense oligonucleotide; antisense technology; ss.
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/note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
15. .20
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/note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
                Gaps
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                Indels
                                                                                                                                                                                                                                                  Human interleukin-18 antisense oligonucleotide segid 96
Pred. No. 1.4e+02;
0; Mismatches 2;
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                                           765
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                                                                                                                                                         BP.
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                                             748 GCTGCCACCTTATGCAGT
                                                                  GCTGCCACCTGCTGCAGT
                                                                                                                                                         ADP64751 standard; DNA; 20
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Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              Key
modified_base
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                                                                                                                                                                                                                   09-SEP-2004
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The invention relates to an antisense compound that modulates interleukin CC -5 (IL-5) signal transduction. The antisense compound is an antisense oligonucleotide targeted to a nucleic acid molecule encoding a mammalian consideration of mammalian IL-5 or IL-5 receptor a. The antisense compound modulates the expression of mammalian IL-5 or IL-5 receptor a. The antisense captesion of mammalian IL-5 or IL-5 receptor a. The antisense coligonucleotide comprises at least one modified internucleoside linkage, consoliditied sugar molety, i.e. 3 -0-methoxyethyl sugar molety, and at modified sugar molety, i.e. 5 -methoxyethyl sugar molety, and at consoliditied mucleobase, i.e. 5-methoxyethyl sugar molety, and at consoliditied nucleobase, i.e. 5-methoxyethyl sugar molety, and at consoliditied mucleobase, i.e. 5-methoxyethyl sugar molety, and at consoliditied mucleobase, i.e. 5-methoxyethyl sugar molety, and at compound so that the ratio of the mammalian IL-5 receptor a in mammalian cells or altered. Treating a mammal having a disease or condition characterised by a reduction associated with a disease or condition characterised by a reduction in approcase comprises compound so that IL-5 receptor a expression, or IL-5 receptor a signal transduction, IL-5 or IL-5 receptor a substitute of an antisense compound so that IL-5 receptor a is modulated, the ratio of IL-5 receptor a is modulated. The antisense compounds, methods and compositions are useful in promoting apoptosis and in treating eosinophilic syndrome and
                                                                                                                                                                                                                                                                                                                               Murine interleukin-5 (IL-5) receptor a DNA antisense oligonucleotide #72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense compound modulating interleukin-5 signal transduction, useful in promoting apoptosis and in treating eosinophilic syndrome or
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                    Mouse; interleukin-5; IL-5; ss; antisense oligonucleotide; IL-5 receptor a; phosphorothioate; 2'-0-methoxyethyl sugar moiety; 5-methylcytosine; IL-5 signal transduction; apoptosis; eosinophilic syndrome; asthma; antiasthmatic; cytostatic.
                                        ö
  Length 20;
                                        Indels
Score 14.8; DB 1;
Pred. No. 1.4e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Manoharan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 25; SEQ ID NO 152; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mckay R,
                                                                               765
                                                                                                                      18
                                                                                                                                                                                                                    ADR12130 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-1999; 99US-00280799.
17-MAR-2000; 2000WO-US007318.
07-MAR-2001; 2001US-00800629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-OCT-2003; 2003US-00679532.
      1.3%;
                                                                                 748 GCTGCCACCTTATGCAGT
                                                                                                                      1 GCTGCCACCTGCTGCAGT
                                                                                                                                                                                                                                                                                                  23-SEP-2004 (first entry)
                                             16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEAN N M.
KARRAS J G.
MCKAY R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Karras JG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-479669/45.
      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2004121376-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KARR/) I
(MCKA/) M
(MANO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dean NM,
                                                                                                                                                                                                                                                             ADR12130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                asthma.
                                                                                                                                                                                    RESULT 169
                                               Matches
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The lambda ZAPII cDNA library was mde from mRNA of a human female fetal CC (17-18 week gestation) brain, using both oligo (dT) and random- sequence (17-18 week gestation) brain, using both oligo (dT) and random- sequence CC primers. A 500-bp PCR product, corresp. to part of the coding region (547 1-1047) of the rat orphan receptor was used to screen the human fetal coling region of the rat orphan receptor was used to screen the human fetal contain cDNA library. PCR was performed using the fetal brain cDNA library cas template and a 23-mer forward primer posns 162-1047 (AAAG2341). Six positive plaques were isolated and sequenced. The DNA was amplified using two oligo primers, USI and JS2 (AAQ52342, AAQ52343). They corresp. to the sequences corresplete to do PCR amplification of a DNA cloned in the plasmid's linker. CC possible to do PCR amplification of a DNA cloned in the plasmid's linker. CC specific synthetic primers (3 forward primers (AAQ52344) was selected for sequencing analysis. 4 creverse primer (AAQ52347) were used for manual sequencing of the hY1-5 clones and its deletion constructs. Three oligos necessary to study the inhibition of the contractile effect of neuropeptide Y on human blood conserved to the mineral sequencing of the human (13 masse mismatched antisense oligo hY1-M (AAQ52330). CC (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                            synthetic forward primer for the manual sequencing of human
asthma. This sequence represents a murine IL-5 receptor a DNA antisense oligonuclectide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding human neuro-peptide Y-peptide YY Y1 receptor - is used to develop drugs for treating e.g. hypertension, depression or obesity.
                                                                                                                                   Gaps
                                                                                                                                   ö
                                                                                          Score 14.8; DB 1; Length 20;
Pred. No. 1.4e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yl receptor; Y-evoked vasoconstriction; primer; ss.
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                                                         Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                           1050 ACTICCTTATCTTTCCAG 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Page 13; 50pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of synthetic forward
Yl receptor cDNA clone hY1-5.
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                                                                                                  1.3%;
                                                                                                                                                                                              2 ACTICCTIACCITICCIG
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(first entry)
                                                                                                      Query Match
Best Local Similarity 88.9
Matches 16, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAY-1992;
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                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
23-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                               AAQ52344;
                                                                                                                                                                                                                                                                        RESULT 170
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1.3%; Score 14.8; DB 1; Length 21;

Query Match

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Human MRP-1 polymorphic DNA region #230.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   renal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a multidrug resistance-associated protein 1 (MRP -1) polynucleotide. The polynucleotide is useful in an in vitro method for identifying and containity a single nucleotide polynucphism and for identifying and obtaining a pro-drug or drug capable of modulating the activity of a molecular variant of MRP-1 or for identifying and obtaining an inhibitor of the activity of a molecular variant of MRP-1. The sequences are useful for diagnosing a disorder related to the presence of a molecular variant of MRP-1 or susceptibility to such a disorder, where the disorder is cancer (particularly renal cancer) or a disease related to multidrug
                                                                                                                                                                                                                                                                                                                                                                                       Novel multidrug resistance-associated protein 1 polynucleotide useful for diagnosis and treatment of cancer and multidrug resistance related diseases, and for identifying single nucleotide polymorphisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                resistance. This sequence represents a human MRP-1 polymorphic DNA region
              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                      Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer; renal cancer; cytostatic; single nucleotide polymorphism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.3%; Score 14.8; DB 1; Length 21; 88.9%; Pred. No. 1.5e+02;
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            Indels
 80.0%; Pred. No. 1.5e+02; cive 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21 BP; 5 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                   Human MRP-1 polymorphic DNA region #229.
                                                                                                                                                                                                                                                                                                                                                Mornhinweg
                                                                                                                                                                                                                                                                                                                            (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 82; 198pp; English.
                                331 TCTTGCTCGTGTGCCTGTGA 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
                                           2 TCTTGCTTATGGRGCTGTGA
                                                                                                      BP.
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                                                                                                      ABS66964 standard; DNA; 21
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                                                                                                                                               (first entry)
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           16; Conservative
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                     multidrug
                                                                                                                                                                                                                                          WO200259142-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                              29-NOV-2002
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                                                                                                                           ABS66964;
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ID ABS6690
XX
AC ABS6690
XX
DT 29-NOV
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                                                                                  RESULT 171
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Matches
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The invention relates to a multidrug resistance-associated protein 1 (MRP -1) polynucleotide. The polynucleotide is useful in an in vitro method for identifying a single nucleotide polymorphism and for identifying and obtaining a pro-drug or drug capable of modulating the activity of a molecular variant of MRP-1 or for identifying and obtaining an inhibitor of the activity of a molecular variant of MRP-1. The sequences are useful for diagnosing a disorder related to the presence of a molecular variant of MRP-1 or susceptibility to such a disorder, where the disorder is cancer (particularly renal cancer) or a disease related to multidrug resistance. This sequence represents a human MRP-1 polymorphic DNA region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel multidrug resistance-associated protein 1 polynucleotide useful for diagnosis and treatment of cancer and multidrug resistance related diseases, and for identifying single nucleotide polymorphisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
          cancer;
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Human, multidrug resistance-associated protein 1, MRP-1, ss. renal cancer, cytostatic; single nucleotide polymorphism.
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Pred. No. 1.5e+02;
0; Mismatches 2; Indels
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Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                       Homo sapiens
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The invention relates to a multidrug resistance-associated protein 1 (WRP-1) polynucleotide. The polynucleotide is useful in an in vitro method cor identifying a single nucleotide polynucphism and for identifying and obtaining a pro-drug or drug capable of modulating the activity of a molecular variant of MRP-1 or for identifying and obtaining an inhibitor
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                                                                                                                                                                                        The invention relates to a multidrug resistance-associated protein 1 (MRP-1) polymucleotide. The polymucleotide is useful in an in vitro method for identifying and sobtaining a single nucleotide polymorphism and for identifying and obtaining a pro-drug or drug capable of modulating the activity of a molecular variant of MRP-1 or for identifying and obtaining an inhibitor of the activity of a molecular variant of MRP-1. The sequences are useful for diagnosing a disorder related to the presence of a molecular variant of MRP-1 or susceptibility to such a disorder, where the disorder is cancer (particularly renal cancer) or a disease related to multidrug resistance. This sequence represents a human MRP-1 polymorphic DNA region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer; renal cancer; cytostatic; single nucleotide polymorphism.
                                                                                Novel multidrug resistance-associated protein 1 polynucleotide uses diagnosis and treatment of cancer and multidrug resistance related diseases, and for identifying single nucleotide polymorphisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.3%; Score 14.8; DB 1; Length 21; Best Local Similarity 88.9%; Pred. No. 1.5e+02; Matches 16; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
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          Mornhinweg
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                                                                                                                                                                Claim 1; Page 82; 198pp; English
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            Hoffmeyer S,
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                                                  WPI; 2002-657475/70.
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                Brinkmann
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The invention relates to a multidrug resistance-associated protein 1 (MRP 1) polynucleotide. The polynucleotide is useful in an in vitro method for identifying a single nucleotide polynucphism and for identifying and obtaining a pro-drug or drug capable of modulating the activity of a molecular variant of MRP-1. The sequences are useful for diagnosing a disorder related to the presence of a molecular variant of MRP-1. The sequences are useful for diagnosing a disorder related to the presence of a molecular variant of MRP-1 or susceptibility to such a disorder, where the disorder is cancer (particularly renal cancer) or a disease related to multidrug cancer. Novel multidrug resistance-associated protein 1 polynucleotide useful for diagnosis and treatment of cancer and multidrug resistance related diseases, and for identifying single nucleotide polymorphisms. resistance. This sequence represents a human MRP-1 polymorphic DNA region ö for diagnosing a disorder related to the presence of a molecular variant of MRP-1 or susceptibility to such a disorder, where the disorder is cancer (particularly renal cancer) or a disease related to multidrug resistance. This sequence represents a human MRP-1 polymorphic DNA region of the activity of a molecular variant of MRP-1. The sequences are useful Gaps Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer; renal cancer; cytostatic; single nucleotide polymorphism. Gaps ; 0 . 0 Length 21; 21; 2; Indels Indels 1.3%; Score 14.8; DB 1; Length 88.9%; Pred. No. 1.5e+02; ve 0; Mismatches 2; Indels Sequence 21 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 1 Other; 1.3%; Score 14.8; DB 1; 88.9%; Pred. No. 1.5e+02; iive 0; Mismatches 2; Sequence 21 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 1 Other; ä Human MRP-1 polymorphic DNA region #232. Hoffmeyer S, Mornhinweg (EPID-) EPIDAUROS BIOTECHNOLOGIES AG. Example 2; Page 82; 198pp; English. 1074 AACCACTTAACCTCTG 1091 1074 AACCACTTAACCTCTG 1091 18 AATCACTMAACCTCTCTG 1 4 AATCACTMAACCTCTCTG 21 BP 25-JAN-2002; 2002WO-EP000796. 26-JAN-2001; 2001EP-00101651. 88.9%; ABS66967 standard; DNA; 21 (first entry) 16; Conservative 16; Conservative WPI; 2002-657475/70. Query Match Best Local Similarity Query Match Best Local Similarity WO200259142-A2. Brinkmann U, Homo sapiens 29-NOV-2002 01-AUG-2002. ABS66967; Matches Matches RESULT 17 g ઠ ð d

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                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a multidrug resistance-associated protein 1 (MRP -1) polynucleotide. The polynucleotide is useful in an in vitro method for identifying a single nucleotide polymorphism and for identifying and obtaining a pro-drug or drug capable of modulating the activity of a molecular variant of MRP-1 or for identifying and obtaining an inhibitor of the activity of a molecular variant of MRP-1. The sequences are useful for diagnosing a disorder related to the presence of a molecular variant of MRP-1 or susceptibility to such a disorder, where the disorder is cancer (particularly renal cancer) or a disease related to multidrug resistance. This sequence represents a human MRP-1 polymorphic DNA region
                                                                                                                                                                                                                                                                                                                       Novel multidrug resistance-associated protein 1 polynuclectide useful for diagnosis and treatment of cancer and multidrug resistance related diseases, and for identifying single nucleotide polymorphisms.
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                                                                                                                Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer; renal cancer; cytostatic; single nucleotide polymorphism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cancer based on CYP3A5 related oligonucleotide SEQ ID NO:296.
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                                                                                                                                                                                                                                                                               Brinkmann U, Hoffmeyer S, Mornhinweg E;
                                                                                            Human MRP-1 polymorphic DNA region #234.
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                             ABS66969 standard; DNA; 21 BP.
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                                                                       (first entry)
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Matches 16; Conservative
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The present invention describes the use of irinotecan (I) or its derivative for the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject having a ganome with a variant allele which comprises a cytochrome p450, subfamily IIIA (nifedipine cridaes), polypeptide 5 (CYPSAS) polynucleotide (II). (I) and (II) have cytostatic activity. The therapeutic applications of (I) is improved, since it is possible to individually treat a subject with an appropriate cost of cosage and/or an appropriate derivative of (I). Therefore, undesirable, harmful treatment of those subjects who do not respond to the cotentially harmful treatment of those subjects who do not respond to the treatment with substances (nonresponders), as well as the development of creatment with substances (nonresponders), as well as the development of cury resistances due to suboptimal drug dosing can be avoided. ACF62200 co ACF62751 and ABM34912 to ABM35013 represent sequences used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New use of irinotecan for preparation of compositions for treating cancer in subject having genome with variant allele comprising cytochrome p450, subfamily IIIA, polypeptide 5 polynucleotide, termed CYP3A5.
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cytochrome p450; subfamily IIIA; nifedipine oxidase; polypeptide
cytostatic; PCR primer; ss.
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Pred. No. 1.5e+02;
0; Mismatches 2; Indels
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24-MAY-2002; 2002EP-00011710.
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24-MAY-2002; 2002EP-00011710.
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WO2003013534-A2
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The present invention describes the use of irinotecan (I) or its derivative for the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant gliona in a subject having a genome with a variant cancer, or malignant gliona in a subject having a genome with a variant cancer, or malignant gliona in a subject having a genome with a variant carcarior control or control or cytostatic activity. The therapeutic applications of (I) and (II) have correctively. The therapeutic applications of (I) is improved, gince it is possible to individually treat a subject with an appropriate derivative of (I). Therefore, undesirable, harmful or toxic effects are efficiently avoided. Unnecessary and treatment with substances (nonresponders), as well as the development of the respondence of the difference of the difference of the difference of the difference of the development of the treatment with substances (nonresponders), as well as the development of the treatment with substances (nonresponders), as well as the development of the treatment with substances (nonresponders), as well as the development of the treatment with substances (nonresponders) is prepresent sequences used in the
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                                                                                                                                 New use of irinotecan for preparation of compositions for treating cancer in subject having genome with variant allele comprising cytochrome p450, subfamily IIIA, polypeptide 5 polynuclectide, termed CYP3A5.
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                 (EPID-) EPIDAUROS BIOTECHNOLOGIE AG
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24-MAY-2002; 2002EP-00011710.
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Best Local Similarity 88.9
Matches 16; Conservative
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ACF62465/
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The present invention describes the use of irinotecan (I) or its derivative for the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject having a genome with a variant cancer, or malignant glioma in a subject having a genome with a variant condase), polypeptide 5 (CTPABA) polynucleotide (II). (I) and (II) have cytostatic activity. The therapeutic applications of (I) is improved, cince it is possible to individually treat a subject with an appropriate derivative of (I). Therefore, undesirable, dasage and/or an appropriate derivative of (I). Therefore, undesirable, containally harmful treatment of those subjects who do not respond to the present with substances (nonresponders), as well as the development of the ACR62751 and ABM34912 to ABM35013 represent sequences used in the cemplification of the present invention
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subfamily IIIA, polypeptide 5 polynucleotide, termed CYP3A5.
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88.9%; Pred. No. 1.5e+02;
iive 0; Mismatches 2;
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                                      Disclosure; Page 40; 86pp; English.
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Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

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oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have cytostatic activity. The therapeutic applications of (I) is improved, since it is possible to individually treat a subject with an appropriate dosage and/or an appropriate derivative of (I). Therefore, undesirable, harmful or toxic effects are efficiently avoided. Unnecessary and potentially harmful treatment of those subjects who do not respond to the treatment with substances (nonresponders), as well as the development of drug resistances due to suboptimal drug dosing can be avoided. ACF62200 to ACF62751 and ABM34912 to ABM35013 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of irinotecan or its derivative for preparation of a pharmaceutical composition for treating cancer in a subject having a genome with a variant allele comprising a multidrug resistance protein 1 polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                irinotecan; colorectal cancer; cervical cancer; gastric cancer;
lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;
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                                                                                                                                                                                                                                                          1.3%; Score 14.8; DB 1; Length 21; 88.9%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                2; Indels
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                                                                                                                                                                                                                     Sequence 21 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                              exemplification of the present invention
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24-MAY-2002; 2002EP-00011710.
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Matches 16; Conservative
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ADB21135
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                                                                                                                                                                                                                                                                                                                                          irinotecan; colorectal cancer; cervical cancer; gastric cancer;
lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of irinotecan or its derivative for preparation of a pharmaceutical composition for treating cancer in a subject having a genome with a variant allele comprising a multidrug resistance protein 1
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              Length 21;
1.3%; Score 14.8; DB 1; Lengua. 2.
88.9%; Pred. No. 1.56+02; Lindels
                                                                                                                                                                                                                                                                                                         MRP1 based cancer related nucleic acid SEQ ID NO:294.
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                                                                                  1074 AACCACTTAACCTCTCTG 1091
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                                                                                                    4 AATCACTAAACCTCTCTG 21
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24-MAY-2002; 2002EP-00011710.
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                                                    Conservative
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Matches, 16, Conservative
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          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
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                                                  Matches
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23-JUL-2002; 2002WO-EP008217.
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                                                                  WO2003013533-A2
                                                                                                                                                                                                                                                                      polynucleotide.
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                                          Unidentified.
                                                                                                                                                                                          Heinrich G,
                                                                                       20-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                              Use of irinotecan or its derivative for preparation of a pharmaceutical composition for treating cancer in a subject having a genome with a variant allele comprising a multidrug resistance protein 1
                                                                                                              irinotecan; colorectal cancer; cervical cancer; gastric cancer;
lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
variant allele; multidrug resistance protein 1; MRPį; cytostatic; gene;
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                                                                                           MRP1 based cancer related nucleic acid SEQ ID NO:296.
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                            ADB21138 standard; DNA; 21 BP.
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24-MAY-2002; 2002EP-00011710.
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                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotide.
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                                                                                                                                                                           Unidentified
                                                                       20-NOV-2003
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                                                  ADB21138;
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       RESULT 183
ADB21138/c
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The present invention describes a method for the use of irinotecan (I) or its derivative for the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject having a genome with a variant allele which comprises a multidrug resistance protein 1 (MRP1) polynucleotide (II). (I) has cytostatic activity. (I) or its derivative can be used for the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject, where the subject is a human (preferably African or Asian) or a mouse. The present sequence represents a sequence which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of irinotecan or its derivative for preparation of a pharmaceutical composition for treating cancer in a subject having a genome with a variant allele comprising a multidrug resistance protein 1
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lung cancer; ovarian cancer; pancreatic cancer; malignant glioma; variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;
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Pred. No. 1.5e+02;
0; Mismatches 2; Indels
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24-MAY-2002; 2002EP-00011710.
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                         Use of irinotecan to treat cancer patient by determining if patient has variant alleles of UGT1A1 gene, administering increased/decreased amounts of irinotecan based on increased/decreased levels of UGT1A1 gene product.
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                                23-JUL-2001; 2001EP-00117608
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                       Kerb R;
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                                                                    24-MAY-2002;
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                                                                                             The invention relates to the novel use of irinotecan to treat a patient suffering from cancer. This involves determining if the patient has one or more variant alleles of the UGTIA1 gene, and if the patient has one or more of such variant alleles, irinotecan is administered in an increased or decreased amount in comparison to the amount that is administered without regard to the patient's alleles in the UGTIA1 gene. The invention has cytostatic activity. A composition of the invention acts as a topoisomerase I inhibitor. The method is useful for treating a patient, an animal e.g. mouse or a human, preferably African or Asian, suffering from cancer such as colorectal, cervical, gastric cancer, lung, ovarian, pancreatic cancer or malignant glioma. The present sequence is udes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the novel use of irinotecan to treat a patient suffering from cancer. This involves determining if the patient has one or more variant alleles of the UGTIAI gene, and if the patient has one or more of such variant alleles, irinotecan is administered in an increased or decreased amount in comparison to the amount that is administered without regard to the patient's alleles in the UGTIAI gene. The invention
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                   of irinotecan based on increased/decreased levels of UGT1A1 gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ss; irinotecan; cancer; UCT1A1; cytostatic; topoisomerase I inhibitor; colorectal cancer; cervical cancer; gastric cancer; lung cancer; ovarian cancer; pancreatic cancer; malignant glioma; uridine diphosphate glycosyltransferasel member A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
variant alleles of UGT1A1 gene, administering increased/decreased
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                                                                                                                                                                                                                                                                                                                                the exemplification of the invention.
                                                            Disclosure; Page 53; 107pp; English.
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24-MAY-2002; 2002EP-00011710.
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hes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of irinotecan to treat cancer patient by determining if patient has variant alleles of UGTIA1 gene, administering increased/decreased amounts of irinotecan based on increased/decreased levels of UGTIA1 gene product.
           topoisomerase I inhibitor. The method is useful for treating a patient, an animal e.g. mouse or a human, preferably African or Asian, suffering from cancer with as colorectal, cervical, gastric cancer, lung, ovarian, pare exemplication or mailgnant glioma. The present sequence is udes in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                     ss; irinotecan; cancer; UGT1A1; cytostatic; topoisomerase I inhibitor; colorectal cancer; cervical cancer; gastric cancer; lung cancer; ovarian cancer; pancreatic cancer; malignant glioma; uridine diphosphate glycosyltransferasel member A1.
                                                                                                                                                     Gaps
 cytostatic activity. A composition of the invention acts as a
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                                                                                                                                                                                                                                                                                                                                                            Human UGT1A1 variant allele sequence fragment SEQ ID NO:267.
                                                                                                                      Score 14.8; DB 1; Length 21;
Pred. No. 1.5e+02;
0; Mismatches 2; Indels
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                                                                                               Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
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24-MAY-2002; 2002EP-00011710.
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al Similarity 88.9%;
16; Conservative (
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Best Local Similarity
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Score 14.8; DB 1; Length 21; Pred. No. 1.5e+02;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New use of irinotecan for preparation of pharmaceutical compositions for treating cancer in subject having genome with variant allele comprising multidrug resistance 1 polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                       irinotecan; colorectal cancer; cervical cancer; gastric cancer; lung cancer; ovarian cancer; pancreatic cancer; malignant glioma; multidrug resistance 1; MDR1; cytostatic; human; ds; Cyp3A5; MRP1; MDR1;
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                                                                                                                                                                                                                                                                                                                                                                        Human MRP1 variant allele sequence fragment SEQ ID NO:293.
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  0; Mismatches
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                                                    1074 AACCACTTAACCTCTCTG 1091
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24-MAY-2002; 2002EP-00011710
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hes 16; Conservative
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for the preparation of pharmaceutical compositions for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or mailgrant glioma in a subject having a genome with a variant allele which comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition of the invention has cytostatic activity. The invention is useful for the preparation of pharmaceutical compositions for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject (preferably human, more preferably African or Asian) or a mouse. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                  New use of irinotecan for preparation of pharmaceutical compositions for treating cancer in subject having genome with variant allele comprising multidrug resistance 1 polynucleotide.
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88.9%; Pred. No. 1.5e+02;
ive 0; Mismatches 2; Indels
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24-MAY-2002; 2002EP-00011710.
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24-MAY-2002; 2002EP-00011710.
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                                                                                                                                                                                                                                Heinrich G, Kerb R;
                                                                                                                                                                                                                                                                          WPI; 2003-268145/26.
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Matches 16; Conserv
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WO2003013537-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating cancer in subject having genome with variant allele comprising multidrug resistance 1 polynucleotide.
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lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
multidrug resistance 1; MDR1; cytostatic; human; ds; Cyp3A5; MRP1; MDR1;
                                                                                                 irinotecan; colorectal cancer; cervical cancer; gastric cancer; lung cancer; ovarian cancer; pancreatic cancer; malignant glioma; multidrug resistance 1; MDR1; cytostatic; human; ds; Cyp3A5; MRP1; MDR1;
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                                                         Human MRP1 variant allele sequence fragment SEQ ID NO:296.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
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24-MAY-2002; 2002EP-00011710.
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                 (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                    WO2003013537-A2
                                                                                                                                                                                                              Homo sapiens.
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                 04-DEC-2003
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18

RESULT 191 ADB97209

Matches

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Gaps

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The invention relates ro a novel use of irinotecan or its derivative for the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject having a genome with a variant allele which comprises
                                                                                                                                                     The invention relates to the novel use of irinotecan or its derivative for the preparation of pharmaceutical compositions for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or maingnant glioma in a subject having a genome with a variant allele which comprises a multidrug resistence I (MDR1) polynucleotide. A composition of the invention has cytostatic activity. The invention is useful for the preparation of pharmaceutical compositions for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject (preferably human, more preferably African or Asian) or a mouse. The present sequence is used in the exemplification of the
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                                           New use of irinotecan for preparation of pharmaceutical compositions for treating cancer in subject having genome with variant allele comprising multidrug resistance 1 polynuclectide.
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
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                                                                                                                              Claim 2; Page 77; 130pp; English
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               WPI; 2003-268145/26.
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                                                                                                                                                                                                                                                                                                                                                           nvention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New use of irinotecan for preparation of pharmaceutical compositions for treating cancer in subject having genome with variant allele comprising multidrug resistance 1 polynucleotide.
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lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
multidrug resistance 1; MDR1; cytostatic; ds; human; UGT1A1; MRP1; TOP1.
a multidrug resistance 1 (MDR1) polynucleotide. A composition of the invention has cytostatic activity. The present sequence is used in the exemplification of the invention.
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                                                                                                     Length 21;
                                                                                                                                                                                                                                                                                                                                                                        Human MRP1 variant allele sequence fragment SEQ ID NO:294.
                                                                                                                                     Indels
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                                                                      Sequence 21 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 1 Other;
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Pred. No. 1.5e+02;
0; Mismatches 2;
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                                                                                                                                                                                          18 AATCACTMAACCTCTCTG 1
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24-MAY-2002; 2002EP-00011710.
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                                                                                                         Query Match 1.3%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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Gaps ; 0 18 AATCACTAAACCTCTCTG

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RESULT 195 ADB92398

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Local Similarity
Les 16; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject having a genome with a variant allele which comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition of the invention has cytostatic activity. The present sequence is used in the exemplification of the invention.
                                                                                           irinotecan; colorectal cancer; cervical cancer; gastric cancer; lung cancer; ovarian cancer; pancreatic cancer; malignant glioma; multidrug resistance 1; MDR1; cytostatic; ds; human; UGT1A1; MRP1; TOP1.
                                                                                                                                                                                                                                                                                                                                                   pharmaceutical compositions for with variant allele comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           irinotecan; colorectal cancer; cervical cancer; gastric cancer;
lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
multidrug resistance 1; MDR1; cytostatic; ds; human; UGT1A1; MRP1; TOP1.
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                                                                      Human MRP1 variant allele sequence fragment SEQ ID NO:293,
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                                                                                                                                                                                                                                                                                                                                                 New use of irinotecan for preparation of treating cancer in subject having genome multidrug resistance 1 polynucleotide.
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24-MAY-2002; 2002EP-00011710.
 ADB92398 standard; DNA; 21
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                                              (first entry)
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nes 16; Conservative
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The invention relates ro a novel use of irinotecan or its derivative for the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject having a genome with a variant allele which comprises a multidrug resistance I (MDR1) polymucleotide. A composition of the invention has cytostatic activity. The present sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotide useful for detecting single nucleotide polymorphisms in human gene.
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                                                                                                                                                                                              treating cancer in subject having genome with variant allele comprising multidrug resistance 1 polynucleotide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                Disclosure; Page 48; 104pp; English.
                                                                                               (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           exemplification of the invention.
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                                     23-JUL-2001; 2001EP-00117608.
24-MAY-2002; 2002EP-00011710.
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further relates to: an oligonucleotide containing single nucleotide polymorphisms; a PCR primer set chosen from the combination of two DNA fragments from any one of 1220 fully defined sequences as given in specification; a labelling probe containing the SNP containing oligo; and a microarray equipped with the SNP containing oligo. The isolated human gene of the invention is useful for detecting the single nucleotide polymorphisms in human gene. The isolated human gene is also useful for diagnosis of disease and determination of side effect to a medical agent. The isolated human gene is also effective in detecting single nucleotide polymorphisms in a human gene. This polymucleotide sequence represents one of the PCR primers used in the single nucleotide polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antidiabetic; Anorectic; Eating-Disorder; feeding behaviour; fat deposition; metabolic rate; lean muscle mass; body fat; Cbl; multi-adaptor protein; feeding disorder; glucose uptake disorder; metabolism disorder; diabetes; obesity; hyperlipidaemia; human; C-Cbl; siRNA; short interfering RNA; ds; RNA interference; gene silencing.
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                            1.3%; Score 14.8; DB 1; Length 21; 8.9%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                              Sequence 21 BP; 3 A; 4 C; 7 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human c-Cbl siRNA sense strand, SEQ ID 75.
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14-NOV-2003; 2003AU-00906285.
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                                                                                                                                                                                                                                                                                          899 ACCAAGAGCCTCAACATT
                                                                                                                                                                                                                                                                                                                     19 ACCAAGGGACTCAACATT
                                                                                                                                                                                                                                              88.98;
                                                                                                                                                                                                                                                                                                                                                                                                ADP46739 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                               Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                     RESULT 198
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The present invention relates to a method for identifying a compound that is capable of modulating feeding behaviour, fat deposition, metabolic rate, or the ratio of lean muscle mass to body fat in a subject. The method comprises performing an assay to measure a metabolism-associated phenotype that has been determined for a genetically modified non-human animal that comprises a genetic modification within an allele of its Cblocus, and determining the effect of the compound on the phenotype. The genetic modification reduces or prevents expression of a functional

identifying compounds capable of modulating feeding behavior, fat deposition, metabolic rate, or the ratio of lean muscle mass to body fat by detecting a proto-oncogene Cbl in disorders such as diabetes, obesity

WPI; 2004-488065/46.

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Molero

Claim 86; SEQ ID NO 75; 213pp; English

and hypolipidemia.

deposition,

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The present invention relates to a method for identifying a compound that is capable of modulating feeding behaviour, fat deposition, metabolic rate, or the ratio of lean muscle mass to body fat in a subject. The method comprises performing an assay to measure a metabolism-associated phenotype that has been determined for a genetically modified non-human animal that comprises a genetic modification within an allele of its Cbl cours, and determining the effect of the compound on the phenotype. The genetic modification reduces or prevents expression of a functional endogenous Cbl in the animal. The c-Cbl protein is a multi-adaptor protein that is involved in ligand-induced down regulation of receptor tyrosine kinases. The method of the invention is useful in the treatment of feeding disorders or disorders of glucose uptake and metabolism, such as diabetes, obesity and hyperlipidaemia. The present sequence is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying compounds capable of modulating feeding behavior, fat deposition, metabolic rate, or the ratio of lean muscle mass to body fat by detecting a proto-oncogene Cbl in disorders such as diabetes, obesity and hypolipidemia.
                 protein that is involved in ligand-induced down regulation of receptor tyrosine kinases. The method of the invention is useful in the treatment of feeding disorders or disorders of glucose uptake and metabolism, such as diabetes, obesity and hyperlipidaemia. The present sequence is the sense strand for a human c-Cb1 siRNA. The siRNA is useful in modulating a metabolism-associated phenotype in a cell, tissue or animal subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antidiabetic; Anorectic; Eating-Disorder; feeding behaviour; fat deposition; metabolic rate; lean muscle mass; body fat; Cbl; multi-adaptor protein; feeding disorder; glucose uptake disorder; metabolism disorder; diabetes; obesity; hyperlipidaemia; human; c-Cbl; siRNA; short interfering RNA; ds; RNA interference; gene silencing.
                                                                                                                                                                                                                                                 Gaps
endogenous Cbl in the animal. The c-Cbl protein is a multi-adaptor
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                                                                                                                                                                                                    1.3%; Score 14.8; DB 1; Length 21; 88.9%; Pred. No. 1.5e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                               Sequence 21 BP; 0 A; 7 C; 5 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human c-Cbl siRNA antisense strand, SEQ ID 193.
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                                                                                                                                                                                                                                                                                            33 AGGAAGCCGGAAGCAGCC 50
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14-NOV-2003; 2003AU-00906285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-DEC-2003; 2003WO-AU001676.
                                                                                                                                                                                                                                                                                                                                     18 AGGGAGCCAGAAGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP46857 standard; DNA; 21
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                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004055181-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP46857;
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RESULT 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method for detecting a cancer cell in a subject. The method comprises determining the level of expression of a GOBLIN gene in a sample of the subject where elevated expression of the gene is indicative of a primary cancer or its micrometastasis or metastasis. Also described: (1) an isolated GOBLIN nucleic acid molecule; (2) a vector comprising the isolated nucleic acid of (1); (3) a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting a cancer, e.g. breast or ovarian cancer, in a subject comprises determining the level of expression of a GOBLIN gene in a sample.
                                                                                                                                                                                                                                                                              cancer; GOBLIN; micrometastasis; metastasis; cytostatic; gene therapy; squamous cell carcinoma; hepatocellular carcinoma; melanoma; head and neck cancer; adenocarcinoma; gastrointestinal cancer; renal cell cancer; bladder cancer; prostate cancer; non-squamous carcinoma; glioblastoma; medullablastoma; ovarian cancer; mucinoma or lear cell carcinoma; elar cell carcinoma; elar cell carcinoma; endometrioid ovarian cancer; ducinoma or cancer; breast cancer; lobular lesion; stromal lesion; ductal adenocarcinoma;
antisense strand for a human c-Cbl siRNA. The siRNA is useful in modulating a metabolism-associated phenotype in a cell, tissue or animal
                                                                                                                                                                                                                                                                                                                                                                    proliferative fibrocystic change; epitheliosis; intraductal papilloma; atypical ductal hyperplasia; hyperproliferative disease; human; small interfering RNA; siRNA; ss.
                                                                                         Gaps
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/note= "3'-extension dinucleotide TT overhang"
                                                                  1.3%; Score 14.8; DB 1; Length 21; 88.9%; Pred. No. 1.5e+02;
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'note= "human GOBLIN mRNA target sequence"
                                                                                        2; Indels
                                             Sequence 21 BP; 7 A; 5 C; 7 G; 2 T; 0 U; 0 Other;
                                                                                        0; Mismatches
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                                                                                                                            2 AGGGAGCCAGAAGCAGCC 19
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                                                                                                              33 AGGAAGCCGGAAGCAGCC
                                                                                                                                                                                          ADR18488 standard; DNA; 21
                                                                                                                                                                                                                                     (first entry)
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/*tag=
not
                                                                                        16; Conservative
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/not
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                                                                         Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                               ADR18488;
                                                                  Query Match
                       subject
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monoclonal or polyclonal antibody that binds specifically to a GOBLIN polypeptide, or its immunogenic coplippe; (5) a fusion protein comprising the isolated polypeptide of (4); (6) a method of identifying a compound that reduces or antagonises carpression of a GOBLIN gene; (7) a process for identifying or determining expression of a GOBLIN gene; (7) a process for identifying or determining expression of a GOBLIN gene; (7) an isolated nucleic acid that antagonises expression of a GOBLIN gene, where the nucleic acid that antagonises expression of a GOBLIN gene, where the nucleic acid comprises a nucleotide sequence comprising any of the 21 bp sequences of SEQ ID NOS:46-353; (9) an isolated antisense nucleic acid comprises a cubleotide sequence capable of selectively hybridising to mRNA encoded by contracted nucleic acid of (1); and (10) a process for monitoring the efficacy of treatment of a cancer in a subject. GOBLIN sequences have cytostatic activity, and can be used for producing an antibody. The efficacy of treatment of a cancer in a subject. GOBLIN sequences have cytostatic activity, and can be used for producing an antibody. The mucleic acid molecule can be used for producing an antibody. The carcinoma, hepatocellular carcinoma, melanoma, head and neck cancer, carcinoma, pastocellular carcinoma, melanoma, head and neck cancer, carcinoma, pastocellular carcinoma, melanoma, head and neck cancer, carcinoma, gastrointestinal cancer, bladder cancer, prostate cancer, con-squamous carcinoma, gastrointestinal cancer, bladder cancer, prostate cancer, con-squamous carcinoma, glioblastoma, melanoma, woratian cancer, con-squamous carcinoma, clear cell carcinoma, endometrioid ovarian cancer, or mucinous ovarian cancer), or breast cancer (e.g. lobular cancer, or mucinous ovarian cancer), or breast cancer (e.g. lobular cancer, or mucinous ovarian cancer), or breast cancer (e.g. lobular cancer, or mucinous ovarian cancer), or breast cancer (e.g. lobular cancer) at special ductal hyperplasia) in a subject. The antagonist o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease, like cancer. The present sequence represents a small interfering RNA (siRNA) oligonucleotide targeted to human GOBLIN, which is used in
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/*tag= a
/note= "human GOBLIN mRNA target sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the exemplification of the present invention.
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Aatches 16; Conservative
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Synthetic.
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The present invention describes a method for detecting a cancer cell in a subject. The method comprises determining the level of expression of a combject. The method comprises determining the level of expression of a bubject. The method comprises determining the level of expression of the combject where a sindicative of a primary cancer or its micrometastasis or metastasis. Also described: (1) an isolated GOBLIN mucleic acid molecule; (2) a vector comprising the isolated GOBLIN bolypeptide, or its immungento opploagatide; (4) an isolated GOBLIN polypeptide, or its immongento opploagatide; (4) an isolated GOBLIN polypeptide, or its immongento opploagatide; (4) an isolated GOBLIN polypeptide, or its immongento opploagation of a GOBLIN gene, where the nucleic acid that antagonises and producing a compound; (8) an isolated nucleic acid that antagonises or syression of a GOBLIN gene, where the nucleic acid comprises a nucleic described antisense nucleic acid comprises a nucleotide sequence capable of selectively hybridishing to mRNA encoded by the isolated mucleic acid of (1); and (10) a process for monitoring the efficacy of treatment of a cancer in a subject. GOBLIN sequences have compound the activity, and can be used in gene therapy. An isolated GOBLIN contesting and the encoded polypeptides and molecules and molecules and the encoded polypeptides, and enthod mucleic acid molecules and the encoded polypeptides, and enthod mucleic acid molecules and the encoded polypeptides, and enthod mucleic acid molecules and the encoded polypeptides, and enthod mucleic acid molecules and the encoded polypeptides, and enthod mucleic acid molecules and the encoded polypeptides, and concertinoma, head and neck cancer. C carcinoma, hepatocellular carcinoma, melanoma, head and neck cancer, corructatic cancer), renal cell cancer (e.g. gastric, colon, or sacronoma, glioblastoma, dicar cancer, prostate cancer, or mucinous ovarian cancer, or breast cancer, prostate cancer, or mucinous ovarian cancer, or breast cancer (e.g. gastric, e.
                                                                                                                                                                                                                                                                                                                                                                             Detecting a cancer, e.g. breast or ovarian cancer, in a subject comprises determining the level of expression of a GOBLIN gene in a sample.
/*tag= b
/note= "3'-extension dinucleotide TT overhang"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 93; SEQ ID NO 268; 217pp; English.
                                                                                                                                                                                                                                                   (GARV-) GARVAN INST MEDICAL RES.
                                                                                                                                                        12-FEB-2004; 2004WO-AU000169.
                                                                                                                                                                                                    14-FEB-2003; 2003US-0447697P.
                                                                                                                                                                                                                                                                                                Harris J,
                                                                                                                                                                                                                                                                                                                                          WPI; 2004-625877/60.
                                                               WO2004072285-A1
                                                                                                              26-AUG-2004
                                                                                                                                                                                                                                                                                                Stanford P,
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Gaps ; Score 14.8; DB 1; Length 21; Pred. No. 1.5e+02; 0; Mismatches 2; Indels Sequence 21 BP; 2 A; 7 C; 6 G; 6 T; 0 U; 0 Other; 1.3%; Sest Local Similarity 88.9 Matches 16; Conservative Query Match

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RESULT 202 ABL52014

The present invention describes an isolated polymucleotide (I) having a sequence (S1) comprising soluble carrier family 18 (vesicular monoamine), comparising soluble carrier family 18 (vesicular monoamine), member 2 (SLC18A2) isogenes with regions of a sequence (SS) of 40023 bp (see ABL51954), and defined by a corresponding set of polymorphisms whose locations and identities are given in the specification; or a sequence (S2) complementary to (S1). (I) has cut infilammatory and neuroleptic activities, and can be used in gene therapy. Methods from the present invention can be used for haplotyping the SLC18A2 gene in an individual. SLC18A2 is a slow known as the vesticular monoamine transporter (WMAT2). (I) is useful in studying the expression and function of SLC18A2, and in expressing the SLC18A2 correcting for candidate drugs to treat diseases content for use in screening for candidate drugs to treat diseases contents and activity of SLC18A2 as well as on the binding affinity of candidate drugs targeting SLC18A2 as well as on the binding affinity of candidate drugs targeting SLC18A2 so the treatment of respiratory of inflammatory diseases such as neuropsychiatric disorders involving contents of prince in systems. The present sequence represents an allele specific coligonal sourcheofied (ASO) primer for human SLC18A2, which is given /\*tag= a /\*tag= "polymorphic site indicated by an ambiguity base" monoamine; Novel genetic variants of soluble carrier family 18 (vesicular monoamine), member 2 gene useful for screening drugs to treat diseases e.g. neuropsychiatric disorders involving monoaminergic brain systems. Human; solute carrier family 18 member 2; SLC18A2; vesicular monoa vesicular monioamine transporter; VMAT2; polymorphic site; SNP; single nucleotide polymorphism; antiinflammatory; neuroleptic; haplotyping; genotyping; respiratory inflammatory disease; neuropsychiatric disorder; monoaminergic brain system; primer; ss. Human SLC18A2 allele specific oligonucleotide primer SEQ ID NO:62 Sausker EA; Location/Qualifiers Claim 17; Page 15; 183pp; English. Kliem SE, (GENA-) GENAISSANCE PHARM INC. 17-SEP-2001; 2001WO-US042217. 15-SEP-2000; 2000US-0232895P ABL52014 standard; DNA; 15 Han J, WPI; 2002-393942/42. WO200222652-A2 Anastasio AE, Homo sapiens misc feature 21-MAR-2002. 11-JUL-2002 ABL52014; 

Gaps ö 1.3%; Score 14.6; DB 1; Length 15; 93.3%; Pred. No. 1.4e+02; ive 1; Mismatches 0; Indels Sequence 15 BP; 0 A; 3 C; 3 G; 8 T; 0 U; 1 Other; TIGITICIGCCTIIG 317 14; Conservative Local Similarity 303 Query Match Matches ઠે

in the present invention

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RESULT 203

Mouse; intermediate-conductance potassium channel; dermatological; antiliflammatory; keratolytic; vulnerary; antilipsoriatic; atopic eczema; contact dermatitis; vitiligo; skin; hyperkeratosis; actinic keratose; hypertrophic scar; keloids; lentigo; aged skin; ulcer; psoriasis; mIKl;

PCR; primer; ss

WO200253171-A2. Mus musculus.

11-JUL-2002.

Mouse intermediate-conductance potassium channel protein mIK1 primer 1.

ABQ78935 standard; DNA; 16 BP.

04-NOV-2002

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The invention relates to single nucleotide polymorphisms in the gene encoding the human cytotoxic T-lymphocyte-associated protein 4 or CTLA4 protein. A method for haplotyping the CTLA4 gene in an individual comprises identifying the nucleotide at one or more polymorphic sites and determining whether one of the copies of the gene is defined by one of the CTLA4 haplotypes given in the specification or whether both copies are defined by a haplotype pair. This method is useful in genotyping, whereby all possible haplotype pairs can be assigned to specific pair of the CTLA4 gene can be identified by comparing the frequency of the haplotype pair in a population exhibiting the trait with the haplotype or haplotype pair in a reference population, where a higher haplotype frequency in the trait is associated with the haplotype or haplotype pair in a reference indicates the trait is associated with the haplotype or studying the expression and function of CTLA4 and its corresponding DNA are used for studying the expression and function of CTLA4 activity, such as autoimmume disorders. The sequences are also useful for studying the effect of variation on the
                                                                                                                                                                                        Human; cytotoxic T-lymphocyte-associated protein 4; CTLA4; haplotyping; haplotype pair; single nucleotide polymorphism; autoimmune disorder; ss; genotyping; gene therapy; drug screening; antisense gene therapy; primer; immunosuppressive; sequencing; PCR; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New genetic variants of human cytotoxic T-lymphocyte-associated protein 4, CTLA4 gene for studying expression, function of the gene and expressing CTLA4 protein useful in identifying drugs to treat autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biological activity of CTLA4 as well as on the binding affinity of candidate drugs targeting CTLA4. Sequences ABK27518-ABK27549 represent allele-specific oligonucleotide probes, sequencing primers and PCR
                                                                                                                                                 Human CTLA4 gene allele-specific oligonucleotide sequencing primer #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 BP; 3 A; 3 C; 1 G; 7 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primers used to detect CTLA4 gene polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 13; 62pp; English.
                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAY-2000; 2000US-0206353P.
                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAY-2001; 2001WO-US016905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Choi JY, Messer C;
                    ABK27525 standard; DNA; 15
                                                                                                       (first entry)
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Best Local Similarity 93.34
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                              WO200190122-A2.
                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                       09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                         29-NOV-2001.
                                                              ABK27525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chew A,
ABK27525
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Use of intermediate-conductance potassium channel proteins for the diagnosis, prevention and treatment of disorders associated with disturbed keratinocyte activity, especially psoriasis.

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Goppelt A, Alzheimer C, Koegel (UYLU-) UNIV LUDWIG MAXIMILIANS.

WPI; 2002-643295/69.

(SWIT-) SWITCH BIOTECH AG

27-DEC-2001; 2001WO-EP015317. 28-DEC-2000; 2000DE-01065475. 20-MAR-2001; 2001US-0277453P. The invention relates to a novel use of intermediate-conductance

Example 3; Page 119; 121pp; German.

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potassium channel proteins. The proteins of the invention have demaclogoical, antiinflammatory, keratolytic, vulnerary, and antipooriatic activity. The method is used especially in the field of damaged skin, e.g. contact dermatitis, atopic eczema, vitiligo, hyperkratosis, actinic keratosis, hypertrophic eczem, by hyperkratosis, actinic keratosis, hypertrophic acars, kebids, lentigo, aged skin, ulcers and especially psoriasis. The sequence represents a PCR primer for the mouse potassium channel protein mIKI of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.3%; Score 14.4; DB 1; Length 16; 93.8%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16 BP; 3 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human TIE-2 substrate sequence SEQ ID NO:1797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 CTGTCGGGAACTGGCA 280
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AAA18571
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Gaps

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586 TCATGTTCACTTTAA 600

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RESULT 204 ABQ78935

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The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNY) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA1761 to AAA1762 represent ribozyme sequences for ARNY, and AAA1761 to AAA1762 and AAA1763 and AAA1763 to AAA19154 represent their recresponding target sequences; corresponding target sequences; cand AAA19155 to AAA1922 represent their corresponding target sequences; cand AAA19155 to AAA1961 and AAA1960 to AAA1963 and AAA1962 represent their corresponding target sequences; cand AAA19159 to AAA2168 to AAA21680 to AAA21680 to AAA21680 represent their corresponding target sequences; cand integrin alpha 6 subunit, and AAA2332 to AAA2333 to AAA21680 to AAA21680 represent their corresponding target sequences; cand integrin subunit beta 3, and AAA23476 to AAA23343 to condition are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNY, are concerning angiofenic retinopathy, age related macular degeneration (ARND), inflammation, and arthritis, as well as macular degeneration (ARND), inflammation, and arthritis, as well as madiate and other syndrome of tuberous sclerosis, pot-wine stains, Sturge Weber conditions, inflammation, beta 3 and diseases related to the levels of ARND; inflammation, and arthritis, as well as and other syndromes and diseases related to the levels of ARNI, Tie-2, and other syndromes and diseases related to the levels of ARNI, Tie-2, and other syndromes and diseases related to the levels of ARNI, Tie-2, integrin subunit, all and the levels of ARNI, Tie-2, and other syndromes and disease related to the levels of ARNI, Tie-2, the arrive and other syndromes and disease related to the levels of ARNI, Tie-2, and other syndromes and disease related to the levels of ARNI, Tie-2, the arrive and oth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors.
age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verruca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      integrin subunit alpha-6, or integrin subunit beta-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 9 A; 1 C; 3 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 56; Page 103; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         Jarvis T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1023 ATCATAGAGAAGTAAA 1038
                                                                                                                                                                                                                                                                               99WO-US006507
                                                                                                                                                                                                                                                                                                                             98US-0079678P
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nes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-591315/50.
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                                                                                                                                     sapiens.
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Matches
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                                                                                                                                     Homo
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Coeshott C, Mcswiggen JA;

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The present invention describes a human genome-derived myosin-like correction 1 (hGDMLP-1). The protein and polynuclectide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 corrected acids can be used as probes to detect, characterise and quantify mucleic acids can be used as probes to detect, characterise and quantify correction variants having desired phenotyptic improvements, and for protein variants having desired phenotyptic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP cused as immunogens to raise antibodies that specifically recognise hGDMLP cused and/or amount specifically of hGDMLP-1 proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polyunclectide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart come and selectal muscle disorders. hGDMLP-1 is localised to chromosome 22. The sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B. The sequence has a contracted in the internal part of the printed the present when the part of the printed the part of the part of the printed the part of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence
    hGDMLP-1; heart;
Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; hear muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shannon ME;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 2566; 214pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         758
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2001WO-US000669.
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-179446/23.
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                                                                                                                                              WO200192524-A2.
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                                                                                                      Homo sapiens.
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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and/or amount specifically of HGDMLP proteins, as specific blomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the HGDMLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                                                               Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shannon ME;
                                                                                                                                Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2565.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 2565; 214pp; English
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                   ABN02573 standard; DNA; 17 BP.
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2001WO-US000663.
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2001US-0266860P.
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2001WO-US000667
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                                                                                            (first entry)
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                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                   06-DEC-2001
                                                       ABN02573;
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at ftp.wipo.int/pub/published\_pct\_sequence

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The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, cumour angiogenesis, diabetic retinopathy, macular degeneration, neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca culgaris, angiofibroma of tumberous sclerosis, port-when stains, Sturge Weber syndrome, Oslar-Weber-rendu syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (I) to the patient in conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or cell, by contacting the cell with (I). (I) is useful for cleaving RNA of ERG gene, by contacting (I) is useful for cleaving and cation such as Mg2+. (I) is useful for diagnosis of conditions and
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                                                                                              Gaps
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                                                   DB 1; Length 17;
                                                                                              Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ERG Amberzyme target sequence Seq ID No 2054.
Sequence 17 BP; 3 A; 5 C; 7 G; 2 T; 0 U; 0 Other;
                                              1.3%; Score 14.4; DB 1;
13.8%; Pred. No. 1.6e+02;
ve 0; Mismatches 1
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                                                                                                                                            758
                                                                                                                                                                                                                                                                                                          ABK19407 standard; RNA; 17 BP.
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                                                                      93.8%;
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                                                                                                                                          743 AGGCAGCTGCCACCTT
                                                                                                                                                                                                                                                                                                                                                                                                    09-APR-2002 (first entry)
                                                                                                                                                                                   17 Accederacion
                                                                        Best Local Similarity 93.8
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-082995/11.
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                                                                                                                                                                                                                                                                                                                                                        ABK19407;
                                                   Query Match
                                                                                                                                                                                                                                                            RESULT 208
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The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, tumour anglogenesis, diabetic retinopathy, macular degeneration, neovascular glaucoma, myopic degeneration, arthritis, psoriasis, vertuca vulgaris, anglofibroma of tuberous sclerosis, port-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more therapies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression of Ets-related gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Baving's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous selevosis; port.wine stain; wound healing; sturge Weber syndrome; Kippel-Trenaunay Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;
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useful for treating cancer, diabetic retinopathy, macular degeneration,
arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes ABK17354-ABK2719 represent nucleic acids, including antisense and enzymatic nucleic acid molecules which regulate expression of ERG, and
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                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ERG hammerhead ribozyme target sequence, Seq ID No 324.
                                                                                                                                                                                                           1.3%; Score 14.4; DB 1; Length 17;
8.8%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                    Sequence 17 BP; 4 A; 3 C; 5 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                               related PCR primers of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ABK17677 standard; RNA; 17 BP.
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                                                                                                                                                                                                                                                                                               959 TGGACCCAGGACATTT 974
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                                                                                                                                                                                                                                   68.88;
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Best Local Similarity 68...
The 11; Conservative
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           unual communications surrected by administering (I) to the patient in angiogenesis is treated by administering (I) to the patient in conjunction with one or more of other therapies such as radiation or chemotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting the cell with RNA, in the presence of a divalent cation such as Mg2+. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes ABK1354-ABK2219 represent nucleic acids, including antisense and enzymatic nucleic acid molecules which regulate expression of ERG, and related PCR primers of the invention
                                                                                                                                                                                                                                                                                                    Gaps
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Leukaemia or tumour
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                                                                                                                                                                                                                                                                 Query Match
1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 12; Conservative 3; Mismatches 1; Indels
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                                                                                                                                                                                                                                     Sequence 17 BP; 5 A; 4 C; 4 G; 0 T; 4 U; 0 Other;
 conditions suitable for the treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUN-2001; 2001US-00877478.
08-JUN-2001; 2001US-0296876P.
24-OCT-2001; 2001US-0335059P.
05-DEC-2001; 2001US-0337055P.
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BLATT L.
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MACEJAK D.
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DRAPER K.
ROBERTS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis B virus.
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08-JUN-2001;
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Draper K,
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(BLAT/)
(MACE/)
(MCSW/)
(MORR/)
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(ROBE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 210
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The present invention relates to nucleic acid molecules which modulate the synchesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes, and erlaws, zinzymes, amberzymes, and G-cleaver ribozymes. DNAzymes, compounds, and aptamers that bind to HBV reverse transcriptuse primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV DNA. The nucleic acids may be used to modulate the expression of HBV C genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and isease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents a substrate for one of the HBV is cibozyme, d-cleaver, zinzyme, DNAzyme or amberzyme sequences
                Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolated nucleic acid, useful for treating viral diseases associated a tumors and cell degeneration, also related polypeptides, antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine; tumour suppression; tumour reversion; apoptosis; virus resistance; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine oligonucleotide associated with tumour supression, SEQ ID 4476.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.3%; Score 14.4; DB 1; Length 17; 37.5%; Pred. No. 1.6e+02; tive 9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 17 BP; 4 A; 2 C; 2 G; 0 T; 9 U; 0 Other;
                                                                                                 Example 1; Page 154; 387pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disclosed in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR ENGINES LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-SEP-2002; 2002WO-IB004210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-SEP-2001; 2001FR-00011979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 UUUAAUGCCUUUAUAU 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACC67229 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       569 TTTAATACCTTTATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 37.5
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and transfected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amson R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-333167/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      schizophrenia; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003025176-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Telerman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-2003
                                                         infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACC67229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Disclosure; Page 554; 738pp; French.

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Gaps

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                  The present invention relates to murine oligonucleotides (ACC62754-
ACC68806), which are associated with tumour suppression, tumour
reversion, apoptosis and virus resistance. The oligonucleotides are
useful as (1) as probes and primers for detecting, identifying,
quantifying and/or amplifying nucleic acid, e.g. as one component of a
gene chip; in vitro as (anti) sense reagents; and (2) for production of
recombinant polypeptides. The oligonucleotides are useful for preparation
of pharmaceuticals for prevention and/or treatment of viral diseases that
are characterised by development of tumours or cell degeneration,
specifically cancer but also Alzheimer's disease and schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic, antiviral, neuroprotective, nootropic, neuroleptic, ss;
primer, probe, tumour suppression, tumour reversion, apoptosis,
virus resistance, transgenic animals, Alzheimer's disease, schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to the isolation of 6327 nuclectide sequences, fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides, or the complement, or corresponding RNA, of the nucleotides. The nucleotides are used as probes or primers for detecting, identifying, quantifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour suppression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies (Ab) against the polypeptide are useful for prevention and/or treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                  Query Match 1.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 1.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour suppression/reversion associated nucleotide #6208.
                                                                                                                                                                                                                                                            Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 757; 771pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hb.
                                                                                                                                                                                                                                                                                                                                                                                            534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-SEP-2002; 2002WO-IB004219.
                                                                                                                                                                                                                                                                                                                                                                                                                                  2 Arccardrecacarde 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful e.g. for treatment o
polypeptide and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB45885 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                          519 ATACATGTGCACATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Telerman A, Amson R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-441574/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003040369-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB45885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB45885/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 212
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Polynucleotides differentially regulated in response to cholesterol and adipogenesis are useful to detect and treat associated conditions such as obesity, athersclerosis, diabetes mellitus and coronary artery heart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes a composition comprising at least one expression vector comprising a polynucleotide of the invention. The composition has anorectic, antiarteriosclerotic, cardiant and antidiabetic properties. The invention is used to detect and tract conditions associated with elevated cholesterol and lipid or during adipogenesis, particularly obesity, athersclerosis, diabetes mellitus or coronary artery heart disease. This sequence represents a polynucleotide differentially
of viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia). Analysis of the expression of the nucleotides can be used for diagnosis and/or prognosis of these diseases. The nucleotides and polypeptides can also be used to screen for their specific interactive molecules, potentially useful for treating diseases associated with abnormal expression of the nucleotides.
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression vector; anorectic; antiarteriosclerotic; cardiant; antidiabetic; elevated cholesterol; elevated lipid; adipogenesis; obsisty; atherselatosis; diabetes mellitus; coronary artery heart disease; cholesterol homeostasis; ss; differntial expression.
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                                                                                                                                                                                                         Query Match 1.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 1.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cholesterol homeostasis/adipogenesis related DNA seq id 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed during cholesterol homeostasis and adipogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17 BP; 5 A; 3 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                         Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; SEQ ID NO 47; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE30660 standard; DNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LYNX-) LYNX THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                         854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JAN-2003; 2003US-00339793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JAN-2002; 2002US-0347286P
                                                                                                                                                                                                                                                                                                                                              16 AAGGCCTGGGTGGATC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                         839 AAGGCCGGGGTGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-830986/77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bowen B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003180764-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE30660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease.
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 213
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This invention relates to novel isolated nucleic acid sequences involved in the phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses. The invention may be useful for the development of compounds with a cytostatic, virucide, neuroprotective, development of compounds with a cytostatic, virucide, neuroprotective, nootropic or neuroleptic activity. The DNA sequences may be useful as noted and primers for detecting, indentifying, quantifying and/or camplifying nucleic acid, for example as one component of a gene chip, in virto as antisense reagents and for production of recombinant plantenticals for prevention may therefore be useful for preparation of plypeptides. The invention and/or treatment of viral diseases that characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. The present sequence data for this patent did not form part of the printed Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                cytostatic; virucide; neuroprotective; noctropic; neuroleptic; probe; primer; PCR; gene chip; antisense; viral disease; tumour; cancer; Alzheimer's disease; schizophrenia; ds; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated mucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                            Human tumour suppression/reversion-related DNA sequence SeqID2567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.3%; Score 14.4; DB 1; Length 17; 33.8%; Pred. No. 1.6e+02; ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                    tumour suppression; tumour reversion; apoptosis; virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/publishedpct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 2567; 30pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       839 AAGGCCGGGGTGGATC 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR ENGINES LAB.
                                                                                                                            ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-SEP-2001; 2001FR-00011980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-2002; 2002WO-IB004523
981 GATCCAAAGGAGTTGT 996
                                1 GATCCAAAGCAGTTGT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGGCCTGGGTGGATC
                                                                                                                            ADIS0064 standard; DNA; 17
                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and transfected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Telerman A, Amson R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-313354/30.
                                                                                                                                                                                                                                                                                                                                                                                                       WO2003025177-A2
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                   15-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-2003
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Best Local
                                                                                                                                                                   ADI50064;
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ID ACC5
                                                                                                                 ADI50064,
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Gaps

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1.3%; Score 14.4; DB 1; Length 17; 93.8%; Pred. No. 1.6e+02; ive 0; Mismatches 1; Indels

93.8%;

Query Match Best Local Similarity

15; Conservative

Matches

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Fri Aug 19

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15-JAN-2003; 2003US-00342902
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                                                                                                                                                                                                                                                                                                                                                The
                                                                                                                                                                                                                                                                          nucleic acid sequences associated with tumor suppression, regression,
                                                                                                                                                                                                                                                                                                                                   This sequence represents an isolated nucleic acid sequence associated with tumour suppression or regression, apoptosis or virus resistance. invention relates to these sequences oc sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                     apoptosis or virus resistance are useful to diagnose and treat viral disease, development of tumor cells and cell degeneration.
                                                                   88; tumour suppressor; antitumour; cytostatic; tumour suppression; tumour regression; apoptosis; virus resistance; diagnosis; cellular degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis B virus, HBV; ss; enzymatic nucleic acid, RNA cleavage, hepatitis B virus infection, hepatitis, hepatocallular carcinoma, cirrhosis, liver failure; lamivudine; interferon, genetic drift, virucide; hepatotropic; antiinflammatory; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 1.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 5 A; 3 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis B virus (HBV) RNA target sequence #948.
                                                 Human tumour suppressor sequence #2498
                                                                                                                                                                                                                                   Amson R;
                                                                                                                                                                                                               SA.
                                                                                                                                                                                                                                                                                                                 Claim 1; Page 617; 798pp; French
                                                                                                                                                                                                               (MOLE-) MOLECULAR ENGINES LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                       20-JUN-2001; 2001FR-00008139.
                                                                                                                                                                                           20-JUN-2001; 2001FR-00008139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 ACATTCTGATGAGATC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADM58814 standard; RNA; 17
                             27-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                969 ACATTTTGATGAGATC
                                                                                                                                                                                                                                   Telerman A,
                                                                                                                                                                                                                                                       WPI; 2003-250498/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2004054156-A1
                                                                                                                               FR2826373-A1.
                                                                                                             Homo sapiens
                                                                                                                                                   27-DEC-2002.
                                                                                                                                                                                                                                  Tuijnder M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAR-2004.
          ACC53731;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 216
                                                                                                                                                                                                                                                                           New
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The invention relates to an enzymatic nucleic acid molecule that specifically cleaves RNA derived from hepatitis B virus (HBV) and comprising one or more binding arms, without requiring the presence of a 2.-OH group within the molecule for activity. The nucleic acids are useful for treating hepatitis B virus infection, hepatitis, either alone or in combination with other therapies such as lamivudine and interferons. The nucleic acids are useful as diagnostic tools to examine genetic drift and wutations within diseased cells, for detecting the presence of HBV RNA in a cell, for the study of RNA and for down-regulating gene expression of target genes in bacterial, fungal, viral, plant or mammalian cells. This sequence represents an HBV RNA target sequence, used in the scope of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel enzymatic nucleic acid molecule such as DNAzymes and inozymes specifically cleaving RNA derived from hepatitis B virus and comprising one or more binding arms, useful for treating hepatitis and cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; ss; probe; myosin-like protein-l; hGDWLP-l;
hGDWLP-l agonist hGDWLP antagonist; hGDWLP inhibitor; heart disorder;
skeletal muscle function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.3%; Score 14.4; DB 1; Length 17; ilarity 37.5%; Pred. No. 1.6e+02; Conservative 9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 4 A; 2 C; 2 G; 0 T; 9 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                            Blatt L, Mcswiggen JA, Morrissey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 948; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human GDMLP-1 probe SEQ ID NO:2565.
14-MAY-1992; 92US-00882712.
07-FEB-1994; 94US-00193627.
08-NOV-1999; 99US-00436430.
20-MAR-2000; 2000US-00531025.
09-AUG-2000; 2000US-00636385.
24-OCT-2000; 2000US-00636387.
08-JUN-2001; 2001US-0069747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 uvuaaugccuuvauau 16
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ID ACN65663 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             569 TITAATACCTITATAT
                                                                                                                                                                                                                                                                                              BLATT L.
MCSWIGGEN J A.
MORRISSEY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-247781/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                      DRAPER K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2004137589-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                Draper K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACN65663;
                                                                                                                                                                                                                                                                                           (BLAT/) (MCSW/) N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                   (DRAP/)
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Matches
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Homo sapiens.
                                                                                                27-SEP-2000;
                                                                                                                     30-JAN-2001;
                                                                                                                               30-JAN-2001;
                                       15-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               function.
                                                                                                                                                                                                                                                                                                         (CHEN/)
                                                                                                                                                                                                                                                                  (JIYY/)
(PENN/)
                                                                                                                                                                                                                                                        (GUYY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 219
                                                                                                                                                                                                                                                                                        (HANZ/
                                                                                                                                                                                                                                                                                                (RANK/
                                                                                                                                                                                                                                                                                                                                       Gu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA85722,
SXXX
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                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel polypeptide (I) comprising a sequence (S1) of myosin-like protein-1 (hGDMLD-1) having 2568 amino acids fully defined in the specification, a fragment of at least 8 amino acids of (S1), 95% deviation from (S1) which are conservative substitutions, and 65% identity to (S1). A polypeptide of the invention acts as a agonist or antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A pharmaceutical composition of the invention is useful for treating or preventing a disorder associated with decreased expression or activity of hGDMLP-1, such as a disorder of heart and/or skeletal muscle function. The present sequence represents a 17-mer nucleotide, used in the invention for scanning the sequence represented in ACN63102
                                                                                                                                                                                                                                                                                                 Novel myosin-like protein-1, useful for treating or preventing disorder associated with decreased expression or activity of human genome-derived myosin-like protein-1 such as disorder of heart and/or skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; ss; probe; myosin-like protein-1; hGDMLP-1;
hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
skeletal muscle function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                           Shannon ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.3%; Score 14.4; DB 1; Length 17; 93.8%; Pred. No. 1.66+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 BP; 3 A; 5 C; 7 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                              Hanzel DK, Rank D,
                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 2565; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human GDMLP-1 probe SEQ ID NO:2566.
                               04-0CT-2000; 2000GB-0024265.
30-JAN-2001; 2001W0-US000661.
30-JAN-2001; 2001W0-US000662.
30-JAN-2001; 2001W0-US000663.
30-JAN-2001; 2001W0-US000664.
30-JAN-2001; 2001W0-US000666.
30-JAN-2001; 2001W0-US000666.
30-JAN-2001; 2001W0-US000666.
30-JAN-2001; 2001W0-US000669.
30-JAN-2001; 2001W0-US000669.
30-JAN-2001; 2001W0-US000669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACN65664 standard; DNA; 17 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-DEC-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 743 AGGCAGCTGCCACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 93.8
nes 15; Conservative
                                                                                                                                                                                                                                                              Ji Y, Penn SG,
                                                                                                                                                                                                                                           SHANNON M E.
                                                                                                                                                                                                                                                                                   WPI; 2004-533378/51.
                                                                                                                                                                                                 PENN S G.
HANZEL D K.
                                                                                                                                                                                                                       RANK D.
CHEN W.
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Best Local Si
Matches 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACN65664;
                                                                                                                                                                                                                                                                                                                                       function
                                                                                                                                                                                 GUYY/)
                                                                                                                                                                                                                         (RANK/)
                                                                                                                                                                                                                                  (CHEN/)
                                                                                                                                                                                                                                           (SHAN/)
                                                                                                                                                                                                            (HANZ/)
                                                                                                                                                                                                    (PENN/)
                                                                                                                                                                                                                                                                Gu Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel myosin-like protein-1, useful for treating or preventing disorder associated with decreased expression or activity of human genome-derived myosin-like protein-1 such as disorder of heart and/or skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 2566; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001W0-US000664.
30-JAN-2001; 2001W0-US000666.
30-JAN-2001; 2001W0-US000666.
30-JAN-2001; 2001W0-US000666.
30-JAN-2001; 2001W0-US000669.
30-JAN-2001; 2001W0-US000669.
30-JAN-2001; 2001W0-US000669.
30-JAN-2001; 2001W0-US000670.
05-PEB-2001; 2001WS-OZ66860P.
25-MAY-2001; 2001US-0266860P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                  2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
                                                                                                                                                                                                                                                                                                                           2001WO-US000662
2001WO-US000663
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                                                                                                            26-NOV-2003; 2003US-00723361
                                                                                                                                                                                                                                                                                                 2001WO-US000661
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les 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PENN S G.
HANZEL D K.
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CHEN W.
US2004137589-A1
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21-JUN-2000; 2000WO-US016951.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnerary; proliferative disease; skin disease; psoriasis; diabetic retinopathy; cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP; matrix metalloproteinase; growth factor; reductase; scarring; cytostatic; antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide; antisickling; ophthalmological; keratolytic; gene therapy; viral wart; atopic dermatitis; actinic keratosis; squamous cell carcinoma; basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar; sickle cell retinopathy; ss.
                                                                                                                                                                                                                                                                                                                The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment
                                          Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
                                                                                                                                                                                                                                               New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19 BP; 4 A; 9 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyclin B1 ribozyme binding site SEQ ID NO:3308.
                                                                                                                                                                                                     Robbins JM;
                      Cyclin B1 ribozyme binding site #51.
                                                                                                                                                                                                                                                                                              Disclosure; Page 96; 109pp; English.
                                                                                                                                                                                                      Barber JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                   99WO-US028772
                                                                                                                                                         98US-0110954P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 GGCTTGGAGAGGCAG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH60884 standard; DNA; 19
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         791 GTGCTTGGAGAGGCAG
                                                                                                                                                                                                     Welch PJ,
                                                                                                                                                                                                                           WPI; 2000-412314/35.
                                                                                                                                                                                (IMMI-) IMMISOF INC
                                                                                                                                                                                                                                                                        PCNA and Cyclin B1.
                                                                                        WO200032765-A2.
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                                                                                                                                   06-DEC-1999;
                                                                                                                                                         04-DEC-1998;
04-DEC-2000
                                                                                                              08-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                     Tritz R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH60884;
                                                                  Mammalia.
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The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme (I) which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (WMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid molecule (II) comprising a promoter antipacitatic, anticlaborrheic, antidabetic, antidiabetic, antidia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; high bone mass; HBM gene; Zmaxl gene; chromosome 11; 11q13.3; sequence tagged site; STS; osteoporosis; osteopathic; gene therapy; antisense therapy; vaccine; bone disorder; Paget's disease; adapter; sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zmax1 gene region physical map preparation STS marker #522.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19 BP; 4 A; 9 C; 2 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 312; 408pp; English.
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                                                                                                      26-OCT-2000; 2000WO-US029500
                                                                                                                                                                                                            99US-0161532P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-2002 (first entry)
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                   (IMMU-) IMMUSOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-300427/31.
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03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                               Robbins JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-OCT-2001
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Disclosure; Page 42; 409pp; English.

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                                                                                                                                                                                                                                                   The present invention describes the human Zmaxl gene and the high bone mass (HBM) gene, which are found on chromosome 11q13.3. The Zmaxl and HBM genes have osteopathic activities. The genes can be used in gene therapy, antisense therapy and in the production of vaccines. They can be used in the diagnosis and treatment of bone disorders including osteoporosis, paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.

ABA82038 to ABA82700 and AAG68168 to AAG66193 represent sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying molecules involved in lipid regulation, useful for diagnosing, treating or preventing e.g., arteriosclerosis, comprises identifying a molecule that binds to high bone mass gene or its corresponding wild type gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                     proteins useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                     New high bone mass (HBM) and Zmaxl genes and proteins useful modulating bone mass for the treatment of e.g. osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                         1.3%; Score 14.4; DB 1; Length 19; 93.8%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 19 BP; 2 A; 1 C; 7 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recker RR, Johnson ML;
                                                                                                      Recker RR, Johnson ML
                                                                                                                                                                                                                                                                                                                                                                           the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Zmax1 cDNA reverse PCR primer #261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENO-) GENOME THERAPEUTICS CORP.
(UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
                                                                                                                                                                                                                          Disclosure; Page 37; 443pp; English.
                                                                      (GENO-) GENOME THERAPEUTICS CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 TGGAATTGTTGTTTCT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAY-2000; 2000US-00578900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TGGAATTGTTGTGTCT 16
                   05-APR-2000; 2000US-00543771.
05-APR-2000; 2000US-00544398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK23360 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 93.8
les 15; Conservative
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                                                                                                        Little RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-097784/13.
                                                                                                                                      WPI; 2001-657171/75.
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                                                                                                         Carulli JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK23360;
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Matches
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The invention relates to a method for identifying a molecule involved in lipid regulation comprising identifying a molecule that binds to or inhibits binding of a molecule to high bone mass (HMM) or its wild type gene, Zmax1. Compounds identified by the method are useful for treating, gene, preventing or screening for normal and abnormal lipid associated conditions, including arteriosclerosis, cardiovascular creatment or prevention of diabetic atherosclerosis, neurovascular treatment or prevention of diabetic atherosclerosis, neurovascular conditions caused by plaque build-up, poor circulation due to plaque conditions caused by plaque build-up, poor circulation due to plaque build-up and associated poor wound healing. The methods may be used in build-up and succeed as surrogate markers in pharmaceutical development, and diagnostic assays for bone development, in diagnosis of human or animal bone disease, and in the concling human Zmax1 and HBM, and PCR primers, probes, linkers and advantage of the invantion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation; gene therapy; bone density modulation; bone strength; trabecular number; bone size; bone tissue connectivity; bone disease; osteoporosis; PCR; osteomalacia; rickets; Paget's disease; neoplasm of the bone; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New transgenic animals (e.g. mice), useful as models for studying bone density modulation, developing drugs for treating or preventing bone diseases (e.g. osteoporosis), or diagnosing diseases characterized by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          March 1.3%; Score 14.4; DB 1; Length 19; Local Similarity 93.8%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19 BP; 2 A; 1 C; 7 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bodine PV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human HBM STS marker reverse primer #261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 58; 603pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENO-) GENOME THERAPEUTICS CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAY-2001; 2001US-0290071P.
17-MAY-2001; 2001US-0291311P.
01-FEB-2002; 2002US-0353058P.
04-MAR-2002; 2002US-0361293P.
                                                                                                                                                                                                                                                                                                                                                                               and adapters of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 TGGAATTGTTGTTTCT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACC45943 standard; DNA; 19 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reduced bone density
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-129278/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200292764-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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The invention relates to novel transgenic animals expressing the high bone mass (HBW) gene, expressing the corresponding wild type HBW gene, comprising an alteration of the gene encoding LRP6 or LRP6, or expressing an LRP5 that is modulated by an altered gene control sequence introduced on LRP5 that is modulated by an altered gene control sequence introduced by homologous or non-homologous recombination. The transgenic animals are for the study of bone density modulation or bone mass modulation. The invention may have a use in gene therapy. The transgenic animals and nucleic acids are for the study of bone density modulation, where the bone mass is modulated relative to non-transgenic animals of the same concerning an more than one parameter selected from bone density, bone strength, trabecular number, bone size, or bone tissue connectivity. The transgenic animals, nucleic acids and mechods are useful for identifying compositions, which may be employed for treating or preventing bone diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or neoplasms of the bone. The transgenic animals and nucleic acids are also needla in methods for diagnasing diseases involved in bone development, or characterised by reduced bone density or mass. The present sequence is used in the exemplification of the invention
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Sequence 19 BP; 2 A; 1 C; 7 G; 9 T; 0 U; 0 Other;

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Gaps
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1.3%; Score 14.4; DB 1; Length 19; 93.8%; Pred. No. 1.7e+02; ive 0; Mismatches 1; Indels
                                                           295 TGGAATTGTTGTTTCT 310
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                                                                             TGGAATTGTTGTGTCT
               Best Local Similarity 93.8
Matches 15; Conservative
   Query Match
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ADB98641 standard; DNA; 19 BP. ADB98641; RESULT 224 

(first entry) 04-DEC-2003 Sequence tagged site #522 used to prepare Zmax1 (LRP5) gene region map. Osteopathic, Gene therapy; High Bone Mass; HBM; LRP5; Zmax1; LRP6, bone mass modulation; osteoporosis; STS; sequence tagged site; ds.

Ното варіелв.

WO200292000-A2

21-NOV-2002

13-MAY-2002; 2002WO-US014877.

11-MAY-2001; 2001US-0290071P. 17-MAY-2001; 2001US-029111P. 01-FEB-2002; 2002US-0353058P. 04-MAR-2002; 2002US-0351293P.

(GENO-) GENOME THERAPEUTICS CORP. (AMHP ) WYETH.

New nucleic acid comprising a mutation in LRP5 or LRP6, useful for diagnosing a HBM-like phenotype in a subject and for preparing a composition for modulating bone mass and/or lipid levels in a subject suffering from e.g. osteoporosis. WPI; 2003-129214/12.

Yaworsky PJ, Liu W;

Morales A,

Graham JR,

Anisowicz A,

Allen K,

Example 2; Page 65; 629pp; English

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The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and LRP6 mutants, which results in a HBM-like phenotype when expressed in a cell. The HBM-like phenotype results in home mass modulation and/or lipid level modulation. The invention is useful for diagnosing a HBM-like phenotype in a subject and for preparing a composition for modulating home mass and/or lipid levels in a subject suffering from e.g. osteoporosis. The present sequence is a Sequence Tagged Site (STS) marker, which was used to prepare a physical map of the Zmax1 (LRP5) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated amino acid protein sequence selected from an amino acid sequence appearing as ADRI6922 or an amino acid sequence appearing set ADRI6922 or an amino acid sequence expearing set ADRI6922 or an amino acide ADRI6922 is encoded by the HBM (high bone mass) allele of the human Zmax1 gene and has sequence similarity to LDL receptors. Also disclosed are nucleic acids, proteins, cloning vectors, expression vectors, transformed hosts, methods of developing pharmaceutical compositions, methods of identifying molecules involved in bone development, and methods of idagnosing and treating diseases involved in bone mass (HBM) allele on chromosome 11q13.3 encoding ADRI6922. The protein is useful for treating, diagnosing, preventing, or screening for normal and abnormal conditions of bone, including metabolic bone diseases, e.g. osteoporosis. The present sequence is a PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, high bone mass; Zmax1; ss; primer; HBM; osteoporosis; osteopathic; LDL receptor; bone development; metabolic bone disease; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New high bone mass gene of chromosome 1.1Q13.3, encoding protein useful for treating, diagnosing, preventing, or screening for normal and abnormal conditions of bone, including metabolic bone diseases, e.g.
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human chromosome 11 Zmax1 region reverse mapping primer #261.
                                                                                                                                                                                                                                       1.3%; Score 14.4; DB 1; Length 19; 93.8%; Pred. No. 1.7e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                    Sequence 19 BP; 2 A; 1 C; 7 G; 9 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 588; 284pp; English.
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98US-0105511P.
99US-00229319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
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                                                                                                                                                                                                                                                                                                                                                 TGGAATTGTTGTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-623529/60.
                                                                                                                                                                                                                                                             Best Local Similarity
Matches 15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JAN-1998;
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                                                                                                                                                                                                                                         Query Match
                                                                                                                                                               region.
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The invention relates to an isolated nucleic acid sequence encoding a high bone mass protein (HBM). The gene exists in two alleles, Zmax1, the netional wild-type (the cDNA for which appears as ADR47570 encoding ADR47571) and the HBM allele (the cDNA for which appears as ADR47571 encoding ADR47572) and the HBM allele differ by a single nucleotide of chording ADR47573. The two alleles differ by a single nucleotide of chording vector comprising HBM/Zmax1 (and a replicon operative in an expression vector comprising HBM/Zmax1 operably linked to a transcription regulatory region, an isolated host cell), an expression vector comprising HBM/Zmax1 operably linked to a transcription regulatory region, an isolated host cell action to bone modulation, a method of identifying a molecule involved in bone modulation, a method of identifying a molecule involved in bone modulation, a method of testing for them activity, a method of developing a pharmaceutical for the treatment of bone development disorders, a method of altering bone development in an animal, a method of altering bone development in a host, a dispnostic screening for a genetic predisposition to a bone development disorders, a method of an experience a method of expressing the HBM protein in bone tissue, a bacterial arriticial chromosome comprising HBM/Zmax1 sequence (appearing as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid sequence encoding high bone mass, useful in diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      development disorder; osteoporosis; chromosome 11; gene therapy;
                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                             Human chromosome 11 Zmax1 region reverse mapping primer #261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ss; PCR; high bone mass; Zmax1; HBM; bone modulation;
                                                                             Length 19;
                                                                                                                  Indels
                                                                         Query Match 1.3%; Score 14.4; DB 1; I
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1;
                                      Sequence 19 BP; 2 A; 1 C; 7 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnson ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 588; 303pp; English.
used in the mapping of the Zmax1/HBM gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating and/or preventing osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recker RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JAN-1998; 98US-0071449P.
23-OCT-1998; 98US-0105511P.
13-JAN-1999; 99US-00229319.
05-APR-2000; 2000US-00544398.
                                                                                                                                                         295 TGGAATTGTTGTTTCT 310
                                                                                                                                                                                                                                                                                             ADR48157 standard; DNA; 19 BP
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                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNIV CREIGHTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                      ADR48157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYCR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer.
                                                                                                                                                                                                                                                          RESULT 226
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ADR47574-ADR47580), a method for amplifying a nucleotide polymorphism in the Zmax1 or HBM gene, a method for identifying a regulatory element of a HBM gene and an isolated nucleic acid segment of at least 15 contiguous nucleotides including a polymorphic site from HBM/Zmax1. The nucleic acid molecule and the encoded polypeptide, composition, and methods are useful in diagnosing, treating and preventing a bone development disorder, i.e. osteoporosis. The gene for HBM/Zmax1 is located on chromosome 11q13.i.e. The present sequence is a primer used in the mapping of the HBM/Zmax1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                  Score 14.4; DB 1; Length 19;
Pred. No. 1.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer used to amplify an ORF of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                     Sequence 19 BP; 2 A; 1 C; 7 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 14.4; DB 1;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 1516; Disclosure; 1912pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                        BP.
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                                                                                                                                                                                                                                                                                                                                                                                         AAX92502 standard; DNA; 20
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                                                                                                                                                                                                                                                                         TGGAATTGTTGTTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydophila pneumoniae.
                                                                                                                                                                                                                    Best Local Similarity 93.8
Matches 15, Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEST ) GENSET
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04-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                         295
                                                                                                                                                                                                                                                                                                                                                                                                                          AAX92502;
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                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                          RESULT 227
                                                                                                                                           gene.
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RESULT 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR primers AAA96393-94 were used to amplify polymorphic microsatellite repeat (PMR) sequences from the human costimulatory receptor gene locus (hCGRL). The primers are used in the method of the invention. The specification describes a method for determining the predisposition of a human subject to develop autoimmune disease. The method comprises detecting a PMR sequence in the CD28, ICOS gene or CTLA4 gene of the human costimulatory receptor gene locus (HCGRL). PMR sequences vary in length among individuals and can be amplified to generate products that differ in size. These products can then be detected by rapid and convenient high resolution processes. The method is useful for determining the predisposition of insulin-dependent diabetes mellitus (IDDM), Addison's disease, Graves disease, autoimmune hypothyroidism, rheumatoid arthritis, Hashimoto's disease, coeliac disease and leprosy. PMR sequences within hCRGL are useful as markers in a variety of assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and in the field of forensic medicine, disease diagnosis and human genome
                                                                                                                                                                                                                                                                                                                        ICOS gene, CTLA4 gene, costimulatory receptor gene locus; CGRL; lupus; insulin-dependent diabetes mellitus; IDDM, Addison's disease; leprosy; Graves disease; autoimmune hypothyroidism; myasthenia gravis; thymoma; thyroiditis; postpartum thyroiditis; rheumatoid arthritis;
                                                                                                                                                                                                                                                             Primer used to amplify a sara25/26 polymorphic microsatellite repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determining predisposition of humans to develop autoimmune disease involves detecting polymorphic microsatellite repeat sequence within human costimulatory receptor gene locus.
                                                                                                                                                                                                                                                                                                     Autoimmune disease; polymorphic microsatellite repeat; PMR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14.4; DB 1; Length 20;
Pred. No. 1.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Hashimoto's disease; coeliac disease; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 9 A; 3 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 18; Page 151; 160pp; English.
                                                                                                                                        AAA96394 standard; DNA; 20 BP.
287 ITCACTACTGGAATTG 302
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                       19 TTCACTACGGGAATTG 4
                                                                                                                                                                                                                       08-FEB-2001 (first entry)
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ling V, Wu P, Gray GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-628257/60.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                  AAA96394;
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                                                                                                  RESULT 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical agents acting on a disease as well as other treatment. N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel biallelic markers used to construct a high density disequilibrium
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                                                                                                                                                                                       Human biallelic marker upstream amplification primer SEQ ID NO:6795.
                                                                                                                                                                                                                                               Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; gentotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chumakov I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Page 1679; 2745pp; English.
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AAZ72439 standard; DNA; 20 BP.
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98US-0109732P.
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                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      map of the human genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                   diagnosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-1999;
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23-NOV-1998;
                                                                                                                         10-SEP-2001
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                                                           AAZ72439;
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721 AAATATATTAACGCAG 736

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Secondary lymphod chemokines (SLC's), variants, fragments, and the polynucleotides encoding the chemokines, variants and fragments, anti-SLC polynucleotides encoding the chemokines, variants and fragments, anti-SLC antibodies or ligands for the CCR7 receptor can be used to modulate can denditatic cell function in a mammal which results in a decreased primary immune response. SLC can be used to treat cancer or hyperproliferative cimmune response. SLC can be used to pigmented skin lesions. SLC is also useful for treating solid tumours such as melanoma, breast cancer, tumours of the head and neck, cancers or metastases of ovary, endometrium, urinary tract, stomach, testicle, prosetate, lung, bladder, pancreas, bone, liver, colon or rectum, or metastases of unknown primary origin. SLC can also be used to suppress angiogenesis particularly angiogenesis involved in recruitment of leukocytes into sites of inflammation and immune responses, particularly, the chemotaxis of dendritic and other cells. SLC is also useful in preventing graft rejection, prevention and treatment of the autoimmune diseases and for enhancing an immune response. Two primers chemokine CCR2
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                                                            Secondary lymphoid chemokine; SLC; cancer; hyperproliferative disorders; prostatic hyperplasia; proliferative breast disease; proliferative retinopathy; melanoma; breast cancer; cancer; metastases; suppression; angiogenesis; tumourigenesis; inflammation; immune response; chemotaxis; graft rejection; autoimmune disease; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating cancer or hyperproliferative disorder and modulating dendritic cell function in a mammal involves administering secondary lymphoid
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                                                                                                                                                                                                                                                                                                                                                                                          Kothakota S, Williams LT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PTP1B antisense oligonucleotide ISIS 142070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 1 A; 4 C; 7 G; 8 T; 0 U; 0 Other;
                                 Primer for amplifying CCR2 chemokine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 28; 53pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                              Keting C, Xin H, Chan VWF,
                                                                                                                                                                                                                                                                                        99WO-US031096
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                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-465631/40.
                                                                                                                                                                                                                                                                                                                                                              (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                  WO200038706-A2.
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                                                                                                                                                                                                                                                                                          28-DEC-1999;
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20-OCT-2000
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                                                                                                                                                                                  Synthetic
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The invention relates to a compound of 8-50 nucleobases in length targeted to a nucleic acid encoding protein phosphatase 18 (PTP1B), where targeted to a nucleic acid encoding protein phosphatase 18 (PTP1B), where the compound specifically hybridises with and inhibiting the expression of PTP1B in cells are (1) and nucleobase portion of an active site on a nucleic acid encoding or PTP1B; (2) inhibiting the expression of PTP1B in cells or tissues with the compound; treating an animal experising contacting the cells or tissues with the compound; treating an animal newprising administering the compound; (4) decreasing blood sugar levels in an animal comprising administering the compound; (5) preventing or delaying the onset of a disease or condition associated breventing or delaying the onset of an increase in blood glucose levels in an animal comprising administering the compound; (6) preventing or delaying the onset of an increase in blood glucose levels in an animal comprising administering the compound; not compound is used to inhibit the expression of PTP1B in cells or tissues, to treat or condition associated with prevent or delay the onset of a disease or condition associated with prevent or delay the onset of a disease or condition, and for animal having or suppected of having the disease or condition, and for decreasing blood sugar levels or preventing or delaying the onset of an inmal animal. The compound is also used in diagnostics, therapeutics, prophlaxis, and in research reagents and kits. The present sequence is an antisense compound of the invention kits. The present enables and animal. The compound is also used in diagnostics, therapeutics, prophlaxis, and in research reagents and treasenting human PTP1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PTP1B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compound for inhibiting the expression of protein phosphatase 1B (PTP: and for treating diabetes, cancer, or obesity, comprises an antisense oligonucleotide targeted to nucleic acid encoding PTP1B.
Antisense; protein phosphatase 1B; PTP1B; ss; probe; human;
type 2 diabetes; obesity; ovarian cancer; chronic myeloid leukaemia;
hyperproliferative disease; antidiabetic; anorectic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mckay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Butler MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monia BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Freier SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 27; 133pp; English.
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                                                                                                                                                                                                                                                                     18-JAN-2000; 2000US-00487368.
31-JUL-2000; 2000US-00629644.
                                                                     olood glucose; gene therapy
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                                                                                                                                                                                                                                                                                                                                                     WYATT J.
FREIER S M.
MONIA B P.
BUTLER M M.
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                                                                                                                                                                                                                                                                                                                                  COWSERT L M.
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                                                                                                                                                 US2002055479-A1
                                                                                                               Homo sapiens.
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(MCKA/)
                                                                                                                                                                                                                                                                                                                                     (COMS/)
                                                                                                                                                                                                                                                                                                                                                        (WYAT/)
(FREI/)
                                                                                                                                                                                                                                                                                                                                                                                                  (/INOM
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BP.

ACC86742 standard; DNA; 20

RESULT 232

ACC86742 ID ACC8

Length 20;

Query Match

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involving angiogenesis
                                                                 (ISIS-) ISIS PHARM INC
                                                                         WPI; 2003-301004/29.
                                                  WO2003022227-A2
                                Key
modified_base
                         sapiens
     04-AUG-2003
                                                                      Bennett CF,
                                                      20-MAR-2003
                           Synthetic.
  ACC86742;
                          Homo
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ADB68675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "This oligonucleotide has a phosphorothioate backbone and 2'-O-methoxyethyl (2'-MOB) wings at the 5' and 3' ends, which are 5 nucleotides in length. Also all cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapeutics, prophylaxis, e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits, and in distinguishing between functions of various members of a biological pathway. The present sequence represents a human VEGFR-2 chimeric phosphorochioate antisense oligonucleotide, which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense oligonucleotide targeted to a nucleic acid encoding vascular endothelial growth factor receptor-1, useful for diagnosing or treating cancer, rheumatoid arthritis, or diseases or conditions
                                                                                                                                                                                                                                                  Vascular endothelial growth factor receptor 1, VEGF receptor; VEGFR, inhibitor; cytostatic; antirheumatic; antiarthritic; antiangiogenic; antialfammatory; antisense gene therapy; hyperproliferative disorder; cancer; rheumatoid arthritis; angiogenesis; infection; inflammation; tumour formation; phosphorothioate; 2'-O-methoxyethyl; 2'-MOE; ss.
                                                                                                                     Human VEGFR-1 chimeric phosphorothioate oligonucleotide SEQ ID NO:37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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(first entry)
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Seguence 20 BP; 5 A; 4 C; 4 G; 7 T; 0 U; 0 Other;

ö The present invention describes compounds (I) comprising 8-50 nucleobases in length targeted to a nucleic acid molecule encoding a microsomal triglyceride transfer protein, where the compounds specifically hybridise with and inhibit the expression of the microsomal triglyceride transfer protein. Also described: (I) a compound 8-50 nucleobases in length which appecifically hybridises with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding microsomal triglyceride transfer protein; (2) a composition comprising (I) and a carrier or Microsomal triglyceride transfer protein antisense oligonucleotide #91. hybridisation; microsomal triglyceride transfer protein inhibitor; cardiant; antiarteriosclerotic; antilipaemic; antisense gene therapy; abnormal lipid metabolism; abnormal cholesterol metabolism; atherosclerosis; cardiovascular disease; mouse; phosphorothioate; ss; New antisense oligonucleotide compounds, useful for diagnosing, preventing and/or treating conditions with aberrant activity of the microsomal triglyceride transfer protein, such as atherosclerosis and Gaps triglyceride transfer protein; antisense oligonucleotide; /note= "phosphorothioate linkages, and all cytidine residues are 5-methylcytidines" ö Indels 1.3%; Score 14.4; DB 1; 13.8%; Pred. No. 1.7e+02; ve 0; Mismatches 1; /mod\_base= OTHER /note= "2'-0-methoxyethyls" 'note = "2'-0-methoxyethyls" Location/Qualifiers mod base= OTHER Claim 3; Page 97; 135pp; English. OTHER BP. 641 13 17-JUL-2002; 2002WO-US022799 30-JUL-2001; 2001US-00917963 93.8%; ADB68675 standard; DNA; 20 /\*tag= c /mod base= (first entry) GTTTTATTCTCAGCAA GTTTTATGCTCAGCAA Д \*tag≔ a Conservative 16. .20 (ISIS-) ISIS PHARM INC. Graham MJ; WPI; 2003-300705/29. Local Similarity -O-methoxyethyl WO2003018600-A2 modified\_base heart disease modified base modified\_base Synthetic. Mus musculus. 04-DEC-2003 06-MAR-2003 15; microsomal Crooke RM, 979 4 ADB68675; Best Loc Matches RESULT 233 

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diluent; (3) inhibiting the expression of microsomal triglyceride

transfer protein in cells or tissues, comprising contacting the cells or

tissues with (1) so that expression of microsomal triglyceride transfer

protein is inhibited; and (4) treating an animal having a disease or

condition associated with microsomal triglyceride transfer protein,

condition associated with microsomal triglyceride transfer protein,

condition associated transfer protein is inhibited. (1) have cardiant,

antisense gene therapy. The methods and compositions of the present

antisense gene therapy. The methods and compositions of the present

conditions associated with aberrant expression or activity of

diseases or conditions associated with aberrant expression or activity of

microsomal triglyceride transfer protein, such as an abnormal lipid or

cholesterol metabolism condition like atherosolarosis and cardiovascular

disease. The present sequence represents a mouse microsomal triglyceride

transfer protein chimeric phosphorothioate antisense oligonucleotide,

which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to producing a cloned cell containing a stably silenced target gene. The method involves introducing a nucleic acid molecule expressing a chimeric repressor fusion protein into a parent cell. The repressor fusion protein comprises a first amino acid sequence comprising a Kruppel-Associated Box (KRAB) domain or its variant that binds to the protein KAPI and has DNA-dependent repressor activity fused to a second amino acid targeting sequence that binds to the target gene, fused to a switch component, that, in the presence of a ligand or inducer, permits the second amino acid sequence to bind to the target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Producing a cloned cell containing a stably silenced target gene, useful in research and drug screening, comprises introducing a nucleic acid molecule expressing a chimeric repressor fusion protein into a parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRAB; repressor fusion protein; Kruppel-associated box; KAP1; Coll1a2; cloned cell production; drug screening; luciferase; RT-PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                1.3%; Score 14.4; DB 1;
Local Similarity 93.8%; Pred. No. 1.7e+02;
hes 15; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collla2 cDNA amplifying RT-PCR primer COL-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 TCTTATGCTGGGATGT
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/mod_base= OTHER
/mod_base= OTHER= 2' methoxyethyl nucleotides. All cytidine
nucleobases are 5' methylcytidine."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleotides. All cytidine
gene, where the fusion protein is under the control of regulatory sequences capplel of directing its expression in the parent cell. The sequences capplel of directing its expression in the particularly useful in research and drug screening, e.g. identifying a test molecule that activates the expression of a stably silenced target gene, or manipulating expression of target gene in a cell. Sequences ACF36598-99 represent primers used in a RT-PCR assay for detecting levels of Colla2mRNA in NIH373 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding PTP1B, useful for treating a disease/condition associated with PTP1B, such as cancer, diabetes or obesity.
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mckay R;
                                                                                                                                                                                                                                                                                                                                                                                                                                      human; ss; antisense; PTP1B; protein phosphatase 1B; PTPN1; phosphorothioate backbone; hyperproliferative condition; cancer; cytostatic; antidiabetic; anorectic; type 2 diabetes; obesity.
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                                                                                                                                                                  1.3%; Score 14.4; DB 1; Length 20; 93.8%; Pred. No. 1.7e+02; rative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "OTHER= phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                               Antisense DNA oligo to target human PTP1B DNA SeqID 297.
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nucleobases are 5' methylcytidine."
                                                                                                                                        Sequence 20 BP; 3 A; 3 C; 7 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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/note= "OTHER= 2'
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31-JUL-2000; 2000US-00629644.
14-MAY-2001; 2001US-00854883.
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                                                                                                                                                                                                                                                                                                                                 ADI14044 standard; DNA; 20
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                                                                                                                                                                                                                                                18 AGCAAGACTTCATAAG
                                                                                                                                                                                                                                 600 AGAAAGACTTCATAAG
                                                                                                                                                                        Query Match
Best Local Similarity 93.8
Matches 15; Conservative
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Freier SM;
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                                                                                                                                                                                                                                                                                                                                                               ADI14044;
                                                                                                                                                                                                                                                                                                        RESULT 235
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                                                            This invention relates to novel compositions and methods for modulating the expression of PTPIB (also known as protein phosphatase 1B and PTPNI). Specifically, it refers to antisense compounds that can target and hybridise with a nucleic acid molecule encoding PTPIB, as well as splice variants thereof and inhibit expression accordingly. PTPIB is a tyrosine phosphatase that plays an essential regulatory role in signalling mediated by the insulin receptor and as such is useful for treating diseases such as type 2 diabetes and obesity. Furthermore, FTPIB can suppress transformation of oncogenic genes, such that compositions of this invention can also be used to treat hyperproliferative conditions including cancer. Accordingly, these compounds can be described as having cytostatic, antisberse DNA oligo that targets human PTPIB DNA, and which has a phosphorothicate backbone and 2'-0-methoxyethyl wings, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense oligonucleotide for modulating endothelial lipase expression, for diagnosing, preventing or treating e.g. dyslipidemia, low high density lipoprotein or cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy; Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL; cardiovascular disorder; metabolic syndrome X; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mod_base= OTHER
/note= "This oligonucleotide has a phosphorothicate
backbone ad 2- methyoxyethyl (2'-MOE) wings at the 5'
and 3' ends, which are 4 nucleotides in length. Also all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human endothelial lipase antisense oligonucleotide, SEQ ID 3422.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.3%; Score 14.4; DB 1; Length 20; 93.8%; Pred. No. 1.7e+02; trive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytidine residues are 5-methylcytidines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                           exemplification of the invention.
                    NO 297; 143pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343 GGCTGTGATCAAATGG 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ25024 standard; DNA; 20 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                  Claim
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IID ADJ2

XXX ADJ2

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BDB Humm

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XXX ADJ2

BDB BDD SPT

BDB BDD SPT

BDB BDD SPT

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BDB BDD SPT

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BDB BDD SPT

XXX ADJ2

XXX ADJ
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Corn; plant; transformable; introgression; chromosomal locus; bin 6.02-6.04; bin 10.04-10.06; bin 1.03-1.06; bin 1.08-1.11; bin 3.05-3.07; corn seed; plant breeding; transgenic plant; chromosome 6; SSR marker; marker assisted breeding; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of producing a transformable corn line by introgressing at least one chromosomal locus mapping to bin 6.02-6.04 or bin 10.04-10.06, where the locus is introgressed from a more transformable corn line into a less transformable corn line. The invention also relates to corn variety 178-187-20 seed (ATCC accession co. PTM-5183) and corn variety 178-187-25 seed (ATCC accession no. PTM-5182); progeny of a plant grown from the seed cited above, where the progeny comprises loci mapping to chromosomal bins 1.03-1.06, 1.08-1.11, 2.05-3.07, and 6.02-6.04; a transgenic corn plant produced by transforming the progeny cited above; and hybrid corn seed and plants produced by crossing a corn line with the progeny cited above. Because
                                                                     The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25511), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are used for diagnostics, prophylaxis, or as research reagents or kits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing a transformable corn line comprises introgressing at least c
chromosomal locus mapping to bin 6.02-6.04 or 10.04-10.06, where the
locus is introgressed from a more transformable corn line into a less
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.3%; Score 14.4; DB 1; Length 20; 93.8%; Pred. No. 1.7e+02; rative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 2 A; 6 C; 11 G; 1 T; 0 U; 0 Other;
Claim 3; SEQ ID NO 3422; 1007pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; SEQ ID NO 23; 77pp; English.
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ADN61693 standard; DNA; 20
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Best Local Similarity 93.8
Matches 15; Conservative
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more transformable lines are typically agronomically poor, while lines with superior or desired agronomic traits tend to be less transformable, the methods of the invention provide a means of testing for the effects of an introduced gene on traits such as yield, kernel quality and plant phenotype in earlier plant generations in a breeding programme. Sequences ADN61671-ADN61702 represent PCR primers used in an example of the invention to amplify corn SSR markers useful in marker assisted breeding.
                                                                                                                                                                                                                                                                                                                                                 Human, antisense; ss; Huntingtin interacting protein 1; HIP1; cellular apoptosis; Huntington's disease; chromosome 7q11.23.
                                                                                                                     Score 14.4; DB 1; Length 20;
Pred. No. 1.7e+02;
0; Mismatches 1; Indels
                                                                                               Sequence 20 BP; 8 A; 5 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                            Human HIP1 antisense target sequence ISIS168127.
                                                                                                                                                                                                                                                         BP.
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                                                                                                                                                                      775 CCTTTTGCTTGGGGAT 790
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                                                                                                                                                                                               19 CCTTTTGCTAGGGGAT 4
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                                                                                                                           Query Match
Best Local Similarity 93.8
Matches 15; Conservative
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New compound that modulates huntingtin interacting protein 1 expression, useful in treating an animal having a disease or condition involving dysregulation of cellular apoptosis.

WPI; 2004-374983/35.

Dobie KW;

Example 15; SEQ ID NO 120; 85pp; English.

The invention relates to a compound targeted to a nucleic acid molecule encoding huntingtin interacting protein 1, HIP1. The compound, 8-80 nucleobases in length, is an antisense oligonucleotide, where the compound specifically hybridises with the nucleic acid molecule encoding huntingtin interacting protein 1 comprising a sequence appearing as ADNO1766 and inhibits the expression of huntingtin interacting protein 1. Also included are inhibiting the expression of huntingtin interacting protein 1 in cells or tissues, screening for a modulator of huntingtin interacting protein 1, a diagnostic method for identifying a disease state, a kit or assay device comprising the compound and treating an animal having a disease or condition associated with huntingtin interacting protein 1 compound so that expression of huntingtin interacting protein 1 is inhibited. The compound and the methods are useful in treating an animal having a disease or condition involving dysregulation of cellular apoptosis e.g. Huntington's disease. The HIPI gene is located on chromosome 7q11.21. The present sequence is an antisense target region from the HIPI cDNA.

Sequence 20 BP; 3 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

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The invention relates to a compound targeted to a nucleic acid molecule encoding huntingtin interacting protein 1, HIP1. The compound, 8-80 nucleobases in length, is an antisense oligonucleotide, where the nucleobases in length, is an antisense oligonucleotide, where the huntingth specifically hybridises with the nucleic acid molecule encoding huntingtin interacting protein 1 comprising a sequence appearing as ADN01766 and inhibits the expression of huntingtin interacting protein 1 has included are inhibiting the expression of huntingtin interacting protein 1 a diagnostic method for identifying a disease interacting protein 1, a diagnostic method for identifying a disease attac, a kit or assay device comprising the compound and treating an animal having a disease or condition associated with huntingtin interacting protein 1 is inhibited. The compound and the methods are interacting protein 1 is inhibited. The compound and the methods are
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                              Gaps
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 Length
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/note= "2'-methoxyethyl residues"
16. .20
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1.3%; Score 14.4; DB 1;
93.8%; Pred. No. 1.7e+02;
cive 0; Mismatches 1;
                                                                                                                                                                                                                                                              Human HIP1 antisense oligonucleotide ISIS251612.
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                                                                                           GCTGCAGCAGGCCTCT
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      Query Match 1.3
Best Local Similarity 93.8
Matches 15; Conservative
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/*tag=
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useful in treating an animal having a disease or condition involving dysregulation of cellular apoptosis e.g. Huntington's disease. The HIP1 gene is located on chromosome 7q11.23. The present sequence is an antisense oligonuclectide of the invention.
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                                                                                                                                                                                                                                                                                      1.3%; Score 14.4; DB 1; Length 20; 93.8%; Pred. No. 1.7e+02; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                          Sequence 20 BP; 3 A; 8 C; 7 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note = "2'-methoxyethyl residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human HIP1 antisense oligonucleotide ISIS251611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 15; SEQ ID NO 44; 85pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |. .20
|*tag= b
|mod_base= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                           828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002US-00293864.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADN01806 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l. .5
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       813 CTGAAGCAGGCCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGCAGCAGGCCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag= c
                                                                                                                                                                                                                                                                                                                            Local Similarity 93.8
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-374983/35.
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                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 240
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Matches
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The invention relates to a compound targeted to a nucleic acid molecule encoding huntingtin interacting protein 1, HIP1. The compound, 8-80 nucleobases in length, is an antisense oligomucleotide, where the compound specifically hybridises with the nucleic acid molecule encoding huntingtin interacting protein 1 comprising a sequence appearing as ADN01766 and inhibitis the expression of huntingtin interacting protein 1.

Also included are inhibiting the expression of huntingtin interacting protein 1, a diagnostic method for identifying a disease interacting protein 1, a diagnostic method for identifying a disease of animal having a disease or condition associated with huntingtin interacting protein 1 compound so that expression of huntingtin interacting protein 1 is inhibited. The compound and treating an animal having a disease or condition involving dysrequiation of cellular apoptosis e.g. Huntington's disease. The HIP1 gene is located on chromosome 7q11.23. The present sequence is an
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                                                                                                                                                     interacting protein 1 compound so that expression of huntingtin interacting protein 1 is inhibited. The compound and the methods are useful in treating an animal having a disease or condition involving dysregulation of cellular apoptosis e.g. Huntington's disease. The HIPI gene is located on chromosome 7q11.23. The present sequence is an antisense oligonucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
protein 1 in cells or tissues, screening for a modulator of huntingti
interacting protein 1, a diagnostic method for identifying a disease
state, a kit or assay device comprising the compound and treating an
animal having a disease or condition associated with huntingtin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.3%; Score 14.4; DB 1; Length 20; 93.8%; Pred. No. 1.7e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 3 A; 5 C; 9 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human HIP1 antisense target sequence ISIS168128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 15; SEQ ID NO 121; 85pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTGCAGCAGGCCTCT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         812 GCTGAAGCAGGCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 93.8
nes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Gaps ö

Length 20; Indels

SXS

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The present invention relates to a compound which specifically hybridizes with a nucleic acid molecule encoding GFAT, and inhibits the expression of GFAT. Specifically claimed are antisense oligonuclectides capable of modulating the expression of GFAT, and which comprise any of the 3063 sequences of 20 base pairs, given in the specification. The compound, composition and methods are useful for treating a disease or condition associated with GFAT, such as a disease or condition. They are also useful in research and disgnostics for modulating the expression of GFAT. The present sequence represents a chimeric expression of GFAT. The present sequence represents a chimeric phosphorochioate oligonucleotide with 2'-MOE wings and a deoxy gap, these oligonucleotides inhibit human GFAT expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase (GFAT), for treating diabetes, a cardiovascular or neurologic disorder, ischemia/reperfusion injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
Sequence 20 BP; 5 A; 2 C; 6 G; 7 T; 0 U; 0 Other;
                                       1.3%; Score 14.4; DB 1;
ilarity 93.8%; Pred. No. 1.7e+02;
Conservative 0; Mismatches 1:
                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric phosphorothioate oligonucleotide #2537.
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/note= "2-methoxyethyl wing"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
/mod_base= other
                                                                                                                                  269
                                                                                                                                                                                                                                                                                BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GFAT; Antidiabetic; Cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-OCT-2003; 2003WO-US03332.
                                                                                                                                                        ADP78738 standard; DNA; 20
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                                                                                                                                  554 TAATATGCTGGGTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PHAA ) PHARMACIA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag=
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                                                                     Local Similarity
nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reperfusion; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004035763-A2
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modified base
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                                                                                                                                                                                                                                                                                                                                                                12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                         ADP78738;
                                                    Query Match
                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a compound which specifically hybridizes with a nucleic acid molecule encoding GFAT, and inhibits the expression of GFAT. Specifically claimed are antisense oligonucleotides capable of modulating the expression of GFAT, and which comprise any of the 3063 sequences of 20 base pairs, given in the specification. The compound, composition and methods are useful for treating a disease or condition associated with GFAT, such as a disease or condition, e.g. diabetes, a cardiovascular or neurological disorder, ischemia/reperfusion injury. They are also useful in research and diagnostics for modulating the expression of GFAT. The present sequence represents a chimeric phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these oligonucleotides inhibit human GFAT expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase (GFAI), for treating diabetes, a cardiovascular or neurologic disorder, ischemia/reperfusion injury.
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFAT; Antidiabetic; Cardiant;
Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
                                                                                                                                           ö
                                                                                             Query Match
1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                        Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric phosphorothioate oligonucleotide #2670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "2-methoxyethyl wing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'not\overline{e}= "2-methoxyethyl wing"
               antisense target region from the HIP1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; SEQ ID NO 2670; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= b
/mod_base= other
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                                                                                                                                                                                                                                                                                                                                    ADP78871 standard; DNA; 20 BP.
                                                                                                                                                                                      813 CTGAAGCAGGCCTCTC 828
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                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PHAA ) PHARMACIA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-348453/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reperfusion; ss
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Key modified\_base

Synthetic.

12-AUG-2004

ADP78871;

RESULT 242 ADP7887

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modified\_base

29-APR-2004

Broschat KO,

Sequence 20 BP; 4 A; 3 C; 4 G; 9 T; 0 U; 0 Other;

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The present invention relates to a Single Condition Amplification/
Internal Primer (SCAIP) sequencing method for direct sequence analysis of
Internal Primer (SCAIP) sequencing method for direct sequence analysis of
In multi-exon genes from genemic DNA samples and identifying mutations
in multi-exon genes e.g. the dystrophin gene, CAPN3 gene and DYSF gene.
Mutations in the dystrophin gene result in both Duchenne Muscular
CAPN3 gene, encoding calpain (calcium-activated neutral protease) result
in limb-girdle muscular dystrophy type 2A (LGMDZA) and mutations in the
DYSF gene, encoding dysferlin, result in limb-girdle muscular dystrophy
CC type 2B (LGMDZB). The method comprises bringing into contact in each of
the reaction chambers an amplicon from a different one of the
amplification reactions and one or more internal sequencing primers
corresponding to the amplicon and analysing the sequences of the
corresponding to the amplicon and analysing the sequences of the
analysis of any large multi-exon gene. It is also useful for the
indentification and analysis of specific individual genemic mutations
indentification and analysis of specific individual genemic mutations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          including deletions, point mutations, or its combinations, gene complexes with multiple exons/introns spanning large genomic regions. The present sequence is a PCR primer, used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                              Human; SCAIP; CAPN3; DYSF; calpain; calcium-activated neutral protease; limb-girdle muscular dystrophy type 2A; LGMD2A; dysferlin; limb-girdle muscular dystrophy type 2B; LGMD2B; PCR; primer; 8B; Single Condition Amplification/ Internal Primer.
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Characterizing a nucleic acid region, useful for detecting genetic mutations in any large multi-exon gene e.g., those indicating dystrophinopathy, comprises using a Single Condition
                                                              ö
                   1.3%; Score 14.4; DB 1; Length 20; 93.8%; Pred. No. 1.7e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.3%; Score 14.4; DB 1; Length 20; 93.8%; Pred. No. 1.7e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amplification/Internal Primer (SCAIP) seguencing method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Von Niederhausern A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 9; Page 45; 174pp; English.
                                                                                                                                                                                                                                                                                                                                                                          CAPN3/DYSF PCR primer, SEQ ID 471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Flanigan KM, Weiss RB, Dunn DM,
                                                                                                      268
                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-DEC-2002; 2002US-0433774P.
                                                                                                                                           5 TTAATAAGCTGGGTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-2003; 2003WO-US040278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UTAH ) UNIV UTAH RES FOUND
                                                                                                                                                                                                                                                  ADQ14074 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                      553 TTAATATGCTGGGTTT
                                                              Conservative
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-525893/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                 07-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-2004
                                                                                                                                                                                                                                                                                        ADQ14074;
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                                                                                                                                                                                                         RESULT 244
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This invention relates to a protein that exhibits calcium ion channel transmissive activity and is activated by pregnenolone sulphate.

Specifically, it refers to a novel screening method for identifying a cubstance that is useful as a memory improving agent, a learning ability improving agent and/ or an antidementia agent. The present invention describes this acreening tool as one that involves contacting a test substance with cells expressing the calcium permeable nonselective cation channel and analysing the channel activity to select only those cubstances, for example pregnenolone sulphate, which can activate the channel. As such, it provides a means to develop pharmaceutical compositions comprising these substances that can be used to treat dementia, as well as improving memory and learning functions.

Accordingly, they act as calcium channel agonists and exhibit nootropic and neuroprotective activities. This oligonucleotide sequence is a PCR primer given in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide with calcium ion channel transmissive activity, activated by pregnenolone sulfate, useful for screening memory improving agent, learning ability improving agent and/or anti-dementia agent.
                                                                                                                                                                                                                                                                                         murine; mouse; transient receptor potential melastatin; TRPM; primer; 88; pregnenolone sulphate; memory; learning ability; antidementia; calcium permeable nonselective cation channel; dementia; nootropic;
                                                                                                                                                                                                                                                        PCR primer used to amplify murine TRPM calcium ion channel DNA Seq 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.3%; Score 14.4; DB 1; Length 20;
93.8%; Pred. No. 1.7e+02;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 9; SEQ ID NO 13; 114pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sano Y, Inamura K, Mochizuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (YAMA ) YAMANOUCHI PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT30234 standard; DNA; 19 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            714
  464
                                                                                                                                   ADQ91206 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JAN-2003; 2003JP-00009884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L6-JAN-2004; 2004WO-JP000333.
                                    1 AGCTGGGAGCAGTTGT 16
                                                                                                                                                                                                                 21-OCT-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            699 ATGTAGTCACGGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 Argaagrcacegreer
449 AGCTGGGAGCAGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.3
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                        neuroprotective; PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-571687/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004065598-A1
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                                                                                                                                                                          ADQ91206;
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                                                                                                RESULT 245
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ID AAT3
                                                                                                                    ADQ91206
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Gaps

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15; Conservative

Best Local Similarity Matches 15; Conserva

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                                                                                                                                                                                                                                                                                                                                                                                                                              characteristics of which change when the probe is hybridised to the target sequence, can be used to detect target mucleic acid in a convenient single step method. The new probes allow homogeneous assays to be performed without the need to seperate unhybridised probe. If the probe is added before PCR amplification of target DNA, the PCR time profile can be monitored by measuring the flourescent intensity of the reaction mixture. The flourochrome is preferably thiazole orange or oxazole yellow. The method avoids the problem of nonspecific intercalation associated with the use of free flourchromes
                                                                                                                                                                                                                                                                                                                                                    Oligo:nucleotide probes with intercalating fluoro:chrome label - only fluoresces when bound to target sequences, removes need to separate unhybridised probes.
                                                                              Probe; intercalating agent; flourochrome; hybridisation; assay;
detection; thiazole orange; oxazole yellow; flourescent; flourescence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                malignant transformation; diagnostic; therapeutic; ner; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                         Target nucleic acid for probe with attached intercalating agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.3%; Score 14.2; DB 1; Length 19; 84.2%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human breast cancer gene CH13-2a12-1 primer pch14-sp6-3fb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                        Sugiura Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19 BP; 0 A; 11 C; 0 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                        Yawata H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                          Inoue
                                                                                                                                                                                                                 95EP-00308660
                                                                                                                                                                                                                                           94JP-00298665
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                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Conservative
                                                                                                                                                                                                                                                                                                          Otsuka M,
                                                                                                                                                                                                                                                                                                                                   WPI; 1996-261625/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    screening; primer;
                                                                                                                                                                                                                                                                                  (TOYJ ) TOSOH CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ношо варіепв
                                                                                                                                                                                                                                            01-DEC-1994;
21-JUL-1995;
                                                                                                                                                                                                                   01-DEC-1995;
                                    12-NOV-1996
                                                                                                                                                                                                                                                                                                          Ishiguro T,
                                                                                                                                                                   EP714986-A1
                                                                                                                                                                                          05-JUN-1996
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                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189
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             AAT30234;
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WO9738085-A2

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Assessing risk of severe iron overload, e.g. in subjects with hereditary
                                                                                                                                                                                                                                                             breast cancer gene CH13-2a12-1 by differential display. The identified genes cancer gene CH13-2a12-1 by differential display. The identified genes or fragments of these genes can be used for identifying genes and gene products that are initimately related to malignant transformation or maintenance of the malignant properties of cancer cells. It can also be used to design or screen diagnostic reagents or therapeutic compounds. Kits are included within the scope of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hereditary hemochromatosis gene; HFE gene; iron overload; hereditary atransferrinemia; hypotransferrinemia; aceruloplasminemia; polymetabolic syndrome; chronic liver disease; hematological disease; delayed cutaneous porphyria; hematochromatosis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                 Breast cancer genes - used to develop products to design or screen diagnostic reagents or therapeutic compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primer used to amplify a fragment of the human HFB gene.
                                                                                                                                                                                                                                                                                                                                                                                               1.3%; Score 14.2; DB 1; Length 19;
84.2%; Pred. No. 1.8e+02;
ative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                          Sequence 19 BP; 7 A; 4 C; 1 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E ;
                                                                                                                       (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clauser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
(INRM ) INST NAT SANTE & RECH MEDICAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poupon R,
                                                                                                                                                                                                                                            Disclosure; Fig 18; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1009 GITIGAGAAGCATCATCAT 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98FR-00013607.
                                                          96US-0015167P.
96WO-US009286.
96US-0019202P.
96US-00678280.
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                                  97WO-US005930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA46190 standard; DNA; 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-387228/33.
                                                                                                                                                                             WPI; 1997-512705/47.
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-SEP-2000
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                                  09-APR-1997;
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                                                                                    06-JUN-1996;
                                                            10-APR-1996
         16-OCT-1997
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                                                                                                                                                     Smith H,
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                                                                             PCR primers AAA46189-90 were used to amplify a fragment of the human hereditary hemochromatosis (HFE) gene. The primers were used in the method of the invention. The specification describes a method for evaluating the risk of developing severe iron overload, particularly in a predisposed subject. The method comprises determining the profile of the different transcripts of the HFE gene in a biological sample. The method origin, e.g. in cases of iron overload, of inherited or acquired origin, e.g. in cases of hereditary or juvenile hematochromatosis, polymetabolic syndrome, chronic liver disease, delayed cutaneous porphyria or hematological alsease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel stabilising reaction reagent for use in the amplification and/or detection of a target nucleic acid comprising: preparing a reaction mixture with e.g. a nucleic acid as template, at least 1 primer and RNaseH; and incubation of the reaction mixture for a defined period of time to form a reaction product during the amplification of such target nucleic acid. The method is useful for stabilising and long-term storage of reaction reagents for highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stabilising reaction reagent; PCR; primer; RNaseH; long-term storage; specific amplification; pathogenic microorganism; chimeric; genetic engineering; clinical medicine; ss.
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kobayashi E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Method for stabilizing and storing reaction reagents for specific amplification and detection of nucleic acids particularly in e.g. identifying pathogenic microorganisms or viruses in sample.
hemochromatosis, by measuring a profile of the various HFE gene
                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                    Score 14.2; DB 1; Length 19;
Pred. No. 1.8e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stabilising reagent method related oligo SEQ ID No 147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tomono J,
                                                                                                                                                                                                                                                                                      Seguence 19 BP; 3 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto J,
                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 15; Page 168; 177pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                       238 CTATGACTCAGATGCAACC 256
                                                                                                                                                                                                                                                                                                                                                                                                          Mukai H,
                                               Claim 4; Page 11; 38pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВЪ.
                                                                                                                                                                                                                                                                                                                   1.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JUN-2001; 2001JP-0017737.
20-AUG-2001; 2001JP-00249689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Uemori T, Muka.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABT23695 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                       16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-148805/14.
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                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2002101042-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                   transcripts.
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                                                                                                                                                                                                                                                                                                                        Query Match
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sensitive and specific amplification and detection of nucleic acids particularly in identifying pathogenic microorganisms or viruses in a sample using chimeric oligonucleotide primers, which is useful in genetic engineering and clinical medicine. This polynucleotide sequence represents an oligo relating to the novel stabilising reaction reagent method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells by
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assessing culture of undifferentiated primate pluripotent stem cells detecting expression of markers e.g., Zic family member 3, other than human telomerase reverse transcriptase/octamer binding transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ss; PCR; embryonic stem cell; pluripotent stem cell; abnormal cell growth; malignancy; differentiation; primer; RTQ-PCR; realtime quantitative PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mandalam R;
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                                                                                                                                                   DB 1; Length 19;
                                                                                                                                                                                     3; Indels
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                                                                                                                  Sequence 19 BP; 6 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                 1.3%; Score 14.2; DB 1;
84.2%; Pred. No. 1.8e+02;
rative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    RTQ PCR primer #2 for Human LEFTB.
                                                                                                                                                                                                                   1064 CCAGTGGCTAAACCACTTA 1082
                                                                                                                                                                                                                                        1 CCAGAGGCTGAACCAGTTA 19
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                                                                                                                                                                                                                                                                                                                                   ADI82218 standard; DNA; 19
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                                                                                                                                               Query Match
Best Local Similarity 84.2
Matches 16; Conservative
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GOLD J D.
IRVING J M.
MANDALAM R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-119701/12.
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SHELTON D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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(MOKM/)
(SHEL/)
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(GOLD/)
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cc zicz, or any other marker (WR4) chosen from PHD protein Jade-1 (Jade-1), kruppal-like zinc finger protein (ZNF300), etc., as given in the geoficiation), causing pPS cells to differentiate into a particular crisque type by causing them to express one of the markers chosen from (MR3) or (MR3) or (MR4) or markers chosen from GATA binding protein 3 (GATA3), core promoter element binding protein in a pluripotent state (involves specification), maintaining pPS cells in a pluripotent state (involves culturing pPS cells or their progeny in the presence of a normally secreted protein that is encoded by a gene that down-regulated upon differentiation of human embryonic stem (hES) cells, chosen from differentiation of human embryonic stem (hES) cells, chosen from differentiate (involves che appecification), causing pPS cells to differentiate (involves culturing pPS cells or their progeny in the presence of a normally secreted protein that is encoded by a gene that up-regulated upon secreted protein that is encoded by a gene that up-regulated upon concern agiven in the specification), causing pPS cells or their progens, concern gene, according sequence to be preferentially expressed in undifferentiated pPS cells, causing an encoding sequence of encoding sequence to be preferentially expressed in differentiated cells, concern gene, etc., as given in the specification), causing pPS cells to proliferate without differentiated cells from less differentiated cells conting (M4) differentiated cells from less differentiated cells conting the during differentiation, identifying genes that are up or proliferate without differentiation, identifying genes that are up or cone of MR1 from cells not expressing the marker), causing pPS cells to proliferate without differentiation of pPS cells, and a kit (I) for assessing culture of undifferentiated cells, and a kit (I) for casessing culture of undifferentiated cells, and a kit (I) for casessing the growth characteristics of a cell population and pell growth. The method further involve detection; RNA interference; siRNA; gene silencing; gene expression; ö 1.3%; Score 14.2; DB 1; Length 19; 84.2%; Pred. No. 1.8e+02; tive 0; Mismatches 3; Indels Sequence 19 BP; 6 A; 6 C; 5 G; 2 T; 0 U; 0 Other; 0; Mismatches RNA interference target sequence #655. 827 TCATGACCCAGGAAGGCCG 845 TCATAAGCCAGGAAGCCCG 19 ADQ27747 standard; DNA; 19 BP. 21-NOV-2003; 2003WO-JP014893. 22-NOV-2002; 2002JP-00340053. 26-AUG-2004 (first entry) Query Match
Best Local Similarity 84.2
Matches 16; Conservative (NATO/) NATORI Y. (SAIG/) SAIGO K. (TEIK/) TEI K. (NAIT/) NAITO Y. WO2004048566-A1. cytotoxicity. Homo sapiens. 10-JUN-2004. ADQ27747; RESULT 251 ð 셤

Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases by selecting a target gene and measuring the functionality of the nucleotide sequences that are complementary to a stretch of nucleotides The invention relates to a method of detecting the base sequence for RNA interference by detecting the regions in the DNA sequence fulfilling the following requirements such as: (i) the base at 3' terminal is adenine, thymine or uracil; (ii) the base at 5' terminal is guanine or cyclosine; (iii) the seven base sequence at 3' terminal is rich in adenine, thymine and uracil, and; (iv) there are bases in a such a number that it causes RNA interference without showing cytotoxicity. The method is used for designing and synthesizing siRNA causing RNA interference. This sequence corresponds to an RNA interference target sequence of the invention. Detecting sequence of RNA interference useful for synthesizing siRNA, by detecting regions in sequence fulfilling specific criteria such as base at 3' terminal is adenine, thymine or uracil, base at 5' terminal is Gaps gene silencing; Bcl-2; optimised; short interfering RNA; The invention relates to a novel method for selecting siRNA (short interfering RNA) comprising selecting an siRNA molecule of 19-25 nucleoside bases by selecting a target gene and measuring the . 0 1.3%; Score 14.2; DB 1; Length 19; 34.2%; Pred. No. 1.8e+02; [ve 0; Mismatches 3; Indels Devin L, William M, Stephen S; Anti-NR2E1 siRNA related DNA sequence SEQ ID NO:1446. Sequence 19 BP; 5 A; 4 C; 3 G; 7 T; 0 U; 0 Other; Example 12; SEQ ID NO 1446; 199pp; English. Disclosure, SEQ ID NO 669; 325pp; Japanese. 709 GGTGCTCTCAGAAAATATA 727 19 14-NOV-2003; 2003WO-US036787. 14-NOV-2002; 2002US-0426137P. 10-SEP-2003; 2003US-0502050P. Grigciciccanantria 84.2%; ADQ61744 standard; RNA; 19 09-SEP-2004 (first entry) Naito Y; Matches 16; Conservative Anastasia K, Angela R, the target sequence (DHAR-) DHARMACON INC. WPI; 2004-420527/39. guanine or cytosine. WPI; 2004-487423/46. Query Match Best Local Similarity ss; siRNA; gene s RNA interference. Tei K, WO2004045543-A2 03-JUN-2004. Synthetic. ADQ61744; н Saigo K, ADQ61744/ RESULT ð 셤 ò Gaps

Disclosure; SEQ ID NO 48; 57pp; English.

GRP receptor.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the specification as DNA, but described as siRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 6 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
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Local Similarity 84.2%; Pred. No. 1.8e
les 16; Conservative 0; Mismatches
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(GOLD/)
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Matches
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Assessing culture of undifferentiated human embryonic stem cells or their progeny, by detecting Cripto, gastrin-releasing peptide (GRP) receptor and podocalyxin-like protein markers, and either hTERT and/or Oct3/4, or

Gold JD, Irving JM, Mandalam R;

Stanton LW, Brandenberger R,

Mok M;

WPI; 2004-675599/66.

GOLD J D. IRVING J M. MANDALAM R.

(IRVI/)

MOK M.

(MAND/) (MOKM/)

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The invention relates to assessing a culture of undifferentiated human embryonic stem (hES) cells (undifferentiated primate pluripotent stem cells) or their progeny, involves detecting or measuring a marker such as cripto (teratocarcinoma-derived growth factor), gastrin-releasing peptide (GRP) receptor and podocalyxin-like protein, and either hTERT (telomerase cripto (teratocarcinoma-derived growth factor), gastrin-releasing peptide (GRP) receptor and podocalyxin-like protein, and either hTERT (telomerase creverse transcriptae) and/or Oct3/4 (also known as POU domain, class 5, transcription factor 1(POUST)), or GRP receptor. The method involves guantifying the proportion of undifferentiated hES colls and detected or measured at the protein level by antibody assay. The method involves quantifying the proportion of undifferentiated hES cells or differentiated cells in the culture from the marker expression. The level of the marker is determined to be at least 100-fold higher than the level of the marker is determined to be no less than 100-fold lower than the level of the marker in medium conditioned with mouse embryonic the relevable than the level of the marker in medium conditioned with mouse embryonic method further involves modifying the culture conditions on as to cause through an extracellular matrix in medium conditions of cancer, for easesing culture. The method is useful for characterising pluripotent stem cells and their differentiated hES cells or their progeny. The marker used in the above method is useful for characterising pluripotent stem cells and their differentiated progeny, for clinical diagnosis of cancer, for assessing and manipulating culture conditions, regulating gene expression. The separation and purification, and to influence differentiation. The separation is useful for characterising deferentiated because the sequence is a real time of influence differentiated to assay mans arreading and purification, and to influence differentiation. The marker used to assay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human apolipoprotein B (ApoB) oligonucleotide segid 434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 6 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA expression in undifferentiated stem cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 827 TCATGACCCAGGAAGGCCG 845
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Les 16; Conservative
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coronary artery disease; CAD; coronary heart disease; CHD; atherosclerosis; hepatic glucose production; glucose-metabolism-related disorder; diabetes; cancer; breast cancer; colon cancer; lung cancer; neurological disease; Huntington disease; spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.

cardiant; vasotropic; antiarteriosclerotic; antidiabetic;

Human apolipoprotein B (ApoB) oligonucleotide segid 3052.

16-DEC-2004 (first entry)

cytostatic; anticonvulsant; nootropic; muscula; anti-HIV; RNA interference; iRNA; antisense technology; lipid metabolism; cholesterol imbalance; dyslipidaemia hypercholesterolaemia;

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The invention describes a RNA interference (IRNA) agent (I) comprising a sense sequence and an antisense sequence, where the sense sequences have one or more asymmetrical phosphorothioate modifications compenses to a cone or more asymmetrical phosphorothioate modifications and the antisense sequence targets a human gene sequence. Also described are:

Cc and the antisense sequence targets a human gene sequence. Also described are:

Cc are: a pharmaccutical preparation comprising (I); reducing (I); involves selecting a sequence with activity and introducing one or more asymmetrical modification in the sequence, where the modification decreasing its activity; a kit comprising (I) and instruction for its use; and a device that can be dispense or administer a composition comprising (I). Ii is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.

Cc that can be dispense or administer or glucose-6-phosphatase levels.

Cc that can be dispense or administer of useful (I). Ii is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.

Cc that can be dispense or administer or glucose-6-phosphatase levels.

Cc that can be dispense or administer or glucose-6-phosphatase levels.

Cc the can be dispense or administer or glucose-6-phosphatase levels.

Cc the can be dispense or administer or glucose-6-phosphatase levels.

Cc the can be dispense or administer or glucose-6-phosphatase levels.

Cc the can be dispense or dispense or dispense (CD) coronary heart or disperse or glucose production or for treating glucose-metabolism-classed (CBD) and atheroselectosis. (I) is administered to a subject to inhibit hepatic glucose production or for treating glucose-metabolism-classed dispenses as mentioned above, cancer (CBD) broast, colon or creating the diseases as mentioned above, cancer (CBD) and adverses or can be appliable or contary heart or contary heart or contary he
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interference RNA agent useful for treating dyslipidemias, coronary artery disease, diabetes, cancer or neurological disease, comprises sense sequence and antisense sequence which has specific modifications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14.2; DB 1; Length 19;
Pred. No. 1.8e+02;
0; Mismatches 3; Indels
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13-MAR-2003; 2003US-0454962P.
13-MAR-2003; 2003US-0455050P.
17-APR-2003; 2003US-0455050P.
17-APR-2003; 2003US-046504P.
25-APR-2003; 2003US-046565P.
25-APR-2003; 2003US-046502P.
09-MAY-2003; 2003US-0469612P.
08-AUG-2003; 2003US-0493986P.
11-AUG-2003; 2003US-0493986P.
11-AUG-2003; 2003US-0493986P.
10-CCT-2003; 2003US-0493986P.
10-CCT-2003; 2003US-0510318P.
07-NOV-2003; 2003US-0510318P.
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Local Similarity 84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ALNY-) ALNYLAM PHARM.
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2003US-0452682P.
2003US-0454265P.
2003US-0454262P.
2003US-045620P.
2003US-0462894P.
2003US-046302P.
2003US-0463612P.
2003US-046341P.
2003US-046341P.
2003US-046341P.

25-APR-2003; 25-APR-2003; 09-MAY-2003;

08-AUG-2003;

11-AUG-2003; 26-SEP-2003;

13-MAR-2003; 14-APR-2003;

13-MAR-2003;

07-MAR-2003;

17-APR-2003;

08-MAR-2004; 2004WO-US007070

WO2004080406-A2

23-SEP-2004.

Homo sapiens.

2003US-0518453P

07-NOV-2003;

09-OCT-2003;

Manoharan M, Bumcrot D; (ALNY-) ALNYLAM PHARM.

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The invention describes a RNA interference (iRNA) agent (I) comprising a sense sequence and an antisense sequence, where the sense sequences have one or more asymmetrical prosphorothioate modifications con or more asymmetrical prosphorothioate modifications sequences have one or more asymmetrical prosphorothioate modifications and the antisense sequence targets a human gene sequence. Also described are: a pharmaceutical preparation comprising (I); reducing (MI) apob-100 evels or glucose-6-phosphatase levels in a subject; producing (II); creations or glucose-6-phosphatase levels in a subject; producing (II); creations one or more asymmetrical modification in the sequence, where introducing one or more asymmetrical modification in the sequence, where crivity; a kit comprising (I) and instruction for its use; and a device crivity; a kit comprising (I) and instruction for its use; and a device crivity; a kit comprising (I) and instruction for its use; and a device useful for reducing apoB-100 levels or glucose-6-phosphatase levels. The subject is suffering from a disorder characterised by elevated or otherwise unwanted expression of apoB-100, elevated or otherwise unwanted expression of apoB-100, elevated or otherwise unwanted construction and processed of the disorder is chosen from the HDL/LDL cholesterol imbalance, dyslipidaemias, hypercholestorolaemia, statin-resistant chosen from the HDL/LDL cholesterol imbalance, disease (CHD) and atherosclerosis: (I) is administered to a subject to inhibit hepatic glucose production or for treating glucose-metabolism-crivity is useful for related disorder e.g. disabetes or type-2 disabetes. (I) is useful for
                                                                                     Interference RNA agent useful for treating dyslipidemias, coronary artery disease, diabetes, cancer or neurological disease, comprises sense sequence and antisense sequence which has specific modifications.
                                                                                                                                                                                                                                                                                                                                                       Example 5; SEQ ID NO 3052; 378pp; English.
WPI; 2004-677362/66.
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Gaps ö

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16; Conservative

Best Loca Matches

ADR78567 standard; DNA; 19 BP.

RESULT 255

ADR78567;

ADR78567/ ID ADR7 XX AC ADR7 XX

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treating the diseases as mentioned above, cancer (e.g. breast, colon or lung cancer), meurological disease (e.g., Huntington disease or spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence represents a human apolipoprotein B (ApoB) antisense oligonucleotide that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interference RNA agent useful for treating dyslipidemias, coronary artery disease, diabetes, cancer or neurological disease, comprises sense sequence and antisense sequence which has specific modifications.
                                                                                                                                                                                                                                                                                                                                                                                                                                  antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic; cytostatic; anticonvulsant; nootropic; muscula; anti-HIV; tNA interference; iRNA; antisense technology; lipid metabolism; cholesterol imbalance; dyslipidaemia hypercholesterolaemia; coronary artery disease; CAD; coronary heart disease; CHD; atherosclerosis; hepatic glucose production; glucose-metabolism-related disorder; diabetes; cancer; breast cancer; solon cancer; lung cancer; anticological disease; Huntington disease; spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
                                                                                                                                                             Gaps
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                                                                                                                          1.3%; Score 14.2; DB 1; Length 19; 84.2%; Pred. No. 1.8e+02; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Human apolipoprotein B (ApoB) oligonucleotide segid 712.
                                                                                             Sequence 19 BP; 2 A; 4 C; 3 G; 10 T; 0 U; 0 Other;
                                                             can be used to control ApoB gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; SEQ ID NO 712; 378pp; English.
                                                                                                                                                                                           1014 AGAAGCATCATCATAGAGA 1032
                                                                                                                                                                                                                         19 AGAAGCATCATCAAGGAAA 1
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17-APR-2003; 2003US-0463772P.
25-APR-2003; 2003US-0465655P.
09-MAY-2003; 2003US-0465612P.
08-AUG-2003; 2003US-0469612P.
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2003US-0454962P.
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                                                                                                                                                                                                                                                                                                         ADR76227 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                          Query Match
Best Local Similarity 84.2<sup>1</sup>
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Manoharan M, Bumcrot D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ALNY-) ALNYLAM PHARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-677362/66.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-SEP-2003;
                                                                                                                                                                                                                                                                                                                                                                       16-DEC-2004
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come or more asymmetrical 2'-0 alkyl modifications, the antisense sequences have one or more asymmetrical 2'-0 alkyl modifications, the antisense sequences have one or more asymmetrical phosphorothioace modifications and the antisense sequence targets a human gene sequence. Also described are: a pharmaccutical preparation comprising (1); reducing (M1) apoB-100 care: a pharmaccutical preparation comprising (1); reducing (M1) apoB-100 care: a pharmaccutical preparation comprising (1); reducing (M1) apoB-100 cativity; a kit comprising (1) and instruction in the sequence, where the modification decreases nuclease sensitivity while not decreasing its activity; a kit comprising (1) and instruction for its use; and a device that can be dispense or administer a composition comprising (1). (1) is useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1) is useful for reducing apoB-100 levels or glucose-6-phosphatase levels. Cherwise unwanted expression of apoB-100, elevated or otherwise unwanted composition of apoB-100, elevated or otherwise unwanted captesion of apoB-100, elevated or otherwise unwanted 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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invention describes a RNA interference (iRNA) agent (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human apolipoprotein B (ApoB) oligonucleotide seqid 3330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 10 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         can be used to control ApoB gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                552 TTTAATATGCTGGGTTTTT 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 rrgaararcercacrrrrr 1
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ID ADR78845 standard; DNA; 19 BP.
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12-MAR-2003; 2003US-0454265P.
13-MAR-2003; 2003US-0454962P.
14-ARR-2003; 2003US-0455559P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-2004; 2004WO-US007070
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RESULT 259
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axxxat
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                                                                                                                                                                                                                                                                                                                                                      The invention describes a RNA interference (IRNA) agent (I) comprising a sense sequence and an antisense sequence, where the sense sequences have cone or more asymmetrical 2'-0 alkyl modifications, the antisense cone or more asymmetrical phosphorothioate modifications and the antisense sequence targets a human gene sequence. Also described are: a pharmaceutical preparation comprising (I); reducing (II); devels or glucose-6-phosphatase levels in a subject; producing (I); stabilising (I), involves selecting a sequence with activity and introducing one or more asymmetrical modification in the sequence; where controducing one or more asymmetrical modification in the sequence, where introducing one or more asymmetrical modification in the sequence, where controducing one or more asymmetrical modification in the sequence, where introducing appense nuclease sensitivity while not decreasing its activity; a kit comprising (I) and instruction for its use; and a device that can be dispense or administer a composition comprising (I). (I) is conseful for reducing apoB-100 levels or glucose-6-phosphatase levels.

The subject is suffering from a disorder characterised by elevated or otherwise unwanted expression of apoB-100, elevated or otherwise unwanted contends and a disorder or disperse or contends and a disease (CD), coronary heart disease (CD) and atherosclerosis. (I) is administered to a subject to inhibit hepatic glucose production or for treating glucose-metabolism.

The attend disorder e.g. diabetes or type-2 diabetes. (I) is useful for relating the diseases as mentioned above, cancer (e.g. breast, colon or treating the diseases as mentioned above, cancer (e.g. breast, colon or currel human apolipoprotein B (ApoB) antisense eleg. it is useful for represents a human apolipoprotein B (ApoB) antisense elegence or epicence or produced or outled or outled 
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                                                                                                                                                                                                                                                                      coronary artery
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                                                                                                                                                                                                                                                                   Interference RNA agent useful for treating dyslipidemias, coronary disease, diabetes, cancer or neurological disease, comprises sense sequence and antisense sequence which has specific modifications.
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14.2%; Pred. No. 1.8e+02;
ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 BP; 10 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                   Example 5; SEQ ID NO 3330; 378pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragment primer HM3P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   552 TTTAATATGCTGGGTTTTT 570
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                 25-APR-2003; 2003US-0465665P.
25-APR-2003; 2003US-0465802P.
09-MAY-2003; 2003US-0469612P.
08-AUG-2003; 2003US-04693986P.
11-AUG-2003; 2003US-0493986P.
26-SEP-2003; 2003US-0494597P.
09-0CT-2003; 2003US-0510346P.
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                                                                                                                                            07-NOV-2003; 2003US-0518453P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 84.2
nes 16; Conservative
                                                                                                                                                                                                          Manoharan M, Bumcrot D;
                                                                                                                                                                             (ALNY-) ALNYLAM PHARM.
                                                                                                                                                                                                                                       WPI; 2004-677362/66.
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The sequences given in AAQ35764-73 were used to generate NYVAC and ALVAC-
based recombinants expressing the Hantaan virus G1 and G2 glycoproteins.

The expression of these glycoproteins was accomplished by insertion of
the M segment into the ALVAC and NYVAC vectors under the control of the
CC 42 kD promoter. NYVAC is derived from a canarypox virus which has been
cc vaccinia virus and ALVAC is derived from a canarypox virus which has been
cc vaccinia virus and ALVAC is derived from a canarypox virus which has been
cc were engineered as recipient loci for the insertion of foreign genes.

The ALVAC is derived from a canarypox virus which has been
cc were engineered as recipient loci for the insertion of foreign genes.

The engineered as recipient loci for the insertion of foreign genes.

The ALVAC is and was fused to a PCR-derived fragment containing the 42
creation (PCR) and was fused to a PCR-derived fragment containing the 42
cc promoter element. The 42 kD promoter was isolated from Amsacta moorei
cutomorpoxvirus (AmsPV). The 3' region of the M segment coding sequence
was also isolated by PCR and the TSV motif was disrupted. The plasmid
containing the M-specific cDNA clone was used to create an expression
cassette. The expression cassette was introduced into the large subunit,
cribonucleotide subunit (141) open reading frame (ORF) of NYVAC or the CALVAC ORF of NYVAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                       M segment; 42 kD promoter; Copenhagen vaccine; vaccinia virus; canarypox virus; virulence factor; deletion loci; recipient loci; for polymerase chain reaction; PCR; Amsacta moorei entomopoxvirus; AmEPV; TSNT motif; expression cassette; large subunit, ribonucleotide subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccinating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccine comprises recombinant, attenuated pox-virus - use for vaccinating against viral infections such as rabies, hepatitis B, HIV, HSV, EBV, CMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cox WI;
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NYVAC; ALVAC; recombinant; Hantaan virus; G1; G2; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Norton EK;
Pincus SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Taylor J, Tartaglia J, N
Limbach KJ, Johnson GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 5 A; 6 C; 2 G; 7 T; 0 U; 0 Other;
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Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 252; 456pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 CATITICCTIACAATICAA 412
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91US-00713967.
92US-00847951.
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84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                    92WO-US001906.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perkus ME, T
De Taisne C,
Gettig RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (VIRO-) VIROGENETICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-331718/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
09-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAR-1991;
11-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAR-1992;
                                                                                                                                                                                                                                                                                      WO9215672-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paoletti E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Riviere M,
Francis J,
                                                                                                                                                               14L; C4; EB.
                                                                                                                                                                                                                                                                                                                                                        17-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PN field.)
                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mumps etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ53275;
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                                                                                                                                                                                                                                                                                                  Detection and identification of viral and sub-viral pathogens, partic. in plants - by immobilisation with antibodies and spectrophotometric quantitation or electrophoretic identification.
                                        cherry leaf roll virus; CMV; cucumber mosaic virus; CTV; citrus tristeas virus; GFLV; grapevine fanleaf virus; PLRV; potato leaf roll virus; PMV; pepper mild mottling virus; PSTV; potato spindle tuber viroid; Lycopersicum esculentum; detection; virus; immobilisation; amplification; tobamovirus; potyvirus; closterovirus; luteovirus; nepovirus; identification; ss.
                                                                                                                                                                                                                                                                                                                                                                 The primers (AAQ53267-86) are used to amplify the genomes of various viral plant pathogens or satallite viruses. The pathogen is then imobilised using antibodies against proteins in the virus coating or against double-chain RNAs in the case of viral pathogens. Detection of the pathogen is carried out by electrophorectic identification of the amplification products. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003)
                               TSWV; tomato spotted-wilt virus; BYMV; bean yellow mosaic virus; CLRV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide nucleic acid; PNA; PKC-alpha; protein kinase C; ss; cell proliferation; cell differentiation; isozyme; antisense; triple helix; cancer; psoriasis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.3%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 1.8e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                 Borja Tome MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNA oligomer targetting coding region of PKC-epsilon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 11 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                           (NAIN-) INST NACIONAL INVESTIGACION & TECNOLOGIA.
                                                                                                                                                                                                                                               Bardosa Nolasco N, De Blas Beorlegui C,
Pons Ascaso F, Torres Pascual V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              Example 2; Page 6; 13pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     857 TCTTTGTGTTGTAGTCCAT 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ97957 standard; DNA; 20 BP
                                                                                                                                                                                 93EP-00500079
                                                                                                                                                                                                      92ES-00001232
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/*tag=
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                                                                                                                                                                                                                                                                               WPI; 1993-396985/50.
                                                                                                                                                                                 10-JUN-1993;
                                                                                                                                                                                                      12-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
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18-OCT-1995
                                                                                                                                      EP574345-A2
           primer
                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ97957;
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New peptide nucleic acid (PNA) oligomers are provided which (a) consist of naturally occurring nucleobases covalently bound to a polyamide backbone and (b) hybridise to the translation initiation AUG region, coding region, 5' untranslated region (5' UTR) or 3' untranslated region (6' UTR) or 6' Extranded DNA (ssDNA) to produce antisense-type gene regulation moieties. They inhibit expression of PKC-alpha and its isoforms (including beta, gamma, delta, epsilon, zeta and eta) and so are useful for treating and diagnosing cell proliferation and differentiation processes such as neoplastic, hyperproliferation and differentiation processes such as neoplastic, hyperproliferation and inflammatory diseases. PNA oligomers have high affinity for complementary single stranded DNA. They are also able to form triple helices in which a first complementary and a second RNA strand binds with the cranding double helix or with the first PNA strand. The PNAs possess no significant charge and are water soluble, which facilitates cellular uptake. Further, since they contain amides of non-biological amino acids, they are biostable and resistant to enzymatic degradation by proteases. The present sequence targets the coding region of PKC-epsilon. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
/note= "at least one (and preferably all) of the backbone subunits are composed of N-acetyl N-(2-aminoethyl)glycine peptide residues, the nucleobase being attached covalently to the acetyl group and the peptide linkage being formed by condensation of the glycine carboxy group of one residue with the amino group of the 2-aminoethyl moiety in the next residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense; protein kinase C; alpha; PKC; beta; gamma; eta; epsilon; zeta; modulation; expression; isozyme; hybridise; S' UTR; human; 3' untranslated region; translation initiation site; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptide nucleic acid oligomers specific for protein kinase C isozyme(s) - useful as anti:sense molecules for treating PKC mediated disease, e.g. cancer, psoriasis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKC-epsilon coding region antisense oligo, ISIS #7941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 38; Page 274; 287pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-US008465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-00099098
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-082040/11.
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les 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1993;
                                                                                                                                                                                                                                                                                                                                     WO9503833-A1
                                                                                                                                                                                                                                                                                                                                                                                                                   09-FEB-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
21-SEP-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ84260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dean NM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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96US-0012061P

Page 130

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Example 16; Col 21; 55pp; English
    22-FEB-1996;
                                                                                                                                                                                                                                                                                                   Matches
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AAX22647/
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                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                 The sequences given in AAQ84252-64 are oligos which are antisense to the protein kinase C-epsilon (PKC-epsilon) cDNA. These antisense molecules can be used in modulating the expression of this particular isozyme of PKC. These oligonucleotides have a %inhibition of PKC of <40%. The coligonucleotides have a %inhibition of PKC of <40%. The coligonucleotides of the invention preferably hybridise with the 5'- or 3' cultranalated regions of the PKC gene, or the translation initiation site, or the coding region. These oligos may be used in the detection of the human PKC, esp. hyperpooliferative diseases such as psoriasis, associated with PKC, esp. hyperpooliferative diseases such as psoriasis, contenia at least one phosphorothioate linkage and/or at least one of the nucleotides comprises a modification on the 2' position of the sugar, correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                            Oligo:nucleotide(s) hybridisable with Protein Kinase C mRNA or gene - also novel PKC-alpha 3'-UTR sequence, useful for diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer; polymerase chain reaction; amplification; UM-STS; universal mammalian sequence tagged site; genomic map; clone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guanylate cyclase 2D PCR primer for universal mammalian STS's.
                                                                                                                                                                                                                                                                                                                                                                                                                                                1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
phosphorothicate linkage, 2'-0-methyl modification; 2'-0-propyl modification;
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                       Example 16; Page 37; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 AGAGGAGATGATTTTAGCT 452
                                                                                                                                                                                                                                  of hyperproliferative disorders.
                                                                                                                                                                        Dean NM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV01278 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-US002403.
                                                                                                 94WO-US007770.
                                                                                                                      93US-00089996
                                                                                                                                94US-00199779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 84.2
Matches 16; Conservative
                     -O-propyl modification;
                                                                                                                                                   (ISIS-) ISIS PHARM INC.
                                                                                                                                                                        Boggs RT,
                                                                                                                                                                                           WPI; 1995-066911/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-FEB-1997;
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                                                            WO9502069-A1
                                                                                                   08-JUL-1994;
                                                                                                                        09-JUL-1993;
                                                                                                                                  22-FEB-1994;
                                                                                                                                                                         Bennett CF,
                                                                               19-JAN-1995.
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                                        Synthetic.
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The present sequence represents a specifically claimed oligonucleotide PCR primer. The oligonucleotide can be used for polymerase chain reaction (PCR) amplification of DNA, specifically regions of specific genes that are conserved among mammalian species, i.e. pairs of oligonucleotides from the present specification represent universal mammalian sequence-tagged site (UM-STS) primers. The primers are used to develop genomic maps, to isolate clones from libraries, to make cross-species comparisons and to develop additional genetic markers. UM-STS allow genomic comparisons to be made between more species
                                                                                                                                                                                         New oligonuclectide primers amplifying gene regions conserved among mammals - useful for developing genomic maps, isolating clones and making
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein kinase C; PKC; human; antisense; primer; inhibitor; treatment; hyperproliferative condition; cancer; colorectal; breast; bladder; lung; brain; glioblastoma multiforme; skin; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human protein kinase C antisense oligonucleotides - useful for treating PKC-related hyperproliferative conditions e.g. cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.3%; Score 14.2; DB 1; Length 20;
84.2%; Pred. No. 1.8e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein kinase C antisense oligonucleotide #86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 2 A; 1 C; 9 G; 8 T; 0 U; 0 Other;
                                                                                      Yuzbasiyan-Gurkan V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    783 TTGGGGATGTGCTTGGAGA 801
                                                                                                                                                                                                                                                                                                                Claim 1; Page 11; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TTGGGGATGGGCTTGTTGA 20
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(UNMI ) UNIV MICHIGAN.
(UNMS ) UNIV MICHIGAN STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                              cross-species comparisons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Conservative
                                                                                            Venta PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bennett CF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-228583/19.
                                                                                                                                               WPI; 1997-435083/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SISI (-SISI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-1992;
09-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US5885970-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-1999
                                                                                               Brewer GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX22647;
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This invention describes antisense oligonucleotides that specifically bland to human protein kinase C (PRC) mRNA. These oligonucleotides can be used to inhibit PKC mRNA and therefore be used to treat PKC-related hyperproliferative conditions, e.g. cancer, especially colorectal cancer, breast cancer, lung cancer, or brain cancer (preferably glioblastoms multiforme). The products of the invention may also be used to treat skin cancer and psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a direct repeat from the Hz-1 persistence-sesociated gene 1 (Hz-1 pagl). The invention relates to the Hz-1 pagl promoter. The pagl gene promoter is useful in insect cells for driving constitutive expression of e.g. genes encoding foreign proteins. The promoter of the pagl gene is constitutively expressed and stronger than that of the polyhedrin gene in insect cells, enabling it to express foreign genes more strongly e.g. lacZ and luciferase, in addition to which it can be expressed more prominently as a short promoter. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hz-1 pag1 promoter; persistence-associated gene 1; insect cell;
constitutive expression promoter; direct repeat; ss.
                                                                                                                                                                                                                                                                                                                    1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 13 A; 2 C; 2 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                           Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HZ-1 virus persistence-associated gene promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hz-1 Pag1 gene direct repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 3c; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      434 AGAGGAGATGATTTTAGCT 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 AGAGAAGAGATTTTGGCT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-00634350.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX76903 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                Query Match 1.3%
Best Local Similarity 84.2%
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NASC-) NAT SCI COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-357167/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-OCT-2003
05-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX76903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 264
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This invention describes novel oligonucleotides (AAX78524-X78644) having up to 50 nucleotides hybridisable with, and able to modulate the expression of, a nucleic acid encoding protein kinase C and its isozymes alpha, beta type II, beta type II, gamma, eta, dalta, epsilon and zeta. The oligonucleotides of the invention have anti-inflammatory and cyprestatic activity and are used for antisense targeting to modulate the expression of PKC or of a particular PKC isozyme or set of isozymes in cells or tissues. The products of the invention also hybridise with number or be involved in the modulation of PKC expression, which is nucleic acids involved in the modulation of PKC expression, which is conditions e.g. psoriasis but to the involved in the modulation of pkC expression, which is conditions e.g. psoriasis but to the their specificity the oligonucleotides are able to overcome the problems of toxicity associated with previous agents designed to modulate PKC expression
                                                                                                                                                                         PKC; human; PKC-alpha; primer; protein kinase C; expression modulator; PKC-beta type I; PKC-beta type II; PKC-gamma; PKC-eta; PKC-delta; PKC-espailon; PKC-esta; anti-inflammatory; cytostatic; antisense targeting; isozyme; growth control; hyperproliferative disease; colon cancer; glioblastoma; bladder cancer; inflammatory condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotides targetted against nucleic acids encoding protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.3%; Score 14.2; DB 1; Length 20;
84.2%; Pred. No. 1.8e+02;
ative 0; Mismatches 3; Indel8
                                                                                                                                             Human PKC-epsilon oligonucleotide primer ISIS # 7941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 16; Col 63-64; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                434 AGAGGAGATGATTTTAGCT 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX83735 standard; DNA; 20 BP
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                   609/c
AAX78609 standard; DNA; 20
                                                                                                      03-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bennett CF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-404471/34.
                                                                                                                                                                                                                                                                          psoriasis; ss
                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-1992;
09-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                  US5922686-A.
                                                                                                                                                                                                                                                                                                                                                                                                      13-JUL-1999
                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                    AAX78609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dean N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 266
AAX83735/c
ID AAX837
XX
RESULT 265
                   AAX78609,
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1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02; ive 0; Mismatches 3; Indels

566 TITITIAAIACCITIAIAI 584

Local Similarity 84.2 tes 16; Conservative

Matches

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Query Match

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AAX94795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method of inhibiting the expression of human protein kinase C (PKC) in cells. The method comprises contacting the cells with an antisense oligonucleotide which has up to 50 nucleotide cunits. AAX83720 represent specifically claimed antisense oligonucleotides for use in the method of the invention. The antisense oligonucleotides for use in the method of the provention. The antisense coligonucleotides modulation of expression of the PKC gene which results in modulation of expression of the PKC gene. This means they can be used for diagnosis, therapeutic or prophylactic treatment of PKC associated diseases such as cancer and psoriasis, and as research agents. Abnormal proliferative states in tissue from patients suspected of diagnosed. Tumours associated with PKC can be distinguished from tumours which are not PKC associated to allow an efficacious treatment regime to be used. The antisense oligonucleotides have specific activity so are called to modulate PKC activity without producing side effects and with greater effectiveness than observed from administration of current carriers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antisense oligonucleotides specific for human protein kinase C useful diagnosis and treatment of cancer and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
                                                                                                                                Human; protein kinase C; PKC; antisense oligonucleotide; diagnosis; ss; hybridisation; cancer; psoriasis; hyperproliferative disease; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                    Human protein kinase C antisense oligonucleotide SEQ ID NO:86.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer used to amplify an ORF of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  examples from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 16; Col 21; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            434 AGAGGAGATGATTTTAGCT 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX92824 standard; DNA; 20 BP
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                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dean N, Bennett CF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-403817/34.
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                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                    16-MAR-1992;
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                                                      27-AUG-1999
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                                                                                                                                                                                                                                                                                                                  29-JUN-1999
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                                                                                                                                                                                                           Synthetic.
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           AAX83735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 267
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Matches
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AAX91991-X97517 represent PCR primers used to amplify open reading frames and other nucleic acid sequences from the genome of Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinuatis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAX1564-AAX15879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 1.8e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR primer used to amplify an ORF of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 8 A; 7 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome sequence of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 1542; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        940 AGAATCTGAAGCCCCACTC 958
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84.2%;
                                                                                                                                                                                                                                                                               98WO-IB001890.
                                                                                                                                                                                                                                                                                                                                97FR-00014673.
98US-0107078P.
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Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                       Chlamydophila pneumoniae.
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04-NOV-1998;
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                                                                                                    Synthetic
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pneumonia and bronchitis and is thought to be a contributing factor in
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                                                                                                               AAX91991-X97517 represent PCR primers used to amplify open reading frames and other nucleic acid sequences from the genome of Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAX34584 - AAX35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae especially where the vector directs the expression of a neutralising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                              Score 14.2; DB 1; Length 20;
Pred. No. 1.8e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primer used to amplify an ORF of Chlamydia pneumoniae.
                                                                                                                                                                                                                                            Sequence 20 BP; 4 A; 3 C; 5 G; 8 T; 0 U; 0 Other;
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                                                                        Genome sequence of Chlamydia pneumoniae.
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                                                                                            Page 1697; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                         771 GAAACCTTTTGCTTGGGGA 789
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                                                                                                                                                                                                                                                               Query Match 1.3
Best Local Similarity 84.2
Matches 16; Conservative
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                                                                                                                                                                                                                      epitope of C. pneumoniae
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                                                   WPI; 1999-357842/30.
           (GEST ) GENSET
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                              Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae mucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; 88.
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                                                                                                                                                                                                                                                                                                     Score 14.2; DB 1; Length 20;
Pred. No. 1.8e+02;
0; Mismatches 3; Indels
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84.2%; Pred. No. 1.8e+02;
ative 0; Mismatches 3; Indel8
                                                                                                                                                                                                                                                    Sequence 20 BP; 1 A; 5 C; 5 G; 9 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       291 CTACTGGAATTGTTGTTC 309
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Best Local Similarity 84.2
Matches 16; Conservative
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04-NOV-1998;
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Human PKC-epsilon antisense oligonucleotide SEQ ID NO:86.
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                                                                                                                                                     16-MAR-1992;
                                                                                                                                                              09-JUL-1993;
                                                                           Homo sapiens
                                                                                             JS5882927-A.
                                                                                                               16-MAR-1999
                                                                  Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                    and other nucleic acid sequences from the genome of Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory disease such as supermoniae and bronchities and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAX1584 - AAX15879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae
                                                                                                                                                   Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
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Pred. No. 1.8e+02;
0; Mismatches 3; Indels
                                                                                                                                   PCR primer used to amplify an ORF of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 1 A; 5 C; 5 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                   Genome sequence of Chlamydia pneumoniae.
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             GTGGTAGCACTTTATTCTG 478
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98US-0107078P
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(first entry)
                                                                              AAX95840 standard; DNA; 20
                                                                                                                    13-SEP-1999 (first entry)
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hes 16; Conservative
                                                                                                                                                                                                     Chlamydophila pneumoniae.
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14-MAY-1999
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                                                                                                                                                                                               Synthetic
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              460
                                                                                                   AAX95840;
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Matches
                                                             RESULT 271
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The present invention specifically describes antisense oligomucleotides of up to 50 nucleotides in length which specifically bind human protein kinase C-alpha (PKC-alpha) mAX19127 to AAX19247 represent antisense coligomucleotides from the present invention which bind human PKC-alpha, -delta, epsilon, -zet and -eta. The antisense coligomucleotides modulate the expression of the PKC gene (i.e. inhibit oligomucleotides modulate the expression of the PKC gene (i.e. inhibit coligomucleotides modulate the expression of the PKC gene (i.e. inhibit colligomucleotides of propomucleotides can be used to diagnose to apport any partients of the PKC gene). The antisense oligomucleotides can be used to distinguish PKC-associated two partiens and to detect and diagnose PKC expression (through the use of 32P cumours and to detect and diagnose PKC expression (through the use of 32P coligomucleotides can also be used to perform autoradiography of tissues coligomucleotides can also be used to perform autoradiography of tissues coligomucleotides eliminate the side effects associated with the antisense oligomucleotides eliminate the side effects associated with the antisense oligomucleotides eliminate the side effects associated with the gene rather than inhibiting the enzyme itself. (Updated on 20-grown are methods because it modulates the amount of PKC protein made con 20-grown and 2003 to correct PF field.)
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Human; PKC; protein kinase C; diagnosis; antisense oligomucleotide;
phosphorothicate linkage; hyperproliferative disease; cancer; psoriasis;
tumour; inhibition; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New synthetic oligonucleotides inhibiting expression of protein kinase (PKC)-alpha - useful for treating and diagnosing conditions associated with abnormal PKC expression.
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Pred. No. 1.8e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 16; Col 23; 56pp; English.
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Best Local Similarity 84.2'
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bennett CF;
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(GEST ) GENSET.
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                                           Cohen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes antisense oligonucleotides up to 50 mucleotides in length which specifically bind mRNA encoding human protein kinase C (PKC). AAZ27266 to AAZ27368 represent human PKC antisense oligonucleotides used in the exemplification of the present invention. The antisense oligonucleotides are useful for the treatment of diseases associated with PKC expression, such as Myperproliferative and inflammatory conditions including psoriasis, tumours and cancer (glioblastoma, bladder, breast, colon and lung cancer)
                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense oligonucleotides useful for treatment of hyperproliferative and
phosphorothioate; hybridisation; isozyme; target; inflammation;
hyperproliferative disorder; psoriasis; tumour; cancer; glioblastoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human biallelic marker downstream amplification primer SEQ ID NO:9409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammatory conditions including psoriasis, tumors and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 16; Col 23; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434 AGAGGAGATGATTTAGCT 452
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98US-0109732P.
                                                                                                                                                                                                                                          92US-00852852.
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                                                                                                                                                                                                                                                                                                       (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-561076/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis; ss
                                                                                 Homo sapiens
                                                                                                                                                                                                      07-JUN-1995;
                                                                                                                                                                                                                                                                 09-JUL-1993;
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23-NOV-1998;
                                                                                                                                                                                                                                            16-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-SEP-2001
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                                                                                                                                                                                                                                                                                                                                              Bennett CF,
                                                                                                                       US5959096-A.
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                                                                                                                                                               28-SEP-1999
                                                            Synthetic.
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AC AAZ75
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DE HUMA:
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M HUMA:
XM HUMA:
XM HUMA:
XM AMDI
XM AMD
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invention, which contain a polymorphic base at position 24 of their invention, which contain a polymorphic base at position 24 of their invention, which contain a polymorphic base at position 24 of their concledes. AAZ69579 to AAZ7740 represent amplification in partice for the biallelic markers of the invention primers for the biallelic markers of the invention primers for the biallelic markers of the invention concerns a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficactions and side effects from pharmaceutical agents acting on a disease as well as other treatment.

N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and in the Sequence Listing from the
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                                                                                                                                       Novel biallelic markers used to construct a high density disequilibrium
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antisense, antiinflammatory, cytostatic, tumour, MOE, phosphorothioate,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mod_base= OTHER
'note= "Optionally the nucleotides are 2'-methoxyethyl"
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/note= "Optionally the internucleotide linkages are
phosphorothioate"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 4 A; 11 C; 0 G; 5 T; 0 U; 0 Other;
Chumakov I;
                                                                                                                                                                                                                                                    Claim 8; Page 2236; 2745pp; English.
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/hote= "Optional"
16. .20
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/mod_base= OTHER
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*tag=
Blumenfeld M,
                                                                                                                                                                                map of the human genome.
                                                               WPI; 2000-013267/01.
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RESULT 277
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                                                                                                                                                                                                      The present sequence is an antisense oligonucleotide designed to inhibit expression of the human X-linked inhibitor of apoptosis. This sequence is trargeted to the start codon region of the gene. The oligonucleotides may be modified to consist of 10 mucleotides flanked on both sides by 5 mucleotide wings. The wings are composed of 2'-methoxyethyl (2'-MOE) nucleotides Cyridine residues in the 2'-MOE wings are 5-methylcytidines. Throughout the modified oligonucleotides, the internucleoside linkages are phosphorothicate. The modified oligonucleotides are more effective inhibitors than unmodified oligonucleotides. The oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis expression in cells and tissues in vitro. The oligonucleotides are also useful for treating animals or humans, prone to a disease associated with X-linked inhibitor of apoptosis. The oligonucleotides may also be used prophylactically to
                                                                                                                                        Antisense compound useful for research reagents, diagnostics, prophylaxis and for treating disorders associated with X-linked inhibitor of apoptosis, modulates expression of X-linked inhibitor of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                            1.3%; Score 14.2; DB 1; Length 20;
34.2%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRN1; vernalisation; flowering; crop; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                   prevent infection, inflammation or tumour formation
                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 6 A; 4 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                Ackermann EJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A thaliana VRN1 gene PCR primer S49.
                                                                                                                                                                                                                                                                                                                                                                                                                                        426 TATTTGGAAGAGGAGATGA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||| ||||| |||||| ||||||| TATTTTCAAGAGAAGATGA 2
                                                                                                                                                                                    Claim 3; Col 40; 33pp; English.
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                                99US-00392580,
                                                      99US-00392580
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Best Local Similarity 84.2%;
Marches 16; Conservative
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                                                                                                Cowsert LM,
                                                                            (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
                                                                                                                    WPI; 2000-498201/44.
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                                09-SEP-1999;
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                                                                                               Bennett CF,
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                                                                                                                                                                                   Arabidopsis thaliana VRNI. This protein is capable of altering the vernalisation responses of a plant. Also provided are a number of PCR primers used to isolate the sequences. The sequences are useful in the production of crop plants, where they are able to control the timing of flowering, the duration of vernalisation required, the optimum temperature, or even eliminate the need for vernalisation completely. The present sequence is a PCR primer used to isolate the VRNI coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a Campylobacter jejuni or Campylobacter coli fibronectin binding protein (CadF). A recombinant expression vector with cadF is useful in an assay for determining the presence of C.jejuni or C.coli in a test sample or for determining whether a test isolate of Campylobacter is a strain of C.coli. cadF is useful in the construction of DNA probes for identifying and quantifying the level of expression of CadF in a cell. The gene can also be used in a vaccine
Novel VRN1 polynucleotide sequence encoding a polypeptide which alters vernalization response of plant in which VRN1 nucleic acid is expressed, useful for influencing and assessing vernalization phenotype of plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fibronectin binding protein; CadF; vaccine; diagnostic assay; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.3%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 1.88+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 5 A; 10 C; 1 G; 4 T; 0 U; 0 Other;
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Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                       Claim 10; Page 76; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             448 TAGCTGGGAGCAGTGGTAG 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          raccreceaacrerecrae 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF23509 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-00080025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Konkel ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coli.
jejuni.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Campylobacter
Campylobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF23509;
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Fri Aug 19

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Length 20;

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Sequences AAC92560-C92639 represent antisense oligonuclectides targetted to the human nucleolin gene, which inhibit its expression. The antisense oligonuclectides were designed to target different respions of the human nucleolin mRNA, and were analysed for their effect on nucleolin mRNA levels by quantitative real-time PCR. Nucleolin (also known as P92 or C32) is the most abundant nucleolar phosphoprotein in actively growing cells. Nucleolin primarily participates in ribosome biogenesis and transport of ribosomal components, being able to transiently bind to preriosomes in the nucleolus via a ribonucleoprotein consensus sequence. Thewever, it has also been shown to be involved in cyrokinesis, nucleogenesis, cell proliferation and growth, transcriptional repression, replication, signal transduction, and chromatin decondensation. Nucleolin replication, signal transduction, and chromatin decondensation. Nucleolin is a member of the Ag-NOR (active ribosomal gene located in the nucleolar or inbosomal genes, and whose expression is associated with the prediction of tumour growth rate. The presence of antibodies against nucleolin are associated with systemic connective tissue diseases such as systemic cincential and sclerodermaliate with systemic connective tissue diseases such as systemic connective diseases. The oligonucleotides of the invention are useful for diagnosis, prevention and treatment of conditions associated with nucleolin Human nucleolin phosphorothioate antisense oligonucleotide, SEQ ID NO:36. Novel antisense compound targeted to human nucleolin which specifically hybridizes with and inhibits the expression of human nucleolin, useful for modulating the expression of nucleolin in cells. expression, such as tumour formation, immune disorders and inflammation Gaps Human nucleolin; P92; C23; phosphoprotein; ribosome biogenesis; ribosome transport; cytokinesis; nucleogenesis; cell proliferation; cell growth; transcriptional repression; replication; esignal transduction; chromatin decondensation; Ag-NOR family; nucleolin antibody; systemic connective tissue disease; SLE; systemic lupus erythematosus; scleroderma-like chronic graft versus host disease; escleroderma-like chronic graft to the chromic praction; cancer; inflammation; immune disorder; phosphorothioate; antisense oligonucleotide; ss. ö 3; Indels Sequence 20 BP; 4 A; 7 C; 2 G; 7 T; 0 U; 0 Other; 0; Mismatches Example 15; Col 41-42; 41pp; English TTATGTTACTTGTTTGGCT 694 || | |||||||||| ||||| TTCTTTTACTTGTT 20 BP 99US-00433699 99US-00433699 AAC92586 standard; DNA; 20 (first entry) 16; Conservative Cowsert LM; (ISIS-) ISIS PHARM INC. WPI; 2001-079848/09. Homo sapiens 03-NOV-1999; 03-NOV-1999; 27-MAR-2001 US6165786-A. 26-DEC-2000. Bennett CF, 919 AAC92586; Matches

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CC PCR primers AAI65595-AAI65646 were used to amplify polymorphic microsatellite markers, for localisation of a human gene encoding inflammatory bowel disease 1 (IBD1) polypeptide, which is associated with intestinal inflammatory disease. The specification also describes a polypeptide which is in proximity to IBD1, and is designated IBD1prox. The IBD1 gene is probably involved in regulation of apoptosis and activation of NF-kappa B. The IBD1 and IBD1prox polymucleotides are is useful as source of probes and primers, as source of (anti)sense of oligonucleotides, for recombinant production of polypeptides, and in screening for interactive compounds. The polypeptides are used to raise specific antibodies which useful for diagnostic detection or purification of IBD1prox, to screen for specific binding agents, potential the reapeutic agents. The IBD1 and IBD1prox polymucleotides and prevention of inflammatory and/or immune diseases or canner, where associated with mutations in genes corresponding to IBD1 and IBD1prox, especially cryptogenetic inflammation of the intestines (hemorrhagic rectocolitis, Crohn's disease
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                                                                                                                                                                                                                                                                                                                                                                                                   88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human nucleic acids associated with intestinal inflammatory disease, useful for diagnosis, prognosis and control of these diseases, also related proteins.
                                                                                                                                                                                                                                                                                                                                                           intestinal inflammatory disease; apoptosis; NF-kappa B; cancer; inflammatory disease; immune disease; cryptogenetic inflammation; hemorrhagic rectocolitis; Crohn's disease; Blau syndrome; PCR primer;
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gape
                                                                                                                                                                                                                                                                                                         Primer for microsatellite marker D16S408, used to localise IBD1.
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                                                                                                                                                                                                                                                                                                                                            inflammatory bowel disease 1 protein; IBD1; IBD1prox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02; ive 0; Mismatches 3; Indels
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chamaillard
Score 14.2; DB 1;
Pred. No. 1.8e+02;
); Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 8 A; 6 C; 5 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lesage S,
                                                                       800 GAGGCAGATAACGCTGAAG 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 84; 97pp; French.
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                                                                                                          19 GAGGAAGATGACTCTGAAG 1
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 1.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAR-2000; 2000FR-00003832.
                                                                                                                                                                                                  AAI65644 standard; DNA; 20
                                                                                                                                                                                                                                                                         (first entry)
                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hugot JP, Thomas G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-608364/70.
                    Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Blau syndrome)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                       03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-SEP-2001,
                                                                                                                                                                                                                                     AA165644;
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     Query Match
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Matches
                                                                                                                                                              RESULT 279
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776 CTTTTGCTTGGGGATGTGC 794

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Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes the human Zmaxi gene and the high bone mass (HBM) gene, which are found on chromosome 11q13.3. The Zmaxi and HBM genes have osteopathic activities. The genes can be used in gene therapy, and in the production of vaccines. They can be used in the diagnosis and treatment of bone disorders including osteoporosis, paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.

ABA82038 to ABA82700 and AAG68168 to AAG66193 represent sequences used in
                                                                                                                                                                                           Human; high bone mass; HBM gene; Zmaxl gene; chromosome 11; 11q13.3; sequence tagged site; STS; osteoporosis; osteopathic; gene therapy; antisense therapy; vaccine; bone disorder; Paget's disease; adapter; sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cell cycle regulatory protein; cancer; cell cycle abnormality;
cytostatic; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell cycle regulatory protein coding sequence related PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New high bone mass (HBM) and Zmaxl genes and proteins useful for modulating bone mass for the treatment of e.g. osteoporosis.
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1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                               Zmax1 gene region physical map preparation STS marker #244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson ML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 34; 443pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recker RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              882 AAAAGTGTGGCCCACAGAC 900
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                                                                          BP.
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                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-2000; 2000US-00543771.
   CTTGTGCTTGGTGATGTCC
                                                                                                                                                                                                                                                                                                                                                                             21-JUN-2000; 2000WO-US016951
                                                                          ABA82285 standard; DNA; 20
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                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Little RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-657171/75.
                                                                                                                                                                                                                                                                                                                   WO200177327-A1
                                                                                                                                                                                                                                                                           sapiens.
                                                                                                                                      25-JAN-2002
                                                                                                                                                                                                                                                                                                                                                 18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carulli JP,
                                                                                                                                                                                                                                                                                          Synthetic
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   20
                                                                                                          ABA82285;
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The present invention provides the protein and coding sequences of several human cell cycle regulatory proteins. These sequences can be used in the diagnosis and treatment of cancers and other diseases associated with cell cycle abnormalities. The present sequence is a PCR primer described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; PKC antisense oligonucleotide; protein kinase C; PKC; PKC-alpha; PKC-beta type I; PKC-beta type II; PKC-gamma; PKC-delta; PKC-epsilon; PKC-zeta; PKC-eta; PKC expression modulation; Ss; hyperproliferative condition; tumour; glioblastoma; bladder cancer; breast cancer; colon cancer; lung cancer; inflammatory condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                Cell-cycle regulatory protein, useful for diagnosis and treatment of cancers and other diseases caused by abnormal cell cycles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein kinase C-epsilon antisense oligonucleotide 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 20; 34pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1079 CITAACCICICIGGGIGIT 1097
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90US-00566977.
91US-00777760.
91US-007777607.
92US-00852852.
93US-00058023.
93US-0008996.
94US-00891063.
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                                                                                                                                                                               02-OCT-2000; 2000JP-00302674.
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                                                                                                                                   02-OCT-2000; 2000JP-00302674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL90939 standard; DNA; 20
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                                                                                                                                                                                                                                                                            WPI; 2002-440460/47.
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nes 16; Conserv
                                           JP2002101891-A.
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11-JAN-1991;
15-OCT-1991;
16-OCT-1991;
16-MAR-1992;
Homo sapiens.
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09-JUL-1993;
29-AUG-1994;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAY-2002
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                                                                                     09-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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The invention comprises antisense oligonucleotides designed to bind mRNA encoding a human protein kinase C (FKC) isoform (i.e. FWC-alpha, FKC-beta type I, FKC-beta type I, FKC-gramma, FKC-delta, FKC-epsilon, FKC-ceta, and FKC-eta). The antisense oligonucleotides of the invention are useful for modulating the expression of the PKC isoforms. The antisense oligonucleotides are useful for treating hyperproliferative conditions (e.g. tumour, glioblastoma, bladder cancer, breast cancer, colon cancer antisense oligonucleotides of the invention are also useful for detection and diagnosis of FKC expression. The present sequence represents a human PKC antisense oligonucleotide of the invention. NOTE: The present
                                                                                                                             New antisense oligonucleotide having nucleoside units which specifically binds mRNA encoding human protein kinase C isoform, useful for treating hyperproliferative and inflammatory diseases e.g. psoriasis, tumor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence contains a phosphorothioate backbone
                                              ö
                                            Hoke
                                                                                                                                                                                                                                              Example 16; Col 47-48; 77pp; English
                                            Cook PD,
  (ISIS-) ISIS PHARM INC.
                                            Dean NM,
                                                                                        WPI; 2002-215022/27
                                            Bennett CF,
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1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02; ive 0; Mismatches 3; Indels 434 AGAGGAGATGATTTTAGCT 452 ч 19 AGAGAAGAGGATTTTGGCT 84.2%; Local Similarity 84.2 nes 16; Conservative Query Match Best Loc Matches g ઠે

AAL45924 standard; DNA; 20 08-JUL-2002 AAL45924; RESULT 283 AAL45924/c 

BP

Antisense oligonucleotide; exon skipping; exon inclusion signal; disease treatment; splice-modulation; gene therapy; dystrophin; haemostatic; antithyroid; muscular; mouse; ss. Murine dystrophin-specific antisense oligonucleotide mAON#6. (first entry)

Mus sp.

EP1191097-A1

27-MAR-2002.

21-SEP-2000; 2000EP-00203283.

21-SEP-2000; 2000EP-00203283.

(UYLE-) UNIV LEIDS MEDISCH CENT.

Den Dunnen JT, Dauwerse JG; Van Deutekom JCT, Van Ommen GB, Datson NA;

WPI; 2002-354071/39.

Decreasing the production of an aberrant protein in a cell, for treatment of inherited diseases such as Duchenne Muscular Dystrophy or Hemophilia, comprises a splice modulation therapy of exons.

Example 1; Page 6; 18pp; English

The present invention relates to a method of decreasing the production of an aberrant protein in a cell containing pre-mRNA of exons coding for the protein, involving providing the cell with an agent capable of specifically inhibiting an exon inclusion signal of one of the exons, and allowing translation of mRNA produced from splicing of pre-mRNA. The new method decreases the production of an aberrant protein in a cell by using a process known as exon-skipping. The process is carried out by providing an agent such as a nucleic acid to inhibit the exon inclusion signal. The nucleic acid agent can therefore be used as a preparation of a medicament for treatment of inherited diseases such as haemophilia A. clotting factor VIII deficiency, some forms of congenital hypothyroidism, Duchenne Muscular Dystrophy. The present sequence is an antisense oligonucleotide directed at the murine dystrophin pre-\*\*\*\*\*\*\*\*\*\*\*\*\*

Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

Gaps ö DB 1; Length 20; Indels 1.3%; Score 14.2; DB 1; 84.2%; Pred. No. 1.8e+02; ive 0; Mismatches 3; Query Match Best Local Similarity 84.2 Matches 16; Conservative

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793 GCTTGGAGAGGCAGATAAC 811 19 GCTGGAAGAAGCAGATAAC 1 ઠે a

ABL45469 standard; DNA; 20 BP ABL45469; ABL45469/ 

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Gaps

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RESULT 284

11-APR-2002 (first entry)

Human chromosome 21q22.1 PCR primer SEQ ID NO:2513.

Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome; primer; 88. PCR

Homo sapiens.

JP2001321190-A.

20-NOV-2001.

12-MAR-2001; 2001JP-00068285.

10-MAR-2000; 2000JP-00066716

(RIKA ) RIKAGAKU KENKYUSHO (GENO-) GENOTEX YG.

WPI; 2002-144136/19.

Arraying genome clones.

Claim 6; Page 54; 528pp; Japanese.

The present invention describes a method of arraying genome clones. The method comprises: (a) clones of the genomic libraries contained in method comprises: (a) clones of the genomic libraries contained in each of the multiwell plates; (b) a primer descrimination are mixed in each of the multiwell plates; (b) a primer designed based on the chromosome marker sequence is added to the mixture to carry out an amplification reaction; (c) a signal corresponding to the marker is detected from the resultant amplified product to specify the discrimination Nos. of the multiwell plates containing the clones having said marker sequence; (d) the order of the maximum in the specified discrimination Nos. to array the multiwell plates; (e) the clones in the multiwell plates of the specified discrimination Nos. are mixed respectively in each wells of longitudinal and lateral directions; (f) the mixed clones are cultured and the resultant cultures are amplified by using the above primer; (g) signals

Fri Aug 19 11:00:00 2005

Sequence 20 BP; 9 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

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detected from the amplified products; (h) the clones in the multiwell
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plates are specified from the detected result, and (i) the clones are reconstituted as the positions on the chromosome and arrayed. The microarray is useful for gene analysis. ABL42957 to ABL45322 represent PCR primers for human chromosome 1936-35 DNA, and ABL45323 to ABL45634 represent PCR primers for human chromosome 21q22.1, which are specifically claimed for use in the present invention

Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

ö Score 14.2; DB 1; Length 20; Pred. No. 1.8e+02; 3; Indels 0; Mismatches 96 CATTATCCTTCAGTGGGGC 114 ~ 1.3%; 20 CATTAGCCTACAGTTGGGC 16; Conservative Query Match Best Local Similarity Matches 16; Conserv 셤 ઠે

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Gaps

BP. ABL44467 standard; DNA; 20 (first entry) 11-APR-2002 ABL44467; Human; 

Human chromosome 1p36-35 PCR primer SEQ ID NO:1511.

chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome; PCR primer; 88

Homo sapiens

JP2001321190-A.

20-NOV-2001

12-MAR-2001; 2001JP-00068285.

10-MAR-2000; 2000JP-00066716.

(RIKA ) RIKAGAKU KENKYUSHO (GENO-) GENOTEX YG.

WPI; 2002-144136/19.

Arraying genome clones.

Claim 13; Page 68; 115pp; English.

Claim 4; Page 34; 528pp; Japanese.

method comprises: (a) clones of the genomic libraries contained in method comprises: (a) clones of the genomic libraries contained in multiwell plates; (b) a primer designed based on the chromosome marker contributed in added to the mixture to carry out an amplification reaction; (c) a signal corresponding to the marker is detected from the resultant corresponding to the marker is detected from the resultant corresponding to the marker is detected from the resultant corresponding to the marker sequence; (d) the order coff the markers is changed so that the same discrimination Nos. of the multiwell plates of the specified discrimination Nos. to array the multiwell containination Nos. are mixed respectively in each wells of longitudinal and lateral directions; (f) the mixed clones are cultured and the constituted as the position from the detected result; and (i) the clones are are detected from the amplified products; (h) the clones in the multiwell creconstituted as the positions on the chromosome and arrayed. The microarray is useful for gene analysis. ABM42957 to ABM45322 represent propresent progressent promare for human chromosome 21q22.1, which are greenfiled for use in the present invention

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                                                                                                                                                                                   Human; methylated gene; methylation; breast cancer; marker; WT-1;
cell proliferative disorder; TWIST; HOXA5; NES-1; RARbeta; cyclin D2;
retinoic acid receptor beta; oestrogen receptor; Wilms' tumour;
14.3.3 sigma; HIN-1; RASSF1A; tumour suppressor gene; hypermethylation;
                                                                                                                                                                                                                                                                                                                                                                                                     Diagnosing and/or determining a predisposition to a cellular proliferative disorder of breast tissue, in particular breast cancer, determining the state of methylation of one or more nucleic acids
                                                                                                                                                                                                                                                                                                                                                                Fackler MJ;
                    Gaps
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Length 20;
                                                                                                                                                                                                                                                                                                                                                                Davidson N,
                    Indels
 1.3%; Score 14.2; DB 1;
84.2%; Pred. No. 1.8e+02;
:ive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                 Sacchi N,
                                                                                                                                                                                                                                                                                                                                               (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                   NES-1 gene methylation specific primer #3.
                                                                                                                                                                                                                                                                                                                                                                  Dooley WC,
                                          403
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                                          CAATGCAGTCATTTTCCTT
                                                           cearecarrearrrecer
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                                                                                                                                                                                                                                                                                                                                                                                                                                     isolated from the subject.
                                                                                                                                                  (first entry)
                       Conservative
                                                                                                            ABT06471 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                   Evron E,
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-599803/64.
          Local Similarity
nes 16; Conserv
                                                                                                                                                                                                                                primer; 88
                                                                                                                                                                                                                                                                    WO200259347-A2.
                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                   07-NOV-2002
                                                                                                                                                                                                                                                                                       01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                    Sukumar S,
                                                                                                                               ABT06471;
                                           385
                                                             20
   Query Match
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                        Matches
                 Best
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The present invention relates to a method of diagnosing a cellular proliferative disorder of breast tissue, which involves determining the state of methylation of one or more nucleic acids isolated from the subject, where the state of methylation of the nucleic acids as compared with a state of methylation from a subject not having the cellular proliferative disorder of breast tissue is indicative of a cellular or proliferative disorder of breast tissue in the subject. The nucleic acids proliferative disorder of breast tissue in the subject. The nucleic acids oestrogen receptor, cyclin D2, Wilms' tumour gene (WT-1), 14.3.3 sigma, control or RASSFIA. The method is useful for diagnosing and/or determining a predisposition to a cellular proliferative disorder, in particular carcinoma, tubular carcinoma in situ, lobular carcinoma, colloid carcinoma, tubular carcinoma in situ, lobular carcinoma in situ and carcinoma in situ. The present sequence is a primer used in the exemplification of the invention ö Gaps ö Length 20; Indels Sequence 20 BP; 3 A; 3 C; 5 G; 9 T; 0 U; 0 Other; Score 14.2; DB 1; Pred. No. 1.8e+02; 0; Mismatches 1.3%; Conservative Local Similarity nes 16; Conserval Query Match Best Loca Matches

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ABS68905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention comprises antisense oligonucleotides designed to inhibit expression of Syntaxin 4 interacting protein. The antisense oligonucleotides of the invention are useful for inhibiting the expression of Syntaxin 4 interacting protein in cells or tissues. The antisense oligonucleotides are also useful for treating an animal having a disease or condition associated with Syntaxin 4 interacting protein (e.g. diabetes, obesity or a skeletal muscle disorder). The antisense inflammation and tumour formation. The present DNA sequence represents a mouse Syntaxin 4 interacting protein antisense oligonucleotide. NoTE: The present sequence contains a phosphorothioate backbone and 2'-0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                 Mouse, antisense gene therapy, Syntaxin 4 interacting protein, ss; antisense oligonucleotide, diabetes; obesity; skeletal muscle disorder; inflammation; tumour formation; phosphorothioate backbone;
                                                                                                                                                                                                                                                                                                                                                                                                         Novel antisense compound that hybridizes and inhibits nucleic acid molecule encoding Syntaxin 4 interacting protein, useful for treating diabetes, obesity and skeletal muscle disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                              Mouse syntaxin 4 interacting protein antisense oligonucleotide 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 3 A; 5 C; 3 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 88; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             932 AGAAATGCAGAATCTGAAG 950
TTAGAGGATTATGGCGTTT 167
                                                                                                                                                                                                                                                                                                                                                               Wyatt JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 AGAACTCCAGAATGTGAAG 1
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                   rrcaagrrrargccgrrr
                                                                                                                                                                                                                                                                                             19-SEP-2001; 2001WO-US029251.
                                                                                                                                                                                                                                                                                                                  22-SEP-2000; 2000US-00668313
                                                                            ABQ62452 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK23082 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                       (first entry)
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nes 16; Conservative
                                                                                                                                                                                                    -O-methoxyethyl wing
                                                                                                                                                                                                                                                                                                                                       (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                               Freier SM,
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-404952/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     methoxyethyl wings
                                                                                                                                                                                                                            Mus musculus.
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                                                                                                                        16-AUG-2002
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149
                                                                                                  ABQ62452;
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ABK23082/C
ID ABK230
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AC ABK230
XX
DT 09-APR
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Matches
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The invention relates to a method for identifying a molecule involved in lipid regulation comprising identifying a molecule that binds to or inhibits binding of a molecule to high bone mass (HBM) or its wild type gene, Zmaxi. Compounds identified by the method are useful for treating, diagnosing, preventing or screening for normal and abnormal lipid-associated conditions, including arteriosclerosis, cardiovascular cateament or prevention of diabetic atherosclerosis, neurovascular conditions caused by plaque build-up, poor circulation due to plaque conditions caused by plaque build-up, poor circulation due to plaque build-up and associated poor wound healing. The methods may be used in gene therapy, pharmaceutical development, and diagnostic assays for bone development disorders. Molecules identified by comparison of Zmaxl and development, in diagnosis of human or animal bone disease, and in the treatment of bone diseases. Sequences ABK22776-ABK21411 represent contact.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                  lipid-associated condition; arteriosclerosis; cardiovascular disease; 88; osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up; neurovascular condition; wound healing; gene therapy; PCR primer; probe; bone development disorder; antiarteriosclerotic; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      molecules encoding human Zmaxi and HBM, and PCR primers, probes, linkers and adapters of the invention
                                                                    mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying molecules involved in lipid regulation, useful for diagnosing, treating or preventing e.g., arteriosclerosis, comprises identifying a molecule that binds to high bone mass gene or its corresponding wild type gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human RecQ protein-like 4 (RECQL4) DNA antisense oligonucleotide #48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnson
Zmax1 cDNA reverse PCR primer #122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 39; 409pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               882 AAAAGTGTGGCCCACAGAC 900
                                                                                                                                                                                                                                                      osteopathic; cerebroprotective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATATTGTGGCCCACACAC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-097784/13.
                                                                                                                                                                                                                                                                                                                                                                                              WO200192891-A2.
                                                                                                                                                                                                                                                                                                                              Ното варіепв.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carulli JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-2001
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   Human
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                                                                                                                                                                                                                                                                                                                 New antisense compounds targeted to nucleic acids encoding RecQ protein-
like 4, useful for modulating expression of the nucleic acid and treating
diseases associated with expression of the nucleic acid in humans.
                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a compound targeted to specific nucleobases of RecQ protein-like 4 (RECQL4) and which hybridises and inhibits the expression of RECQL4. The compound is useful for inhibiting the expression of RECQL4 in cells or tissues and for treating an animal, particularly a human suspected of having or being prone to a disease or condition associated with expression of RECQL4. The compound is useful for disgnostics, therapeutics and as a research reagent, e.g. prophylactically to prevent or delay infection, inflammation or tumour formation. This sequence represents an antisense oligonucleotide used in
Human; RecQ protein-like 4; RECQL4; ss; chromosome 8q24; infection; inflammation; tumour formation; cancer; cytostatic; antiinflammatory; antimicrobial; antisense therapy; antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.2; DB 1; Length 20;
Pred. No. 1.8e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 2 A; 8 C; 8 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inhibition of human RECQL4 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGCAGGCTGCCCGTCACG 19
                                                                                                                                                                                                                                                                                                                                                                                    Claim 14; Col 45; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 GGGCAGGCTGCCCGGGCCG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.3%;
illarity 84.2%;
Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAY-2001; 2001US-00851520
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                                                                                                                                                             23-FEB-2001; 2001US-00792594.
                                                                                                                                                                                            23-FEB-2001; 2001US-00792594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD41640 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                            (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 16; Conservat
                                                                                                                                                                                                                                                                                       WPI; 2002-689941/74.
                                                                                                                                                                                                                                                           Watt AT;
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                                                                    Homo sapiens
                                                                                                  US6436706-B1
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                                                                                                                                 20-AUG-2002
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Matches
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The present invention relates to novel antisense oligonucleotides which specifically hybridise with specific regions of nucleic acids encoding interleukin-12 (II-12) p35 subunit and inhibit the expression of human IL-12 p35 subunit and inhibit the expression of human IL-12 p35 subunit in human cells or tissues and for treating animals, particularly humans suspected of having or being prone to diseases or conditions associated with expression of IL-12 p35 subunit. They are useful for diagnostics, therapeutics and as research reagent, e.g. prophylactically to prevent or delay infection, tumour formation or inflammation. Sequences of the invention are useful for antisense therapy. The present DNA sequence is a PCR primer which is used for amplifying human IL-12 p35 subunit DNA. This sequence is used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Preparing lipopeptide synthetases, useful for producing new combinations of lipid molecules and amino acid modules, comprises modifying the lipid moiety and optionally a peptide moiety of one or more known (lipo) peptide
                                                                     Novel antisense compounds targeted to nucleic acids encoding interleukin-12 p35 subunit, useful for modulating interleukin-12 p35 subunit expression and treating diseases associated with expression of the subunit in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lipopeptide synthetase; multifunctional enzyme; lipid module; peptide module; DNA libzary; lipopeptide synthesis; antimicrobial; solid surface; immobilisation; ss.
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84.2%; Pred. No. 1.8e+02;
.ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 6 A; 8 C; 4 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                            Example 13; Col 53; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                822 GCCTCTCATGACCCAGGAA 840
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             Freier SM;
                                             WPI; 2002-535980/57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
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             Baker BF,
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Matches
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ABX10661
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                            The invention relates to a method of preparing novel lipopeptide synthetases by modifying the lipid module and optionally the peptide synthetases. The method involves providing a range of DNA fragments encoding lipopeptide synthetases. The method involves providing a range of DNA fragments encoding lipopeptide synthetase encoding lipopeptide synthetase non-palindromaic sticky ends; selecting and ligating at least two of these DNA fragments, at least one of which is specific for the lipid moiety of the lipopeptide synthetase encoding DNA molecule; introducing the lipopeptide synthetase-encoding DNA molecule; call; and expressing the DNA molecule in the host cell. The invention of cell; and expressing the DNA molecule in the host cell. The invention of cell; and method for non-ribosomal preparation of novel peptides synthetases constants and method for non-ribosomal preparation of novel peptides using the novel lipopeptide synthetases of the invention have a lipid constant and peptide module configuration that does not exist in nature, and the DNA library is useful in the production of a range of lipopeptide synthetases. The lipopeptide synthetases of the invention are useful for producing very large numbers of novel lipopeptides, which differ from existing lipopeptides in their fatty acid composition and optionally their amino acid composition. Such lipopeptides, which differ from existing lipopeptides in their fatty acid composition and optionally their and/or activities compared to known lipopeptides, which differ from existing lapopetides in their fatty acid composition and optionally their and/or activities compared to known lipopeptides may have novel structures and/or activities compared to known lipopeptides may have novel structures and/or activities compared to known lipopeptides may have novel structures cand/or activities compared to known lipopeptides sunder to permit the assembly of lipopeptide synthetase modules of containing an Sfil sticky and an Sfil sticky and an Sfil sticky and an Sfil sticky a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    form an Sfil sticky end which facilitates ligatinucleic acid also containing an Sfil sticky end.
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(BRHO-) BRITISH HORSERACING BOARD.
Example 6; Page 46; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multiplex group PCR primer #179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 GGGCAGGCTGCCCGGGCCG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABT21432 standard; DNA; 20 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAY-2001; 2001GB-00011886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-APR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-129314/12.
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                                                                                                                                                 The invention relates to a novel method for determining racing potential of a horse. The method comprises measuring: whether grandpaternal DNA is over-represented in the genome of the horse; or in the case where one of the grandmothers was selected for breeding on the basis of racing performance, whether grandmaternal DNA from the selected grandmother is over-represented in the genome of the horse which indicates that the horse has good racing potential. The method of the invention is useful for determining the racing potential. The method of the invention is useful for determining the racing potential of a horse or for obtaining a progeny horse with good racing potential. This polynucleotide sequence represents a PCR primer used in the detection method of over-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying antibiotic tolerant bacteria, especially antibiotic tolerant Streptococcus pneumoniae, by determining whether the bacteria has type 4 or R6 allele of vex2 and pep27 gene.
Determining the racing potential of a horse comprises measuring whether grandpaternal or grandmaternal DNA from the selected grandmother DNA is over-represented in the genome of the horse.
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antibiotic tolerance; type 4 allele; R6 allele; pep27; penicillin;
vancomycin; vex/pep27/vncr/s operon; pneumococcus; autolytic enzyme;
LytA; signal peptide; VncS; VncR; beta-lactam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reverse PCR primer amplifying vncS SNP containing gene fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02;
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                                                                                                         Example 2; Page 24; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 GGATTTCCTGTTATTCTTG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; Page 4; 11pp; English.
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Matches 16; Conservative
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amplify the regions of the vex2 and pep27 genes which contain the single nucleotide polymorphisms (SNPs). The genes are located within the vex/pep27/vncr/s operon encoding the major pneumocoocal autolyric enzyme, byth. The operon encodes for a signal peptide, Pep27 that is transported out of the cell via the vex dedicated transporter. Once it reaches a critical density in the supernatant, it signals through the two-component regulatory system, vncS and vncR, which subsequently induces activation of LytA. Mutations in any one of the operon genes prevents proper signaling, resulting in a lack of LytA activation and antibiotic signaling, resulting in a lack of LytA activation and antibiotic signaling whether a bacteria is colerance. The method is useful for determining whether a percent signaling and vancomycin and, therefore, for determining whether a subject suffering from a bacterial infection can be effectively treated with those antibiotics. The method is rapid and correctly predicts whether a subject can be successfully treated with a particular antibiotics can be succided as or that alternative therapies can be administered without delay. The sequence presented is the reverse pcR primer which was used to amplify the S. pneumoniae vncS SNP containing
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Best Local Si
Matches 16;
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Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation; gene therapy; bone density modulation; bone strength; trabecular number; bone size; bone tissue connectivity; bone disease; osteoporosis; PCR; osteomalacia; rickets; Paget's disease; neoplasm of the bone; primer; ss.
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                                                                                                                                                                                                                                                                                  Human HBM STS marker reverse primer #122.
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17-MAY-2001; 2001US-0291311P.
01-FEB-2002; 2002US-035958P.
04-MAR-2002; 2002US-0361293P.
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Disclosure, Page 56; 603pp; English.

The invention relates to novel transgenic animals expressing the high commass (HBM) gene, expressing the corresponding wild type HBM gene, comprising an alteration of the gene encoding LRPS or LRPG, or expressing an LRPS that is modulated by an altered gene control sequence introduced by homologous or non-homologous recombination. The transgenic animals are for the study of bone density modulation or bone mass modulation. The invention has osteopathic and cytostatic activity. The polymucleotides of the invention may have a use in gene therapy. The transgenic animals and concleic acids are for the study of bone density modulation, where the nucleic acids are for the study of bone density modulation, where the concleic acids are selected from bone density, bone strength, trabecular number, bone size, or bone tissue connectivity. The transgenic animals moduled and methods are useful for identifying molecules involved in bone development, and for developing pharmaceutical compositions, which may be employed for treating or preventing bone diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or neoplasms of the bone. The transgenic animals and nucleic acids are also useful in methods for diagnosing diseases involved in bone development, or characterised by reduced bone density or mass. The present sequence is useful in the exemplification of the invention 0 ABZ80408 to ABZ80418 encode the human proteins ABP96551 to ABP96561 which have cancer inhibiting functions. Also described is a method for preparing the proteins using recombination techniques. The human proteins from the present invention, and nucleotide sequences encoding them, can be used for treating diseases such as cancer. The present sequence represents a PCR primer for a human cancer inhibiting function related protein from the present invention Human protein that suppresses cancer cell growth and its coding sequence. Gaps Human; cancer; cancer suppression; cancer inhibitor; PCR primer; ss. ; 0 1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02; rative 0; Mismatches 3; Indels Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other; Example 2; Page 10 (Disclosure); 36pp; Chinese. Human protein PP13671 PCR primer #2. 882 AAAAGTGTGGCCCACAGAC 900 AATATTGTGGCCCACACAC 1 (SHAN-) SHANGHAI INST ONCOLOGY ABZ80435 standard; DNA; 20 BP 08-FEB-2001; 2001CN-00105310. 08-FEB-2001; 2001CN-00105310. 28-MAY-2003 (first entry) 16; Conservative WPI; 2003-112778/11. Local Similarity Homo sapiens. 11-SEP-2002. CN1368509-A. ABZ80435; 13 Query Match Matches RESULT 295 Gu J; ABZ80435 8 셤

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a new pharmaceutical composition comprising: (a) an oligonucleotide sequence having up to 50 base pairs (bp); and (b) carboplatin and paclitearl, cisplatin and gencitabine, 5-fluorouracil and leucovorin, or docetaxel. The pharmaceutical composition is useful for treating diseases associated with protein kinase C such as hyperproliferative and inflammacory conditions e.g. psoriasis, tumours and cancer e.g. non-small cell lung cancer, non-Hodgkin's lymphoma, glioblastoma, bladder cancer, lung cancer, colon cancer, breast cancer, ovarian cancer and pancreatic cancer. The present sequence represents an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammation; psoriasis; cancer; non-small cell lung cancer; lung cancer; non-Hodgkin's lymphoma; glioblastoma; bladder cancer; colon cancer; breast cancer; ovarian cancer; pancreatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ss; antisense; PKC; protein kinase C; hyperproliferation; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New pharmaceutical composition, useful for treating cancer, e.g., non-small cell lung cancer or non-Hodgkin's lymphoma.
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protein kinase C-epsilon targeted oligonucleotide ISIS#7941.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antisense oligonucleotide targeted against protein kinase C
                                                      1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02; ative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3%; Score 14.2; DB 1; Length 20;
84.2%; Pred. No. 1.8e+02;
iive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Holmlund JT, Dorr FA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 16; Col 22; 56pp; English.
                                                                                                                                                                                 819 CAGGCCTCTCATGACCCAG 837
                                                                                                                                                                                                                                           1 casscrrcrcrrcacscas 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-00089996.
95US-00478178.
97US-00829637.
                                                                                                                                                                                                                                                                                                                                                                                                  ACH11218 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2001; 2001US-00025139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                    16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dean NM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-531084/50.
                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6537973-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JUL-1993;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bennett CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACH11218;
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                                                                                                                       Matches
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The invention relates to a method of inhibiting growth of a microsatellite instability (MSI)-positive tumour, which involves introducing into the tumour a nucleic acid molecule encoding a retinoblastoma protein-interacting zinc finger gene (RIZ)-1 polypeptide and expressing the polypeptide in the tumour in an effective amount to inhibit growth of the tumour. The method is useful for inhibiting growth of a microsatellite instability (MSI)-positive tumour. The tumour contains cells having an abnormal number of adenosine nuclectides in a RIZ poly(A) tract. The MSI-positive tumour is colorectal tumour, gastric tumour, endometrial tumour or hereditary nonpolyposis colon carcinoma. Also disclosed is a method for determining MSI status of the tumour. Both methods are are useful for detecting and treating MSI(+) tumours and for inducing apoptotic cell killing both in vitro and in vivo. The present sequence represents the RIZ(A) & tract primer RIZA8-F
                                                                                                                                                                                                                                                                                                                                               RIZ1; microsatellite instability; tumour; apoptosis; ss; PCR; primer; retinoblastoma protein interacting zinc finger gene; colorectal tumour; endometrial tumour; hereditary nonpolyposis colon carcinoma; MSI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting growth of microsatellite instability-positive tumor, by introducing a nucleic acid molecule encoding a retinoblastoma protein-interacting zinc finger gene-1 polypeptide into the tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
ACA62693/C

ACA62693;

ACA62693;

XX

ACA62693;

XX

CO-AUG-2003 (first entry)

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XX

XX

XX

XX

RIZ1; microsatellite instability,

XX

RIZ1; microsatellite instability,

XX

RIZ1; microsatellite instability,

XX

Homo sapiens.

YX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             966 AGGACATTTTGATGAGATC 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 Accacarrrrscreascre 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-2003 (first entry)
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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ID ABT4.

XX ABT4.

XX OF 06-NC

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Gaps

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434 AGAGGAGATGATTTTAGCT 452

16; Conservative

Matches

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Local Similarity

19 AGAGAAGAGGATTTTGGCT 1

RESULT 297

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This invention relates to novel chimeric antisense oligonucleotides that specifically hybridise to and inhibit the expression of the nucleotide binding oligonucleotide domain 1, NOD1 protein. NOD1, also known as CARD4 (caspase associated recruitment domain 4) is a domain that is involved in the elimination of cells via programmed cell death and in the host defence against pathogens, i.e. it works to regulate apoptosis. Apoptosis of a naturally occurring process, however, if it becomes overstimulated it can lead to cell loss and neurodegenerative conditions including cli can lead to cell loss and neurodegenerative conditions including programments and blood cell disorders. Conversely, insufficient apoptosis con contribute to the development of cancer, autoimmune disorders and contribute to the development of cancer, autoimmune disorders and contribute to the development of cancer, autoimmune disorders and coligonucleotides that can modulate NOD1 expression and variants there can modulate NOD1 expression fand variants cheat various human diseases caused by aberrant apoptosis. This oligonucleotide sequence is the chimeric antisense oligo used to inhibit expression of human NOD1, the aim of the invention. Note that it has two certain and its procession of human NOD1, the aim of the invention. Note that it has two certain and procession of human NOD1, the aim of the invention. Note that it has two certain and procession of human NoD1, the alm of the invention is phosphorothicate the chimerical procession of the oligonucleotide backbone is phosphorothicate.
Antisense; nucleotide binding oligonucleotide domain 1; gene therapy; ss; caspase associated recruitment domain 4; programmed cell death; cancer; apoptosis; Alzheimer's; neurodegenerative; Parkinson's; ALS; NOD1; CARD4; amyotrophic lateral selerosis; retinitis pigmentosa; autoimmune disorder; viral infection; human; chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New compound, comprising a sequence targeted to a nucleic acid encoding nucleotide-binding oligomerization domain 1 (NOD1), useful for preparing a composition for treating hyperproliferative disease, e.g., cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence tagged site #244 used to prepare Zmax1 (LRP5) gene region map.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Osteopathic, Gene therapy; High Bone Mass; HBM; LRP5; Zmax1; LRP6; bone mass modulation; osteoporosis; STS; sequence tagged site; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 15; Page 76; 138pp; English.
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                                                                                                                                                                                                                                                                                                                            05-DEC-2001; 2001US-00006883.
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                                                                                                                                              Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                       (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                    Dobie KW, Roach MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-577293/54.
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The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and LRP6 mutants, which results in a HBM-like phenotype when expressed in a cell. The HBM-like phenotype results in bone mass modulation and/or lipid level modulation. The invention is useful for diagnoshing a HBM-like phenotype in a subject and for preparing a composition for modulating bone mass and/or lipid levels in a subject suffering from e.g. osteoporosis. The present sequence is a Sequence Tagged Site (STS) marker, which was used to prepare a physical map of the Zmax1 (LRPS) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single nucleotide polymorphism; SNP; fish; Salmo salar;
Orechromis niloticus; Atlantic halibut; microsatellite; cod;
polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid comprising a mutation in LRP5 or LRP6, useful for diagnosing a HBM-like phenotype in a subject and for preparing a composition for modulating bone mass and/or lipid levels in a subject
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14.2; DB 1; Length 20;
Pred. No. 1.8e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Morales A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Graham JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 62; 629pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      suffering from e.g. osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                     (GENO-) GENOME THERAPEUTICS CORP. (AMHP ) WYETH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 AATATTGTGGCCCACACAC 1
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                                                                                                                                                                                                                                 11-MAY-2001; 2001US-0290071P.
17-MAY-2001; 2001US-0291311P.
01-FEB-2002; 2002US-0353058P.
04-MAR-2002; 2002US-0361293P.
                                                                                                                                                                             13-MAY-2002; 2002WO-US014877
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hes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Allen K, Anisowicz A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oreochromis niloticus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-129214/12.
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                                                         WO200292000-A2
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUL-2003
                                                                                                                21-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADD20426;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 300
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Page 147

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The present invention describes an isolated nucleic acid (I) comprising a single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of salmo salar SNPs, Orecohromis niloticus SNPs or Atlantic halibut SNPs; and (ii) a nucleic acid having nuclectide sequence that hybridises to cand it is nucleic acid having nuclectide sequence that hybridises to comprisions to its complement under highly stringent hybridisation conditions. The described: (i) an isolated oligonucleotide (II) comprising at least of an ucleotide sequence of S. salar SNPs, O. niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod polymorphic sites and seabass polymorphic sites, or their complement; (2) a primer pair (III) suitable for use in PCR, comprising two (II) capable of amplifying a nucleotide sequence chosen from S. salar SNPs and, O. colloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod polymorphic sites and seabass polymorphic sites; and determining (MI) the comprising a parentage genotype database comprising providing a parentage genotype database comprising a parentage genotype to the parentage genotypes; where each of the sample genotype to the parentage genotype database, where a match between the sample genotype and one of the candidate parent genotype identifies configuration of the sample senotype and one of the candidate parent genotype identifies a fish sample such as family salmonidae, S. salar, Tilapia, O. niloticus, rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for carinbow trout, halibut, seabass and Atlantic cod. (II) is useful for candidate parent genotype contacting the sample containing nucleic acid that hybridises to salar SNPs and identifying nucleic acid that hybridises to salar SNPs and identifying nucleic acid that hybridises to salar sNPs and identifying a parentage genoted to salar sNPs and of the sample solar acid that hybridises to salar sNPs and identifying the sample acid molecule configuration acid that hybridises to salar sNPs and identifying t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic sites is seabass polymorphic sites, and identifying a nucleic acid that hybridises to (II). (III) is useful for detecting nucleic acid molecule comprising a microsatellite sequence in sample. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for detecting nucleic acid molecule comprising a polymorphic sequence in a sample, comprising contacting the sample containing nucleic acids with one or more (II) which is derived from O. niloticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule comprising single nucleotide polymorphism associated with fish, useful for forming PCR primers which are used for detecting single nucleotide polymorphisms in fish nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 18; SEQ ID NO 1061; 233pp; English.
                                                                                                                                                                                                                                                         Lingaas
                                                                                                                                                                                                                                                         Hoyum M,
16-AUG-2002; 2002US-0404200P
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-627388/59.
                                                                                                                            (GENO-) GENOMAR ASA
                                                                                                                                                                                                                                                   Slettan A,
                                                                                                                                                                                                                                                         Lie O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acids.
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Gaps ö 1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02; 3; Indels 0; Mismatches 782 CTTGGGGATGTGCTTGGAG 800 CTTGGGTTTGAGCTTGGAG 20 Conservative Similarity 16; N Query Match Best Local S Matches 셤 ઠ

ADD90778 standard; DNA; 20 ADD90778; RESULT 301 ADD90778 0×2×6×6×6×2××

BP

S. pneumoniae vncS gene PCR primer #2.

(first entry)

29-JAN-2004

Determining predisposition to inverted nipples useful e.g. for selecting breeding animals comprises detecting specific microsatellite markers.

(FOER-) FOERDERVEREIN BIOTECHNOLOGIEFORSCHUNG DE

03-FEB-2003; 2003WO-EP001045. 05-FEB-2002; 2002EP-00002632

WO2003066891-A2

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14-AUG-2003

Wimmers K;

Hardge T, Schellander K,

WPI; 2003-671539/63.

The present invention relates to the use of a nucleic acid to determine

Disclosure; Page 24; 63pp; German.

88; PCR; primer; antibiotic; antibiotic tolerance; bacterial resistance; beta-lactam; penicillin; vancomycin; vncS.

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Determining whether a bacteria is likely to be tolerant to beta-lactam, penicillin or vancomycin by determining the genotype of the vex2 and
                                                                                                                                                                                                                                              The invention relates to a method of determining whether a bacteria is likely to be tolerant to antibiotics. The methods are used for determining bacterial resistance to beta-lactam, penicilini and/or vancomycin. The present sequence represents the S. pneumoniae vncS PCR
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalian inverted nipple associated microsatellite PCR primer #144.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inverted nipple; microsatellite; PCR; primer; ss; pig
                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 4 A; 5 C; 1 G; 10 T; 0 U; 0 Other;
                                                                                                            (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
                                                                                                                                                                                                                         Claim 16; SEQ ID NO 12; 11pp; English
                                                                                                                                                                                                                                                                                                                                                                                    507
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                                                                02-MAY-2003; 2003US-00428617.
                                                                                                                                                                                                                                                                                                                                                                                    489 ATTGAATTTCTTAGAACTC
                                                                                     13-NOV-2001; 2001US-00054225
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACH00690 standard; DNA; 20
                                                                                                                                 Atkinson RM, Tuomanen EI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
Streptococcus pneumoniae.
                                                                                                                                                       WPI; 2003-852128/79.
                     US2003175796-A1
                                                                                                                                                                                                    pep27 genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-FEB-2004
                                           18-SEP-2003
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                                                                                                                                                                                                                                                                                             primer
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where the nucleic acid is identical to the region of microsatalites \$80200, \$87443, \$50097, \$80007, \$811301 or \$50164 on chromosomes 6, 2, 4, 14, 1 and 3, respectively, in pigs, or homologous positions in the genomes of other mammals. The nucleic acids can be used to select pets, breeding or farm animals that lack inverted nipples, particularly by genomic arcenting of many related mammals in a population. The present sequence is a PCR primer used in the exemplification of the invention to identify microsatellite markers associated with the inverted nipple phenotype predisposition of appearance or inheritance of inverted nipples, 88888888888888

Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Gaps ö 1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02; ive 0; Mismatches 3; Indels Query Match
Best Local Similarity 84.2
Matches 16; Conservative

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406 AATTCAAGGGTTTTTCCTT 424 Н 19 AACTCAAGGGGTTTGCCTT à 셤

RESULT 303

ABZ91305 standard; DNA; 20 ABZ91305/ 

BP.

17-OCT-2003 (first entry)

ABZ91305;

Human oligonucleotide sequence.

Human, antisense; lung dysfunction, nasal airway dysfunction, antinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antisathmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo

WO200285308-A2.

31-OCT-2002

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P

(EPIG-) EPIGENESIS PHARM INC

Aguilar D; Pabalan J, Katz E, Shahabuddin Li Y, Sandrasagra A, Tang L, Shahabuddin Miller S, Nyce JW.

WPI; 2003-229219/22.

Pharmaceutical composition for treating allments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone

Disclosure; SEQ ID NO 6547; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5 or 3 end genomic flanking regions, 5 and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or masal airway dysfunction and a second active agent comprising an antinflammatory steroid and ubiquinone. A composition of the invention has antinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also

antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO enhancing the prophylactic or therapeutic respiratory effect at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 20 BP; 5 A; 6 C; 2 G; 7 T; 0 U; 0 Other; 88888888888

Gaps ö Score 14.2; DB 1; Length 20; Pred. No. 1.8e+02; 0; Mismatches 3; Indels 0 1.3%; Local Similarity 84.2 nes 16; Conservative Query Match Matches

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TTGGAAGAGGAGATGATTT 447 rrescanassasarcacrr 2 429 20 ð 셤

RESULT 304 ABZ9931E

ABZ99318 standard; DNA; 20

ABZ99318;

17-OCT-2003 (first entry)

Human PDE4C oligonucleotide sequence.

Human; antisense; lung dysfunction, nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; fumunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

EPIG-) EPIGENESIS PHARM INC

ä Aguilar Pabalan J, Katz E, Li Y, Sandrasagra A, Tang L, Shahabuddin Nyce JW, 1 Miller S,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone 

Disclosure; SEQ ID NO 14560; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5 or 3 end genomic flanking regions, 5 and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or ansal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, impropersity, antiallergic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also

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for enhancing the prophylactic or therapeutic respiratory effect of an antinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
      88888888888
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Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other;

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                           Gaps
                          ;
Score 14.2; DB 1; Length 20;
Pred. No. 1.8e+02;
0; Mismatches 3; Indels
 1.3%;
                          16; Conservative
             Best Local Similarity
Matches 16; Conserv
  Query Match
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191 TTCCACGCCATCTCCCCCA 209
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8
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Human oligonucleotide sequence. ABZ88740 standard; DNA; 20 (first entry) 17-0CT-2003 ABZ88740; 

ВР

Human; antisense; lung dysfunction; nasal airway dysfunction; antinflammatory steroid; ubiquinone; antinflammatory; antiallergic; antiathmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

WO200285308-A2 Homo sapiens.

31-OCT-2002

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Aquilar Katz E, Pabalan J, ŝ Sandrasagra A, Li Y, Sar Tang L, Nyce JW, Miller S,

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WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 3982; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonuclectide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or ansal alraway dystunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also

The present invention describes a new isolated nucleic acid sequence (I) comprising a DPP10 mRNA sequence. DPP10 is a dipeptidyl peptidase (also known as prolyloligopeptidase). (I) has antinflammatory, antiasthmatic, antiasthmatic, antiasthmatic, antiastrhritic and antirheumatic activities, and can be used in vaccines and gene therapy. A composition comprising (I) can be used for the manufacture of a medicament for regulating DPP10 expression or for preventing or treating inflammatory disease e.g., inflammatory bowel disease, asthma, atopy, rheumatoid arthritis or psoriasis. (I) can also be used in an assay for detecting or measuring DPP10 in a sample. A

Claim 43; Page 313; 321pp; English.

disease

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for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid sequence comprising DPP10 mRNA, useful for the manufacture of a medicament for regulating DPP10 protein expression or for preventing or treating inflammatory disease e.g., inflammatory bowel
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPP10; dipeptidyl peptidase; prolyloligopeptidase; enzyme; asthma; antiinflammatory; antiathmatic; antiathmaticy; antiaththitic; antitheumatic; vaccine; gene therapy; inflammatory disease; inflammatory bowel disease; atopy; rheumatoid arthritis; psoriasis;
                                                                                                                                                                                                                   ö
                                                                                                                                                                                   1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                       Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                 540 TTTACTATGAAATTTAATA 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome 2q14; PCR primer; ss.
                                                                                                                                                                                                                                                                   20 TTCACCATGACATTTAATA 2
                                                                                                                                                                                                                                                                                                                                                         BP
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12-OCT-2001; 2001GB-00024575.
12-OCT-2001; 2001GB-00024594.
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                                                                                                                                                                                                                                                                                                                                                         ABQ84375 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moffat MF,
                                                                                                                                                                                                                                                                                                                                                                                                                    20-FEB-2003 (first entry)
                                                                                                                                                                                  Query Match
Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPP10 PCR primer #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-093132/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens.
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                                                                                                                                                                                                                                                                                                                              RESULT 306
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host cell comprising (I) can be used for producing recombinant DPP10 gene products, or in drug screening systems to identify agents for diagnosis or treatment of individuals having or susceptible to inflammatory disease. Human DPP10 is located on chromosome 2, more specifically chromosome 2914. ABQ84254 to ABQ84612 and ABP5569 to ABP5569 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with the
                                                                                                                                                                                                                                                                                                                                                                                                          Human, stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl; 2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic; antiliflammatory; antisense therapy; antisense oligonucleotide; tumour; abnormal lipid metabolism; abnormal cholesterol metabolism; infection; atherosclerosis; cardiovascular disease; inflammation; inhibition; se;
                                                                                                                                                                                                                                                                                                                                                                                   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:73.
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense oligonucleotides targeted to nucleic acids encoding stearcyl-COA desaturase, useful for treating diseases associated wesaturase, e.g. atherosclerosis, and in diagnostic and research
                                                                                                                                                               ;
0
                                                                                                                            1.3%; Score 14.2; DB 1; Length 20;
ilarity 84.2%; Pred. No. 1.8e+02;
Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gapmer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mod_base= OTHER
/note= "2'-O-methoxyethyl (2'-MOE) gapmer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "phosphorothioate linkages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "2'-O-methoxyethyl (2'-MOE)
                                                                                                     Sequence 20 BP; 8 A; 4 C; 3 G; 5 T; 0 U; 0 Other
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1. .20
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 95; 117pp; English.
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/note= "2'-0-met
                                                                                                                                                                                           472 TATTCTGATTACAGTGCAT 490
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                                                                                                                                                                                                                                                                                                ABZ77118 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-248160/24.
                                                                                                                                              Local Similarity
es 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                           ABZ77118;
                                                                                                                                  Query Match
                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                   RESULT 307
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The present invention describes a compound (I) that is 8-50 nucleobases

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in length targeted to a nucleic acid molecule encoding human stearoyl-CoA desaturase, and which specifically hybridises with and inhibits the expression of human stearoyl-CoA desaturase, or which specifically convicts a specifically hybridises with at least an 8-nucleobase portion of an active site on another acid molecule encoding human stearoyl-CoA desaturase. Human cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory activities, and can be used in antisense therapy. The antisense compounds (1) can be used for modulating the expression of human stearoyl-CoA desaturase and for treating diseases or conditions associated with expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The antisense compounds (1) can also be used for diagnostics, therapeutics and prophylaxis, e.g. to prevent or cally infection, inflammation or tumour formation, as research reagents and kits, and in distinguishing between functions of various members of a biological pathway. The present sequence represents a human stearoyl-CoA desaturase inhibiting chimeric phosphorothioate antisense oligonucleotide, which is given in an example component in the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (I) is useful for producing antidotes. Also disclosed are a recombinant vector containing the coding sequence for (I); a transformant transformed by the recombinant vector; and a method for preparing cytochrome P450, comprising culturing the transformant and recovering cytochrome P450 from the culture. The present sequence is a PCR primer, which was used in an example from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a novel cytochrome P450 (see ABP70653)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A new polypeptide with cytochrome P450 activity useful for producing antidotes.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14.2; DB 1;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytochrome P450; antidote; PCR; primer; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAAGCAGGCCTCTCATGA 832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABV99953 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (WARI/) WARIISHI H.
(KUBI ) KUBOTA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coriolus versicolor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-096531/09
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
hes 16; Conserv
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Matches
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The invention describes a method of diagnosing a cellular proliferative disorder of breast tissue in a subject comprising determining the state of methylation of one or more nucleic acid isolated from the subject, where the state of methylation of one or more nucleic acids is compared with the state of methylation of one or more nucleic acids from a subject on having the cellular proliferative disorder of breast tissue. Also proliferative disorder of breast tissue, and a captular proliferative disorder of breast tissue in a subject; and a kit for the detecting a cellular proliferative disorder of breast tissue in a cellular proliferative disorder of breast tissue in a cellular proliferative disorder of breast tissue in a subject. The method is useful for diagnosing a cellular proliferative disorder of breast tissue in a subject. The method is useful for diagnosing a cellular proliferative disorder of breast tissue in a subject. The method is useful for diagnosing a cellular proliferative disorder of breast tissue in a subject. The method is useful for diagnosing a cellular proliferative disorder of breast tissue in a subject. The method is useful for diagnosing a cellular proliferative disorder of breast tissue in a subject. The method is useful for diagnosing a cellular proliferative disorder of breast tissue in a subject for primer used in the analysis of the methylation state of the serine protease NES-1 gene CpG islands in normal mammary epithelium, breast cancer cell lines and in
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                                                                                                                                                                                                                                                                                                                                                                                                     cellular proliferative disorder; breast cancer; methylation; predisposition; methylation specific PCR; PCR; primer; CpG island; ss; human; serine protease-like protease; NES-1.
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                                                Gaps
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1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02; ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                 Serine protease-like protease NES-1 primer #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; SEQ ID NO 79; 59pp; English.
                                                                                    952 CCCACTCTGGACCCAGGAC 970
                                                                                                                CCCACCACGACCCAGGAC 20
                                                                                                                                                                                                                                     ADM83692 standard; DNA; 20 BP
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                                                                                                                                                                                                                                                                                                                       (first entry)
                 Best Local Similarity 84.2
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUKUMAR S.
EVRON E.
DOOLEY W C.
SACCHI N.
DAVIDSON N.
FACKLER M J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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    Query Match
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(DOOL/)
(SACC/)
(DAVI/)
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                                                                                                                                                                                         RESULT 309
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disorder of breast tissue in a subject comprising determining the state of methylation of one or more nucleic acid isolated from the subject, where the state of methylation of one or more nucleic acids is compared with the state of methylation of one or more nucleic acids from a subject not having the cellular proliferative disorder of breast tissue. Also described are: a method for determining a predisposition to a cellular proliferative disorder of breast tissue in a subject; and a kit for the detecting a cellular proliferative disorder of breast tissue in a subject; and a kit for the detecting a cellular proliferative disorder of breast tissue in a subject. The method is useful for diagnosing a cellular proliferative disorder of breast tissue in a subject. This sequence represents a methylation specific primer used in the analysis of the methylation state of the servine protease NES-1 gene Ogislands in normal mammary epithelium, breast cancer cell lines and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a method of diagnosing a cellular proliferative
                                                                                                                                                                                                                                                            cellular proliferative disorder; breast cancer; methylation; predisposition; methylation specific PCR; PCR; primer; CpG island; ss; human; serine protease-like protease; NES-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing a cellular proliferative disorder of breast tissue in a subject comprises determining the state of methylation of one or more nucleic acid isolated from the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sacchi N, Davidson N, Fackler MJ;
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84.2%; Pred. No. 1.8e+02;
ative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 3 A; 3 C; 5 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                              Serine protease-like protease NES-1 primer #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 158; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dooley WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 TTAGAGGATTATGGCGTTT 167
149 TTAGAGGATTATGGCGTTT 167
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                                  Trcgaagrtrarggcgrrr 19
                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JAN-2002; 2002US-00059579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JAN-2001; 2001US-00771357
                                                                                                                       ADM83766 standard; DNA; 20
                                                                                                                                                                                           03-JUN-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sukumar S, Evron E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOOLEY W C.
SACCHI N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-851722/79.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FACKLER M J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAVIDSON N.
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Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                      US2003138783-A1.
                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                          ADM83766;
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(SACC/)
(DAVI/)
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                                                                                                        ADM83766
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Gaps ;

1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02; ive 0; Mismatches 3; Indel8

Query Match 1.3 Best Local Similarity 84.2 Matches 16; Conservative

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The invention describes a novel composition, all at like active agent, comprising oligonucleotides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and bronchoconstriction, respiratory tract inflammation, allergies and creducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, creducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, congrated associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery of device, in separate containers, (b) the oligomucleotides, (c) restructions for adding a carrier and for use of the kit. The composition of the invention has antiallargic, antiinflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered containing or treating a respiratory, lung or malignant disease. The administered containing or reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung confidence the amount of target polypeptide present in the lungs. The chilammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory transplantation rejection, pulmonary infections, bronchitis or cancer transplantation rejection, pulmonary infections, bronchiting present in the target RNA serves to prevent the breakdown o
                                                                                                                                                                                                                                                                                                                                                                                          Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ss; primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Katz E, Pabalan J, Aguilar D;
                                                                                                                                                                                                                                                                                                         AA486238-derived oligonucleotide SEQ ID 6547.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sandrasagra A, Ka
i, Shahabuddin S;
ABD27535 standard; DNA; 20 BP.
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                                                                                                                                                                                                             (first entry)
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Tang L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200285309-A2.
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                                                                                                      ABD27535;
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This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating comprising oligonucleotides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, curfactant depletion or hyposecretion, when administered to a mammal. The cigonucleotides are derived from a gene encoding or regulating cyreaprassion of a target polypeptide associated with lung airway or lung dysfunction also describes a kit, that comprises: (a) a delivery of the invention also describes a kit, that comprises: (a) a delivery constructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antiinflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a confosition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to
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                                                                                                                                                                                                                                                                                                                                                                                                                         Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cycostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ss; primer.
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2
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pharmaceutical composition for treating asthma, has antisense oligonucleotide containing less percentage of adenosine, targeted trucleic acids associated with lung airway or lung dysfunction, and
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                                                                      Length 20;
                                                                                                           Indels
                                   Sequence 20 BP; 5 A; 6 C; 2 G; 7 T; 0 U; 0 Other;
                                                                    Score 14.2; DB 1;
Pred. No. 1.8e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                          All38216-derived oligonucleotide SEQ ID 3982.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 15; SEQ ID NO 3982; 763pp; English.
prevent any unwanted effects due to it
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                                                                          1.3%;
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                                                                                           84.2%;
                                                                                                                                                                                                                                                                                 ABD24970 standard; DNA; 20
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                                                                                                               Conservative
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                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200285309-A2.
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ö inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distresses syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ss; primer. comprising oligonucleotides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, This invention describes a novel composition (a) a first active agent, Gaps Pharmaceutical composition for treating asthma, has antisense oligonucleotide containing less percentage of adenosine, targeted trucleic acids associated with lung airway or lung dysfunction, and reduce the amount of target polypeptide present in the lungs. The Katz E, Pabalan J, Aguilar D; ö 1.3%; Score 14.2; DB 1; Length 20; 4.2%; Pred. No. 1.8e+02; ve 0; Mismatches 3; Indels Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 U; 0 Other; Human PDE4C-derived oligonucleotide SEQ ID 14560. 84.2%; Pred. No. -Claim 15; SEQ ID NO 14560; 763pp; English. Li Y, Sandrasagra A, Ka Tang L, Shahabuddin S; 540 TITACTATGAAATTTAATA 558 20 rrcaccardacarrraara 2 ABD32349 standard; DNA; 20 BP 23-APR-2002; 2002WO-US013143. 24-APR-2001; 2001US-0286036P. (EPIG-) EPIGENESIS PHARM INC. (first entry) 16; Conservative bronchodilating agent Query Match Best Local Similarity WPI; 2003-093058/08 WO200285309-A2 Homo sapiens. 29-JUL-2004 31-OCT-2002. Nyce JW, ] Miller S, ABD32349; RESULT 313 Matches ABD32349

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cutyonnotectures are certived from a gene encouring or regulating cyression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA.

The invention also describes a kit, that comprises: (a) a delivery device, in separate containers (b) the oligonuclectides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallargic, antiinflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to raduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or bronchoconstriction and/or lung distress or condition such as pulmonary vasoconstriction, and sease or conditions with a submanary disease, pulmonary contension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary impeded respiration, respiratory transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to the oligonucleotides into products that free adenosine into the system c., lung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it ö cytostatic; protein-kinase-inhibitor-C-alpha; gene therapy; carboplatin; paclitaxel; docetaxel; cisplatin; gemcitabine; 5-fluorouracil; leucovorin; procein kinase C alpha inhibitor; PKC-alpha inhibitor; cancer; non-small cell lung cancer; non-Hodgkin's lymphoma; antisense technology; ss; PKC-epsilon. Gaps oligonucleotides are derived from a gene encoding or regulating ö Protein kinase C epsilon antisense oligonucleotide seq id 86 1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02; Indels ٠. ص Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other; FA; Pred. No. 1.86 ); Mismatches Dorr Holmlund JT, · • 191 TICCACGCCATCTCCCCCA 209 rregaggicarcriciccica 19 92US-00852852. 93US-00089996. 95US-00478178. ВР 21-JAN-2003; 2003US-00348485 97US-00829637 2001US-00025139 ADH47993/c ID ADH47993 standard; DNA; 20 25-MAR-2004 (first entry) Local Similarity 84.2 (ISIS-) ISIS PHARM INC. Bennett CF, Dean NM, WPI; 2004-106519/11. US2003148989-A1 18-DEC-2001; 16-MAR-1992; 09-JUL-1993; 07-AUG-2003 31-MAR-1997 Synthetic. ADH47993; Query Match RESULT 314 Matches В ઠે

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                                                                                                                                                                                                                                                         The invention describes new pharmaceutical compositions comprising an oligonucleotide up to 50 nucleotide units in length of a sequence having 20 bp (dnal), in combination with any of the following: carboplatin and paclitaxel; docetaxel; cisplatin and gementable; or 5-fluorourali and leucovorin. Also described are: a method of inhibiting protein kinase C (PKC)-alpha expression in human cells by contacting the cells with any of the pharmaceutical compositions; and methods of treating a condition associated with expression of human PKC-alpha by administering to an animal, or its cells, tissues or bodily fluid any of the pharmaceutical compositions are useful for inhibiting PKC-alpha expression in human cells. The compositions are useful for treating a condition associated with the expression of human PKC-alpha, particularly cancer. In particular, the compositions are useful for treating an condition associated with the expression of human PKC-alpha, particularly cancer. In particular, the compositions are useful for treating on-small lung cancer or non-Hodgkin's lymphoma in a human. This sequence
New pharmaceutical compositions comprising oligonucleotide in combination with e.g. arboplatin or cisplatin, useful for inhibiting protein kinase C expression, particularly for treating cancer, e.g. non-Hodgkin's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises antisense oligonucleotides that are targeted to CDC-like kinase 1. The antisense oligonucleotides of the invention are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antisense oligomucleotide; CDC-like kinase 1; cancer; autoimmune disorder; infection; inflammation; tumour formation; human; ss; 2'-O-methoxyethyl gapmer; phosphorothioate backbone.
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Pred. No. 1.8e+02;
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                                                                                                                                                                                               SEQ ID NO 86; 52pp; English
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1.3%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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                                                                                                                                                                                                  Example 16;
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                                                                                                                        lymphoma.
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ö ö The invention comprises antisense oligonucleotides that are targeted to CDC-1ike kinase 1. The antisense oligonucleotides of the invention are useful for modulating the expression of CDC-1ike kinase 1, and for treating diseases or conditions associated with expression of CDC-like kinase 1 (e.g. cancers and autoimmune disorders). The antisense oligonucleotides may also be used to prevent or delay infection, inflammation and tumour formation. The present DNA sequence represents an antisense oligonucleotide of the invention that is targeted to human CDC-like kinase 1. NOTE: The present sequence is a 2'-0-methoxyethyl gapmer with a phosphorothioate backbone. treating diseases or conditions associated with expression of CDC-like kinase 1 (e.g. cancers and autoimmune disorders). The antisense oligonuclectides may also be used to prevent or delay infection, inflammation and tumour formation. The present DNA sequence represents an antisense oligonuclectide of the invention that is targeted to human CDC-like kinase 1. NOTE: The present sequence is a 2'-O-methoxyethyl gapmer with a phosphorothioate backbone. New antisense oligonucleotides targeted to nucleic acid molecules encoding CDC-like kinase 1, useful for treating diseases or conditions associated with expression of CDC-like kinase 1, e.g. cancers or antisense oligonucleotide; CDC-like kinase 1; cancer; autoimmune disorder; infection; inflammation; tumour formation; human; ss; 2'-O-methoxyethyl gapmer; phosphorothioate backbone. Gaps Gaps .. 0 .. Query Match
1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02; rative 0; Mismatches 3; Indels Human CDC-like kinase 1 antisense oligonucleotide #73. Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other; Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other; Claim 1; SEQ ID NO 86; 64pp; English. 220 CATTGCCAAAAGAGTCACC 238 22-MAY-2002; 2002US-00154708. 22-MAY-2002; 2002US-00154708 ADH58791 standard; DNA; 20 25-MAR-2004 (first entry) 16; Conservative (ISIS-) ISIS PHARM INC autoimmune disorders. WPI; 2004-051714/05. Query Match Best Local Similarity US2003219895-A1. Homo sapiens. 27-NOV-2003. ~ Watt AT; Matches ADH58791, 8888888888 ð 셤

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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                           New antisense compound targeted to a nucleic acid molecule encoding mammalian glucocorticoid receptor, useful for treating diabetes, obesity, cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the human glucocorticoid receptor gene. NOTE: The present sequence contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
                                                                                                                                                                        antisense oligonucleotide; glucocorticoid receptor; infection; inflammation; tumour formation; diabetes; obesity; cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss; phosphorothioate backbone; 2'-methoxyethyl; 2'-MOB.
                                                                                                                                                    Human glucocorticoid receptor-specific antisense oligonucleotide #1961.
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Pred. No. 1.8e+02;
0; Mismatches 3; Indels
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         CATTGCCAAAAGAGTCACC 238
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Best Local Similarity 84.2
Matches 16; Conservative
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                                                               RESULT 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense compound targeted to a nucleic acid molecule encoding mammalian glucocorticoid receptor, useful for treating diabetes, obesity, cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
antisense oligonucleotide; glucocorticoid receptor; infection; infalmalton; tumour formation; diabetes; obesity; cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss; phosphorothioate backbone; 2'-methoxyethy1; 2'-MOB.
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Best Local Similarity 84.2<sup>5</sup>
warches 16; Conservative
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to nucleic acids encoding a mammalian glucocorticoid receptor. The antienne coligonucleotides of the invention are useful for preventing or delaying infection, inflammation or tumour formation. The antisense oligonucleotides are also useful for treating diabetes, obesity, cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The present DNA sequence repersents an antisense oligonucleotide that targets the human glucocorticoid receptor gene. NOTE: The present sequence contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
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                                                                                                              New antisense compound targeted to a nucleic acid molecule encoding mammalian glucocorticoid receptor, useful for treating diabetes, obesity, cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
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Pred. No. 1.8e+02;
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Local Similarity 84.2%;
les 16; Conservative
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                                               Crosby SD, Nalseth AE
              (PHAA ) PHARMACIA CORP
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Matches
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The invention comprises an antisense oligonucleotides that are targeted to nucleic acids encoding a mammalian glucocorticoid receptor. The antisense oligonucleotides of the invention are useful for preventing or delaying infection, inflammation or tumour formation. The antisense oligonucleotides are also useful for treating diabetes, obesity, cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The present DNA sequence represents an antisense oligonucleotide that targets the human glucocorticoid receptor gene. NOTE: The present sequence contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
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antisense oligonucleotides of the invention are useful for preventing or delaying infection, inflammation or tumour formation. The antisense oligonucleotides are also useful for treating diabetes, obesity, cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The present DNA sequence represents an antisense oligonucleotide that targets the human glucocorticoid receptor gene. NOTE: The present sequence contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense compound targeted to a nucleic acid molecule encoding mammalian glucocorticoid receptor, useful for treating diabetes, obesity, cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antisense oligonucleotide; glucocorticoid receptor; infection; inflammation; tumour formation; diabetes; obesity; cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss; phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
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llarity 84.2%; Pred. No. 1.8e+02;
Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                       1.3%; Score 14.2; DB 1; Length 20;
84.2%; Pred. No. 1.8e+02;
tive 0; Mismatches 3; Indels
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                                                                                                                                                    Sequence 20 BP; 1 A; 12 C; 0 G; 7 T; 0 U; 0 Other;
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Best Local Similarity 84.2
Matches 16; Conservative
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Matches
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The invention comprises an antisense oligonucleotides that are targeted antisense oligonucleotides of the invention are useful for preventing or delaying infection, inflammation or unour formation. The antisense oligonucleotides are also useful for treating diabetes, obesity, cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The present DNA sequence represents an antisense oligonucleotide that targets the human glucocorticoid receptor gene. NOTE: The present sequence contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense compound targeted to a nucleic acid molecule encoding mammalian glucocorticoid receptor, useful for treating diabetes, obesity, cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
                                                                                                                                                                                                    Human glucocorticoid receptor-specific antisense oligonucleotide #1849.
                                                                                                                                                                                                                             antisense oligonucleotide; glucocorticoid receptor; infection; inflammation; tumour formation; diabetes; obesity; cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HMG-CoA reductase; 3-hydroxy-3-methylglutaryl-Coenzyme A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 1 A; 12 C; 0 G; 7 T; 0 U; 0 Other;
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CTCCATCTCCCTCTTCCCC 20
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Best Local Similarity 84.2
Watches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HMG-CoA reductase; 3-hydroxy-3-methylglutaryl-Coenzyme A;
HMG-CoA reductase; cardiant; antiarteriosclerotic; antilipaemic;
antisense gene.therapy; cardiovascular disorder; cholesterol metabolism;
HMG-CoA reductase; cardiant; antiarteriosclerotic; antilipaemic; antisense gene therapy; cardiovascular disorder; cholesterol metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel compounds of 8-80 nucleobases in length
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                                                                                                                                                                                                                                                                                                                        compounds, particularly antisense oligonucleotides targeted to a
                                                                                                                                                                                                                                                                                                                                         nucleic acid encoding HMG-COA reductase, useful for treating atherosclerosis, or a disease involving cholesterol metabolism or
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es 16; Conserv
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                                                                 Homo sapiens
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                                                                                                                          08-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; ss.
                                 human; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADI79785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95
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                                                                                                                                                                                                                                                          Dean NM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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RESULT 326
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                                                                                                                                                                                     The invention relates to novel compounds of 8-80 nucleobases in length targeted to, and which specifically hybridises with, a nucleic acid molecule encoding 3-hydroxy-3-methylglutary1-Comaryme A (HMG-COA) reductase, and inhibits the expression of HMG-COA reductase. The novel compounds have cardiant, antiarteriosclerotic, and antilipaemic activities. The compound can be used to treat disorders by antisense gene therapy. The compound can be used to treat disorders by antisense gene therapy. The compounds associated with HMG-COA reductase, such as a disease or condition associated with HMG-COA reductase, such as a cardiovascular disorder e.g. atherosclerosis, or a disease or condition involving cholesterol metabolism. They are also useful in research and diagnostics for modulating the expression of HMG-COA reductase. This polynucleotide sequence represents an antisense oligonucleotide of the
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                            New compounds, particularly antisense oligonucleotides targeted to
nucleic acid encoding HMG-CoA reductase, useful for treating
atherosclerosis, or a disease involving cholesterol metabolism or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genetic marker;
human cystic fibrosis transmembrane conductance regulator; CFTR;
PCR assay; cystic fibrosis; PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                      Match 1.3%; Score 14.2; DB 1; Length 20; Local Similarity 84.2%; Pred. No. 1.8e+02; les 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cystic fibrosis CFTR 1-related PCR primer SeqID333
                                                                                                                                                                                                                                                                                                                                                  G; 6 T; 0 U; 0 Other;
                                                                                                                                                                    Example 16; SEQ ID NO 308; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     95 GCATTATCCTTCAGTGGGG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                          2 gcarrarcricagaaggg 20
                                                                   Dobie KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI44833 standard; DNA; 20 BP.
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08-WAY-2001; 2010US-00851501.

19-NOV-2001; 2001US-0333531P.

08-WAY-2002; 2002US-00142722.
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02-JUL-2002; 2002US-00190366.
                       02-JUL-2002; 2002US-00190366.
                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 6 A; 3 C; 5
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                                            (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DUNLOP C L M. WEISEL J M.
                                                                   Freier SM,
                                                                                         WPI; 2004-081743/08
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                                                                                                                                                 angiogenesis.
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                                                                                                                                                                                                                                                                                                                                  invention.
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                                                                    Dean NM,
                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel single or multiple target oligonucleotide anti-sense to e.g. initiation codons and introns of respiratory disease-relevant genes e.g., CCRI, RANTES, MCP4, useful for prophylaxis or treating respiratory
                                                                                                                           Identifying the presence or absence of a genetic marker in the human cystic fibrosis transmembrane conductance regulator gene of a subject by contacting the DNA and primer set and separating the extension product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interleukin; IL-4 receptor; IL-5 receptor; lung disease; airway inflammation; allergy; asthma; impeded respiration; cystic fibrosis; acute respiratory distress syndrome; pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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84.2%; Pred. No. 1.8e+02;
ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; SEQ ID NO 2467; 85pp; English
                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 333; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the exemplification of the invention.
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in S, Lu H, Cong H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 670 CICAAATTAIGTTACTIGT 688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADJ61611 standard; DNA; 20
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nes 16; Conservative
Dunlop CLM, Weisel JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease e.g., asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-203534/19.
                                                               WPI; 2004-070574/07.
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The present invention relates to an oligonuclectide anti-sense to e.g., initiation codon, coding region with 2-10 nuclectides of 5'-end and 3'-end of nucleic acid target comprising gene(8) chosen from e.g. interleukin (IL)-4 receptor, IL-5 receptor or salts of the cligonuclectide and optionally surfactant operatively linked to the cligonuclectide. The method is useful for preventing or treating a respiratory or lung disease, which involves administering to the airways of a subject an effective amount of an inhibitor. The oligonuclectide is useful for production of a medicament for the prevention and/or treatment of a respiratory or lung disease. The respiratory or lung disease is chosen from airway inflammation, allergy(ies), asthma, impeded respiratory criticities (RP), chronic obstructive pulmonary diseases (CP), chronic obstructive pulmonary diseases (CPD), allergic rhinitis (AR), acute respiratory distress syndrome (ARDS), pullmonary hypertension, lung inflammation, bronchitis, airway continuation. The present sequence represents an oligonucleotide of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interleukin; IL-4 receptor; IL-5 receptor; lung disease;
airway inflammation; allergy; asthma; impeded respiration;
cystic fibrosis; acute respiratory distress syndrome;
pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                 1.3%; Score 14.2; DB 1; Length 20;
84.2%; Pred. No. 1.8e+02;
iive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 8 A; 5 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide associated to PDE4C #269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; SEQ ID NO 2059; 85pp; English.
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H, Cong H;
                                                                                                                                                                                                                                                                                                                                                                                                                                           676 TTATGTTACTTGTTTGGCT 694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 TAAAGTTACTGGTTTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                       16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease e.g., asthma.
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                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                invention
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                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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ADJ61203
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The present invention relates to an oligonucleotide anti-sense to e.g., intitation codon, coding region with 2-10 nucleotides of 5'-end and 3'-end of nucleic acid target comprising gene(8) chosen from e.g. interleukin (IL)-4 receptor, IL-5 receptor or salts of the

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oligonucleotide and optionally surfactant operatively linked to the oligonucleotide. The method is useful for preventing or treating a respiratory or lung disease, which involves administering to the airways of a subject an effective amount of an inhibitor. The oligonucleotide is useful for production of a medicament for the prevention and/or treatment of a respiratory or lung disease. The respiratory or lung disease is chosen from airway inflammation, allergy(ies), asthma, impeded respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases (COPD), allergic rhinitis (AR), acute respiratory distress syndrome (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel compound 8-80 nucleobases in length targeted to a nucleic acid molecule encoding integrin beta 5 (Itgb5). The compound specifically hybridises with the nucleic acid molecule encoding integrin beta 5, thus inhibiting the expression of integrin beta 5. The compound of the invention demonstrates cytostatic, antiinflammatory and antimicrobial activities and may be useful for inhibiting the expression of integrin beta 5, via antiseanse gene therapy and thus for treating diseases associated with expression of integrin beta 5, via antiseanse gene therapy and thus for treating diseases associated with as cancer, inflammation or infection. The current sequence is that of an antiseanse 2-MOB (2'-methoxyethyl) gapmer oligo targeted to human Itgb5 of the invention. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense compounds targeted to nucleic acid molecules encoding integrin beta 5, useful for treating diseases associated with expression of integrin beta 5, e.g. hyperproliferative disorder, infection or
                                                                                                                                                                                                                  obstruction. The present sequence represents an oligonucleotide of the
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               integrin beta 5; Itgb5; cytostatic; antiinflammatory; antimicrobial; antisense; gene therapy; hyperproliferative; cancer; inflammation; infection; 2-MOE wing; 2'-methoxyethyl gapmer; 88; human; phosphorothioate backbone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense 2-MOE gapmer oligo targeted to human Itgb5 - SEQ ID 69.
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16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                  Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                               191 TICCACGCCATCTCCCCCA 209
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Local Si.
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                                                                                                                                                                                                                                               invention.
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/note= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All
cytidine nucleobases are 5-methylcytidine."
                                                                                                                                                                                                                                              human; 88; liver related homologue-1; LRH1; NR5A2; antisense; phosphorothicate; 2' MOE; breast cancer; dyslipidaemia; atherosclerosis; low HDL; high density lipoprotein; high LDL; hypercholesterolaemia; gall stone; triglyceridaemia; obseity; hepatitis; hepaticis; hepaticis; antilipaemic; antiarteriosclerotic; anorectic, hepatotropic; litholytic; antilinflammatory; virucidal.
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oligonuclectide has central "gap" region flanked on both sides by 2-MOE "wings". The backbone linkages are phosphorothioate and all cytidine residues are 5-methylcytidines.
                                                                                                                                                                                                                              Antisense DNA oligo used to modulate human LRH1 expression SeqID 3340.
                                                                              Gaps
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                                                          Query Match 1.1%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 1.88+02; Matches 16; Conservative 0; Mismatches 3; Indels
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/label= OTHER= phosphorothioate backbone
                                        Seguence 20 BP; 9 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
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the expression of liver related homologue-1 (LRH1) and splice variants thereof. Specifically, it refers to compositions 8-30 nucleobases in length that target a portion of an active site on the nucleic acid molecule encoding LRH1 (also known as NRSA2). LRH1 is a monomeric orphan nuclear receptor protein that functions as a tissue specific ranscription factor. The present invention describes antisense oligonucleotides that comprise at least one modified internucleoside linkage, a phosphorothioate linkage, at least one modified sugar moiety, a 2'-0-methoxyethyl (2' MOE) and at least one modified sugar moiety, a 2'-0-methoxyethyl (2' MOE) and at least one modified sugar moiety, a 2'-0-methoxyethyl (2' MOE) and at least one modified sugar moiety, dyslipidaemia, atherosclerosis, low HDL (high density lipoprotein), high crid lipoprotein), hypercholesterolaemia, gall stones, triglyceridaemia, obesity, hepatitis B virus-mediated acute or chronic hepatitis, as well as hepatocellular carcinoma or a condition associated with excmatase activity. Accordingly, these compositions exhibit cytostatic, antiliflammatory and virucidal activities. This liboprotein, beand virucidal activities. This consequence is an antisense DNA oligo used to modulate the consequence.
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/label= OTHER= phosphorothioate backbone
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                                                                                                                                                                             New antisense oligonucleotides targeted to a nucleic acid encoding liver related homologue-1 (LRH1), useful for treating breast cancer, dyslipidemia, atherosclerosis, hypercholesterolemia, or hepatitis.
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                                   01-JUL-2002; 2002US-0392813P.
01-JUL-2003; 2003WO-US020865.
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This invention relates to novel antisense compounds useful for modulating the expression of liver related homologue-1 (LRH1) and splice variants thereoffically, it refers to compositions 8-30 nucleobases in clength that target a portion of an active site on the nucleic acid molecule encoding LRH1 (also known as NR5A2). LRH1 is a monomeric orphan cuclear receptor protein that functions as a tissue specific cranical factor. The present invention describes antisense componition factor. The present invention describes antisense continuage, a phosphorothoate linkage, at least one modified uncleobase, a 5-comethoxycthy1 (2' MOE) and at least one modified uncleobase, a 5-comethoxycthy1 (2' MOE) and at least one modified sugar moiety, a 2'-O-methoxycthy1 (2' MOE) and at least one modified sugar moiety. Ca 2'-O-methoxycthy1 (2' MOE) and at least one modified successivation associated with LRH1, such as beast cancer, disgnosing a disease associated with LRH1, such as beast cancer, disglosing a disease associated with LRH1, such a condition associated with aromatase activity. Accordingly, these compositions exhibit contining an antilippendic, antiliarensions continual activities. This cycostatic, antilipenmatory and virucidal activities. This colisonucleotide sequence is an antisense DNA oligo used to modulate the expression of the human LRH1 protein of the invention.
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cytidine nucleobases are 5-methylcytidine."
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                        /label= OTHER= phosphorothioate backbone
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/mod base= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kane CD;
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phosphorothioate; 2' MOE; breast cancer; dyslipidaemia; atherosclerosis; low HDL; high density lipoprotein; high LDL; hypercholesterolaemia; gall stone; triglyceridaemia; obesity; hepatitis; hepatocellular carcinoma; aromatase; cytostatic; antilipaemic; antiarteriosclerotic; anorectic; hepatocropic; litholytic; antiinflammatory; virucidal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleotides. All
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mod_base= OTHER //mote= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All cytidine nucleobases are 5-methylcytidine."
Antisense DNA oligo used to modulate human LRH1 expression SeqID 2516.
                                               ss; liver related homologue-1; LRH1; NR5A2; antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mod_base= OTHER /nethoxyethyl (2' MOE) nu cytidine nucleobases are 5-methylcytidine.
                                                                                                                                                                                                                                                                                                                                                                                   /mod_base= OTHER
/label= OTHER= phosphorothioate backbone
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                    Key
modified_base
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                                                                                                                                                                                                                                                                        Synthetic.
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01-JUL-2003; 2003WO-US020865

01-JUL-2002; 2002US-0392813P

(PHAA ) PHARMACIA CORP.

Kane CD;

WPI; 2004-083058/08.

New antisense oligonucleotides targeted to a nucleic acid encoding liver related homologue-1 (LRH1), useful for treating breast cancer, dyslipidemia, atherosclerosis, hypercholesterolemia, or hepatitis.

Example 15; SEQ ID NO 2516; 909pp; English.

This invention relates to novel antisense compounds useful for modulating the expression of liver related homologue-1 (LRH1) and splice variants thereof. Specifically, it refers to compositions 8-30 nucleobases in clength that target a portion of an active site on the nucleic acid molecule encoding LRH1 (also known as NRSA2). LRH1 is a monomeric orphan nucleuse receptor protein that functions as a tissue specific or transcription factor. The present invention describes antisense coligonucleotides that comprise at least one modified sugar moiety, a 2'-O-methoxyethyl (2' MDE) and at least one modified sugar moiety, a 2'-O-methoxyethyl (2' MDE) and at least one modified sugar moiety, a 2'-O-methoxyethyl (2' MDE) and at least one modified sugar moiety, a chaspenborothioate linkage, at least one modified sugar moiety, a 1'-O-methoxyethyl (2' MDE) and at least one modified sugar moiety, a 2'-O-methoxyethyl (2' MDE) and at least one modified sugar moiety, a 3'-O-methoxyethyl (2' MDE) and at least one modified sugar moiety, dispansing a disease associated with LRH1, such as becast cancer, dispansion, in proportion, and a sensoriated with LRH1, such as becast cancer, chaptitis as well as hepatocellular carcinoma or a condition associated with aromatase activity. Accordingly, these compositions exhibit with aromatase activity. Accordingly, these compositions exhibit colliponucleotide sequence is an antisense DNA oligo used to modulate the correspondence.

Sequence 20 BP; 6 A; 4 C; 1 G; 9 T; 0 U; 0 Other;

315 TTGGATTTCCTGTTATTCT 333

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mcd_base= OTHER
/note= "This oligonucleotide has a phosphorothioate
/note= "This oligonucleotide has a phosphorothioate
backbone and 2-"methyoxethyl (2'-MOE) wings at the 5'
and 3' ends, which are 4 nucleotides in length. Also all
cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                     Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy; Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL; cardiovascular disorder; metabolic syndrome X; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25517), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for anoulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are
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                                 Gaps
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                                                                                                                                                                                                                                                                      Human endothelial lipase antisense oligonucleotide, SEQ ID 2517.
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                                 Indels
   Length
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Score 14.2; DB 1;
Pred. No. 1.8e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; SEQ ID NO 2517; 1007pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
                                                                  409
                                                                                                 13
                                                                                                                                                                               BP
   1.3%;
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                                                                  391 AGTCATTTTCCTTACAATT
                                                                                                 AGTCATTTCCCTTAATATT
                                                                                                                                                                               ADJ24119 standard; DNA; 20
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                                                                                                                                                                                                                                               (first entry)
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                                    Conservative
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                  Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                         modified base
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                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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        Query Match
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Matches
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(first entry)

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ADJ24120 standard; DNA; 20 BP
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                                     ADJ24120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense oligonuclectide for modulating endothelial lipase expression, for diagnosing, preventing or treating e.g. dyslipidemia, low high density lipoprotein or cardiovascular disorders.
                                                                                                                                                                                                                                      Antilipaemic, Cardiovascular, Analgesic, Antianginal, Antisense therapy;
Human, Endothelial Lipase, dyslipidaemia, high density lipoprotein, HDL;
cardiovascular disorder, metabolic syndrome X; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "This oligonucleotide has a phosphorothioate backbone and 2-"methyoxyethyl (2-'MOB) wings at the 5' and 3' ends, which are 4 nucleotides in length. Also all cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25511), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are used for diagnostics, prophylaxis, or as research reagents or kits.
                                                                                                                                                                                                      Human endothelial lipase antisense oligonucleotide, SEQ ID 2534
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84.2%; Pred. No. 1.8e+02;
iive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 7 A; 5 C; 3 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              /mod_base= OTHER
                                                                                                    ADJ24136 standard; DNA; 20 BP
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TTGGCTTTCCTATTTTTCT
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                                                                                                                                                                        (first entry)
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Best Local Similarity 84.2
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            modified base
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                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                      ADJ24136;
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                                                                                                                                                                                                                                                                                                                                                                                              /mod_base= OTHER
/note= "This oligonucleotide has a phosphorothioate
/note= "This oligonucleotide (2'-MOE) wings at the 5'
backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5'
and 3' ends, which are 4 nucleotides in length. Also all
cytidine residues are 5-methylcytidines"
                                                              Antilipaemic, Cardiovascular, Analgesic, Antianginal, Antisense therapy, Human, Endothelial Lipase, dyslipidaemia, high density lipoprotein, HDL, cardiovascular disorder, metabolic syndrome X, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25511), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are used for diagnostics, prophylaxis, or as research reagents or kits.
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Human endothelial lipase antisense oligonucleotide, SEQ ID 2518
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                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                          1. .20
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004009541-A2
                                                                                                                                                                                                                                                                                                                                   modified base
                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2004
                                                                                                                                                                                                                                            Synthetic
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ADK80500
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Gaps

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867 GTAGTCCATGCTATTAAAA 885

1 GTAGCCAATGCTATTACAA 19

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RESULT 335 ADJ24120/c

26-FEB-2004.

Synthetic

Roberds SL;

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The present invention relates to an antisense compound targeted to a nucleic acid molecule encoding Nav1.3, where the antisense compound and composition are useful for treating a disease or condition compound and composition are useful for treating a disease or condition associated with Nav1.3, e.g. pain including but not limited to neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain, clabelic neuropathy, trigeminal neuropathy, arthritic pain, acute pain, pain from burns, migraine headache, cluster headache, mild-to-moderate headache; seizure disorder such as childhood seizure disorder, including but not limited to neonatal or infantile epilepsy; or ataxia. The present sequence represents a chimeric phosphorothicate oligonucleotide with 2 MoDE wings and a deoxy gap. Used during the antisense inhibition of human Nav1.3 expression, the oligonucleotides are designed to target different regions of the human Nav1.3 RNA.
                                                                                                                                                                                                                                                                     New antisense compound targeted to a nucleic acid molecule encoding Navl.3, useful for useful for treating a disease or condition associated with Navl.3, e.g. pain, seizure disorder such as childhood seizure disorder, or ataxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Osteopathic; calvarial osteoblast differentiation; osteoblast differentiation; calvarial osteoblast mineralization; calvarial osteoblast mineralization; NBLL-1; bone fracture repair; bone density;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 1.3%; Score 14.2; DB 1; Length 20; Local Similarity 84.2%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 5 A; 8 C; 2 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; SEQ ID NO 8317; 417pp; English.
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ADL97965 standard; DNA; 20 BP.
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                                                                                         14-AUG-2002; 2002US-0403416P.
                                            14-AUG-2003; 2003WO-US025465
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                                                                                                                                        (PHAA ) PHARMACIA CORP
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                                                                                                                                                                                                                                    WPI; 2004-203785/19.
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26-FEB-2004
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                                                                                                                                                                                        Roberds SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADL97965;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to an antisense compound targeted to a nucleic acid molecule encoding Nav1.3, where the antisense compound and compositions with and inhibits the expression of Nav1.3. The compound and composition are useful for treating a disease or condition associated with Nav1.3, e.g. pain including but not limited to neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain, diabetic neuropathy, trigeminal neuropathy, arthritic pain, lower back pain, can from burns, migraine headache, cluster headache, mild-to-moderate headache; seizure disorder such as childhood seizure disorder, including but not limited to neonatal or infantile epilepsy; or ataxia. The present sequence represents a chimeric phosphorchhoad pain, sequence represents a chimeric phosphorchhoad eligencelectide with 2. WMOE wings and a deoxy gap. Used during the antisense inhibition of human Nav1.3 expression, the oligonucleotides are designed to target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense compound targeted to a nucleic acid molecule encoding Navl.3, useful for useful for treating a disease or condition associated with Navl.3, e.g. pain, seizure disorder such as childhood seizure disorder, or ataxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Navl.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia; diabetic neuropathy; arthritic pain; migraine headache; infantile epilepsy; ataxia; ss.
                                          Navl.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia; diabetic neuropathy; arthritic pain; migraine headache; infantile epilepsy; ataxia; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric phosphorothioate oligonucleotide to target Nav1.3 #8317.
    Chimeric phosphorothioate oligonucleotide to target Nav1.3 #7834.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 5 A; 9 C; 1 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; SEQ ID NO 7834; 417pp; English.
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                                                                                                                                                                                                                                                                                                                                             14-AUG-2002; 2002US-0403416P.
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Synthetic.

ADK80983;

RESULT 337

g 8

ADK80983

Query Match

Matches

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Gaps

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Indels

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The present invention relates to a method for modulating calvarial osteoblast differentiation and mineralization. The method comprises altering expression or activity of NELL-1, where the increased expression or activity of NELL-1 increases osteoblast differentiation or mineralization and decreased expression or activity of NELL-1 decreases osteoblast differentiation or mineralization. The methods and NELL-1 gene are useful for facilitating repair of bone fractures and/or to generally increase bone density. The present sequence is a PCR primer, used to
                                            Modulating calvarial osteoblast differentiation and mineralization, useful for facilitating repair of bone fractures and/or to generally increase bone density, comprises altering expression or activity of Nell-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCR1; CCR3; Botaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a; tryptase b; PDE4 A; PDR4 B; PDE4 C; PDE4 D; respiratory disease; lung disease; hyper-responsiveness; adenosine; adenosine A receptor; asthma; lung allergy; inflammation; inflammatory disease; airway inflammation; allergy; impeded respiration; cystic fibrosis; chronic obstructive pulmonary disease; CCP9; allergy chinitis; acute respiratory distress syndrome; pulmonary hypertension; until and inflammation; bronchitis; airway obstruction; bronchoconstriction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
                                                                                                                                                                                                                                                                                                                                                   Score 14.2; DB 1; Length 20; Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                       1.3%; Sco...
84.2%; Pred. No. ...
... 0; Mismatches
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                                                                                                                        Example 2; Page 54; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               697 TCATGTAGTCACGGTGCTC 715
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23-APR-2002; 2002WO-US013143.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                    illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                Local Similarity 84.2
Les 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nyce JW, Sandrasagra Shahabuddin S, Lu H,
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             WPI; 2004-329478/30.
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AGUILAR D.
MILLER S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Si
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADO46593;
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(LUHH/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 339
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셤
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The invention relates to oligonuclectides anti-sense to an initiation codon, coding region, 5' or 3' intron-exon junction, intron or region with 2-10 nuclectides of the 5'-end or 3'-end of a nucleic acid target chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL) consen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL) consent from a gene encoding interleukin (IL)-4 receptor, interleukin (IL) consent from a gene encoding interleukin (IL)-4 receptor, interleukin (IL) consent from the consent from and/or treatment of a respiratory or lung disease. The prevention and/or treatment of a respiratory or lung disease. The consent from Encoding interleukin-4 receptor, interleukin-5 receptor, consecut from Tryptase b, PDE4 B, PDE4 C, or PDE4 D. The oligonuclectides are useful for receptor, interleukin-5 receptor, capiratory or lung disease is associated with hyper-responsiveness to and/or increased levels of, adenosine and/or lung disease. The creeptor (S), and/or asthma and/or lung allergie associated with cinflammation or an inflammation, allergy, asthma, impeded respiration, cystic fibrosis (CP), chronic obstructive pulmonary disease (COPD), allergic rhinitis, acute respiratory distress syndrome, pulmonary chypertension, lung inflammation, distress syndrome, pulmonary chypertension, lung inflammation, allergy, asthma, an oligonucleotide of the pronchoonstriction. This sequence represents an oligonucleotide of the ô Novel single or multiple target oligonucleotide anti-sense to e.g. initiation codon, intron of respiratory disease-relevant gene e.g. CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g. CCRI; CCR3; Eccaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptess a; tryptess b; PDB4 A; PDB4 C; PDB4 D; respiratory disease; lung disease; hyper-responsiveness; adenosine; adenosine A receptor; asthma; lung allergy; inflammation; inflammatory disease; airway inflammation; allergy; impeded respiration; cystic fibrosis; CF; chronic obstructive pulmonary disease; COD9; allergic rhinitis; acute respiratory distress syndrome; pulmonary hypertension; lung inflammation; bronchitis; airway obstruction; bronchoconstriction. 88; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5; Gaps .; 0 1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02; 7ative 0; Mismatches 3; Indels Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other; Claim 2; SEQ ID NO 2059; 174pp; English. 209 1 Tregadeccarcrececa 19 25-JUL-2003; 2003US-00627930. 191 TTCCACGCCATCTCCCCCA Human oligonucleotide #2367. ADO47001/c ID ADO47001 standard; DNA; 20 15-JUL-2004 (first entry) Conservative WPI; 2004-293804/27. Query Match Best Local Similarity Matches 16; Conserv US2004049022-A1 Homo sapiens 11-MAR-2004 invention ADO47001; asthma RESULT 340 2225282255528255528255555 용

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Gaps ö Page 166

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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to oligonuclectides anti-sense to an initiation codon, coding region, 5' or 3' intron-exon junction, intron or region with 2-10 nuclectides of the 5'-end or 3'-end of a nucleic acid target chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)-5 receptor, CCRI, CCR3, Ectaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, CTAPA repase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention also relates to a method of screening a candidate compound that binds to one or more nucleic acid target(s) or expressed product(s), for the prevention and/or treatment of a respiratory or lung disease. The oligonuclectides are useful for reducing or inhibiting expression of a cene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a, tryptase b, PDE4 B, PDE4 C, or PDE4 D. The oligonuclectides are useful for preventing a respiratory or lung disease. The respiratory or lung disease is associated with hyper-responsiveness to and/or increased levels of, adenosine and/or levels of adenosine A inflammation or asthma and/or levels of adenosine A inflammation or an inflammation, allergy, asthma, impeded respiration, alleric fibrosis (FF), chronic obstructive pulmonary disease (COPD), allered and an inflammation, allergy, asthma, impeded respiration, alleric fibrosis (FF), chronic obstructive pulmonary disease (COPD), allered and an inflammation, allered such an entermination or allergy asthma, impeded respiration, allered such and an entermination or allergy, asthma, impeded respiration, allered such and an entermination or allergy asthma, impeded respiration, allered such and an entermination or allergy asthma, impeded respiration, allered such and an entermination, allered such and an entermination of allered such and an entermination, allered such and and an entermination and and and an entermination and and an ente
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                                                                                                                                                                                                                                                                                          Novel single or multiple target oligonucleotide anti-sense to e.g. initiation codon, intron of respiratory disease-relevant gene e.g. CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       allergic rhinitis, acute respiratory distress syndrome, pulmonary
hypertension, lung inflammation, bronchitis, airway obstruction or
bronchoconstriction. This sequence represents an oligonucleotide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transplant rejection; immune system; rheumatoid arthritis; lupus; inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; probe.
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84.2%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                            A, Tang L, Aguilar D, Miller S; Cong H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 8 A; 5 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Claim 2; SEQ ID NO 2467; 174pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     676 TTATGTTACTTGTTTGGCT 694
20 TAAAGTTACTGGTTTTGGCT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP12146 standard; DNA; 20 BP
               23-APR-2002; 2002WO-US013135.
23-APR-2002; 2002WO-US013143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ilarity 84.2%;
Conservative
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Shahabuddin S, Lu H, C
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                                                                NYCE J W.
SANDRASAGRA A.
                                                                                                                              MILLER S.
SHAHABUDDIN S.
                                                                                                                                                                                                                                                             WPI; 2004-293804/27.
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Les 16; Conserv
                                                                                               TANG L.
AGUILAR D.
                                                                                                                                                                 LU H.
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                                                                                                            (AGUI/)
(MILL/)
(SHAH/)
(LUHH/)
(CONG/)
                                                                (NYCE/) 1
(SAND/) (TANG/)
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Matches
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The present invention relates to diagnosing or monitoring transplant crejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an xenotransplant rejection or mechanical organ replacement rejection, in an individual. The methods are also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatorid arthritis, or ultra, bacterial or fungal infection. The present sequence represents a probe for a 50 mer oligonaleotide marker for diagnosis and monitoring of allograft rejection and other disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; gene therapy; PPAR-alpha; peroxisome proliferator-activated receptor-alpha; PPAR-alpha modulator; PPAR-alpha associated disorder; hyperproliferative disorder; human; antisense oligonucleotide; antisense technology; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                     Fry K, Woodward R, Ly N, Prentice J, Morris M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PPAR-alpha antisense oligonucleotide seqid 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 5 A; 8 C; 6 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 58; SEQ ID NO 2155; 1762pp; English.
                                                                                                                                                                                                                                                                                                                     (EXPR-) EXPRESSION DIAGNOSTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccrececcrrererresc 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
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                                                                                                                                   24-APR-2003; 2003WO-US012946.
                                                                                                                                                                                                           24-APR-2002; 2002US-00131831
20-DEC-2002; 2002US-00325899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 84.2
nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-400724/37.
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WO2004042346-A2
                                                                                                                                                                                                                                                                                                                                                                                            Wohlgemuth J,
Rosenberg S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUN-2004.
                                                                       21-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the genes
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(APPL-) APPLERA CORP.
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                                                                                                                                                                                                The invention describes a compound, having a sequence comprising 8-80 bp targeted to a nucleic acid encoding PPAR-alpha (peroxisome proliferator-activated receptor-alpha), that specifically hypridises with the nucleic acid encoding PPAR-alpha comprising 86001-bp sequence and inhibits expression of PPAR-alpha comprising 86001-bp sequence and inhibiting the expression of PPAR-alpha. Also described are: a method of inhibiting the modulator of PPAR-alpha in cells or tissues; a method of screening for a modulator of PPAR-alpha; a diagnostic method for identifying a disease state; a kit or assay device comprising the compound; and a method of treating an animal having a disease or condition associated with PPAR-alpha. The oligonuclectide compound is useful for preparing a composition for treating hyperproliferative disorder e.g. cancer. This sequence represents a human peroxisome proliferator-activated receptor-alpha (PPAR-alpha) antisense oligonuclectide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ss; primer; single nucleotide polymorphism; SNP; diagnosis; disease association; linkage analysis; autoimmune disease; rheumatoid arthritis; diabetes; multiple sclerosis; systemic lupus erythematosus; inflammatory bowel disease; psoriasis; thyroditis; celiac disease; pernicious anaemia; asthma; vitiligo; glomerulonephritis; Graves' disease; myocarditis; Sjogren disease; primary systemic vasculitis; genotyping; gene therapy; PCR primer.
                                                                                                                         New oligonucleotide compound that inhibits expression of PPAR-alpha, useful for preparing a composition for treating hyperproliferative disorders, e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                        1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human single nucleotide polymorphism detection primer #126.
                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                         Example 15; SEQ ID NO 76; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 TGTCGGGAACTGGCATATT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 TGTAGGTAACCGGCATATT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2003US-0443566P.
2003US-0455444P.
2003US-0465241P.
2003US-0495115P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR27036 standard; DNA; 20 BP.
 11-DEC-2002; 2002US-00317500.
                         11-DEC-2002; 2002US-00317500.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 84.2
                                                (ISIS-) ISIS PHARM INC
                                                                                                WPI; 2004-449378/42.
                                                                         Mckay R, Dobie KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004067779-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADR27036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 343
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The invention relates to an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is a single nucleotide polymorphism (SNP) selected from any one of the nucleotide enclocitied polymorphism (SNP) selected from any one of the nucleotide concleotide polymorphism (SNP) selected from any one of the nucleotide caguences of SEQ ID NOS:1-669 and 1339-49582, or their complements. The SNPs are useful for identifying an increased or decreased risk for developing an individual who is at an increased or decreased risk for developing an altiphe selectes, systemic lupus erythematosus, inflammatory bowel diseases, psoriasis, thyroiditis, celiac disease, pernicious anaemia, multiphe selectes, systemic lupus erythematosus, inflammatory bowel disease, psoriasis, thyroiditis, celiac disease, pernicious anaemia, altifilgo, glomerulonephritis, Graves disease, myocarditis, cathem, vitiligo, glomerulonephritis, creliac disease, pernicious anaemia, system information for the prevention and/or treatment of the autoimmune disease particularly rheumatoid arthritis, and for the autoimmune diseases particularly rheumatoid arthritis, and for the autoimmune diseases particularly rheumatoid arthritis, and for the autoimmune diseases defined above. The NNPs are useful for human creating the diseases defined above. The nucleic acid molecules are useful for constructing the call expressing a part or all of the useful for constructing or screening drugs that modaled and stand encleic acid molecules and variant peptides, for constructing transgenic animals, for assaying or screening drugs that modaled and stated as hybridises to the nucleic acide of the invention to amplify the SNP containing region. Note SEQ ID NOS 1-49582 are claimed and stated as the printed apecification, however these sequences are not provided in the printed apecification).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                      New single nucleotide polymorphisms (SNPs) associated with rheumatoid arthritis (RA), useful in identification of individuals at risk of developing RA or other autoimmune disease, and in development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Alexander HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.3%; Score 14.2; DB 1; Length 20; 34.2%; Pred. No. 1.8e+02; ve 0; Mismatches 3; Indels
Schrodi SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 4 A; 9 C; 1 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                 Claim 21; SEQ ID NO 49708; 141pp; English.
Carlton VE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1046 CCCAACTTCCTTATCTTTC 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 cccaacarcercarerers 19
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ADR17228 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-NOV-2004 (first entry)
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Matches 16; Conservative
Begovich AB,
                                                                                 NPI; 2004-594223/57.
                                                                                                                                                                                                                                                                                            therapeutic agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS6780609-B1
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Cargill M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADR17228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADR17228,
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The invention relates to an isolated amino acid protein sequence selected from an amino acid sequence appearing as ADR16922 or an amino acid sequence appearing of consisting of the extracellular domain of sequence computating or consisting of the extracellular domain of mass) allele of consisting of the extracellular domain of consisting of the extracellular domain of consisting of the extracellular domain of consisting of consisting of consisting of consisting of consisting of consisting mass of consisting consisting extractions, methods of developing pharmaceutical compositions, methods of identifying molecules involved in bone development, and methods of diagnosting and treating diseases and the high bone mass (HBM) allele on chromosome 11q13.3 encoding and the high bone mass (HBM) allele on chromosome 11q13.3 encoding and the high bone mass (HBM) allele on chromosome 11q13.3 encoding and the high connormal and abnormal conditions of bone, including metabolic bone diseases, e.g. osteoporosis. The present sequence is a PCR primer used in the mapping of the Zmaxl/HBM gene.
                                                                                                                                                                                                                            New high bone mass gene of chromosome 1.1013.3, encoding protein useful for treating, diagnosing, preventing, or screening for normal and abnormal conditions of bone, including metabolic bone diseases, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 absorption; ABCG2; ATP-binding cassette gene; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer used to amplify human ABCG2 DNA - SEQ ID 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KOKU-) KOKURITSU IYAKUHIN SHOKUHIN EISEI KENKYU.
(IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
                                                                                                                                                        Recker RR, Johnson ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 310; 284pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome 4q22; ss; PCR; primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           882 AAAAGTGTGGCCCACAGAC 900
                                                                                                                        (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 AATATTGTGGCCCACACAC 1
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                                                 98US-0071449P.
                                                                 98US-0105511P.
             05-APR-2000; 2000US-00543771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADK67431 standard; DNA; 20
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nes 16; Conservative
                                                                                                                                                            Little RD,
                                                                                                                                                                                              WPI; 2004-623529/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP2004016042-A.
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                                                                                                                                                                                                                                                                                          osteoporosis
                                                                 23-OCT-1998;
13-JAN-1999;
                                                    13-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-NOV-2004
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                                                                                                                                                            Carulli JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADK67431;
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                                                                                                                              The invention relates to a novel polynucleotide having a mutation in the codon encoding a glutamine residue present at the 126 position of a 655 amino acid sequence. The polynucleotide of the invention may be useful for the estimation or diagnosis of a condition which is associated with abnormal drug absorption and in which the ABCG2 (ATP-binding cassette gene) protein is associated. The current sequence is that of a PCR primr which was used to amplify the human ABCG2 DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid sequence encoding high bone mass, useful in diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ss; PCR; high bone mass; Zmax1; HBM; bone modulation; bone development disorder; osteoporosis; chromosome 11; gene therapy;
                                                                                                                                                                                                                                                                                                                                            Gaps
                         Novel ABCG2 polynucleotide having a mutation at a specific position, useful for gene diagnosis of abnormality of medicine absorption associated with ABCG2 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human chromosome 11 Zmax1 region reverse mapping primer #122.
                                                                                                                                                                                                                                                                                                      1.3%; Score 14.2; DB 1; Length 20;
84.2%; Pred. No. 1.8e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                     Sequence 20 BP; 7 A; 1 C; 8 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnson ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 310; 303pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treating and/or preventing osteoporosis.
                                                                                                 Example 1; SEQ ID NO 61; 53pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recker RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENO-) GENOME THERAPEUTICS CORP. (UYCR-) UNIV CREIGHTON.
                                                                                                                                                                                                                                                                                                                                                                                432 GAAGAGGAGATGATTTTAG 450
                                                                                                                                                                                                                                                                                                                                                                                                              2 GCAGAGAGAGAGTTTAG 20
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98US-0105511P.
99US-00229319.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-DEC-2003; 2003US-00731739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADR47879 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-DEC-2004 (first entry)
                                                                                                                                                                                                                                                                                                                             Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carulli JP, Little RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-661408/64.
WPI; 2004-113852/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2004176582-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-1998;
13-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADR47879;
                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADR47879,
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artificial chromosome comprising HBM/Zmax1 sequence (appearing as ADR47574-ADR47580), a method for amplifying a nuclectide polymorphism in the Zmax1 or HBM gene, a method for identifying a regulatory element of a HBM gene and an isolated nucleic acid segment of at least 15 contiguous nucleotides including a polymorphic site from HBM/Zmax1. The nucleic acid molecule and the encoded polymeptide, composition, and methods are useful in diagnosing, treating and preventing a bone development disorder, i.e. osteoporosis. The gene for HBM/Zmax1 is located on chromosome 11q13.i. The present sequence is a primer used in the mapping of the HBM/Zmax1 cloning vector comprising HBM/Zmax1 (and a replicon operative in an isolated host cell), an expression vector comprising HBM/Zmax1 operably linked to a transcription regulatory region, an isolated host cell transformed with the vector(8), a method for testing a substance as a therapeutic agent for bone modulation in a host, a method of identifying a molecule involved in bone modulation, a method for identifying a (candidate) protein involved in bone modulation, a method of testing for HBM activity, a method of developing a pharmaceutical for the treatment of bone development disorders, a method for treating a bone development method for diagnostic assay for bone development disorder, a diagnostic assay for bone development disorder, a diagnostic assay for bone development disorders, a method for a pone development disorder, a method for dispnostic assay for bone development disorders, a method of expressing the HBM protein in bone tissue, a bacterial Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other; 

ch 1.3%; Score 14.2; DB 1; Length 20; 1 Similarity 84.2%; Pred. No. 1.8e+02; 16; Conservative 0; Mismatches 3; Indels 882 AAAAGTGTGGCCCACAGAC 900 19 AATATTGTGGCCCACACAC 1 Query Match Best Local Similarity Matches 16; Conserv 셤 ઠ

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Gaps ö

> ADS31697 standard; DNA; 20 BP 02-DEC-2004 ADS31697; RESULT 347 ADS31697

Gene expression inhibition method erbB2 gene PCR primer #8. (first entry)

cytostatic; gene promoter methylation inducer; cell growth inhibitor; erbB2 gene expression inhibitor; DMA methylation inducer; dsRNA; CpG; human; gene expression; erbB2; tumour; gene transcription; promoter; small interfering RNA; siRNA; gene silencing; ss; primer.

sapiens Synthetic Ношо

WO2004076663-A1.

10-SEP-2004.

27-FEB-2004; 2004WO-JP002448.

27-FEB-2003; 2003US-0449860P.

(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

Taira K, Kawasaki H;

WPI; 2004-662014/64.

Novel DNA methylation inducer containing double-stranded RNA targeting region having CpG on DNA in mammalian cell, useful in suppressing gene expression, and as cell growth inhibitor.

Example 4; SEQ ID NO 58; 98pp; Japanese

The invention relates to a DNA methylation inducer (I) containing doublestranded (ds)RNA that targets the region which contains CpG or CpNG (N is
CC Ar, T, C or G) no DNA in mammalian cell, or expression vector (V1) having
CD DNA that codes dsRNA that targets the region which contains CpG or CpNG
CC on DNA in mammalian cell. (I) is useful in the DNA methylation process,
which involves introducing (I) in a mammalian cell, where the mammalian
CC cll is obtained from human. (I) is useful as gene expression inhibitor.
CC call is obtained from human. (I) is useful as gene expression inhibitor.
CC suppressing gene expression, where the gene is a disease related gene
CC suppressing gene expression, where the gene is a disease related gene
CC The gene is erbB2 and the disease is the tumour. (I) is useful for
CC controlling various biological activities in a mammal by controlling the
CC controlling various biological activities in a mammal by controlling the
CC containing domain on a gene promoter of the target gene.
CC DNA. (I) or (II) enables specific methylation of the carget gene.
CC containing domain on a gene promoter of the target gene.
CC containing domain on a gene promoter of the target gene.
CC (I) induces sequence specific gene at the transcription level. (I)
CC enables DNA methylation in a plant, and controls
CC enables DNA methylation in a plant, and controls
CC enables DNA methylation of the promoter region of agene, where the
CC enables DNA methylation in the promoter region of the corresponds to an erbB2 gene PCR primer used in the method to silence ö Gaps ö Score 14.2; DB 1; Length 20; Pred. No. 1.8e+02; 0; Mismatches 3; Indels Sequence 20 BP; 1 A; 8 C; 7 G; 4 T; 0 U; 0 Other; 1.3%; gene expression in cells. Query Match 1.3 Best Local Similarity 84.2 Matches 16, Conservative 

840 AGGCCGGGGTGGATCCCTC 858 2 AGGCCTGGGTGCGTCCCTC 20 a ò

ADS31698 standard; DNA; 20 ADS31698; RESULT 348 ADS31698, 

BP.

02-DEC-2004 (first entry)

Gene expression inhibition method erbB2 gene PCR primer #9.

cytostatic; gene promoter methylation inducer; cell growth inhibitor; erbB2 gene expression inhibitor; DNA methylation inducer; dsRNA; CpG; human; gene expression; erbB2; tumour; gene transcription; promoter; small interfering RNA; siRNA; gene silencing; 88; primer.

sapiens. Ното

Synthetic.

WO2004076663-A1.

10-SEP-2004.

27-FEB-2004; 2004WO-JP002448

27-FEB-2003; 2003US-0449860P

(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

Taira K, Kawasaki H;

WPI; 2004-662014/64.

Novel DNA methylation inducer containing double-stranded RNA targeting region having CpG on DNA in mammalian cell, useful in suppressing gene expression, and as cell growth inhibitor.

Example 4; SEQ ID NO 59; 98pp; Japanese

The invention relates to a DNA methylation inducer (I) containing doublestranded (ds)RNA that targets the region which contains CpG or CpNG (N is Cp G) on DNA in mammalian cell, or expression vector (V1) having CC DNA that codes dsRNA that targets the region which contains CpG or CpNG on DNA in mammalian cell. (I) is useful in the DNA methylation process, which involves introducing (I) in a mammalian cell, where the mammalian ccl is obtained from human. (I) is useful as gene expression inhibitor or cell growth inhibitor. A gene expression inhibitor (II) is useful for suppressing gene expression, where the gene is a disease related gene crelevant to a disease, and the expression of the gene causes the disease. CC relevant to a disease, and the expression of the gene causes the disease. CC relevant to a disease, and the expression of the gene causes the respective controlling various biological activities in a mammal by controlling the controlling various biological activities in a mammal by controlling the containing domain on a gene promoter of the target gene, where the containing domain on a gene promoter of the target gene, where the containing domain on a gene promoter of the transcription level (I) induces sequence specific methylation in a plant, and controls containing domain on the promoter region of a gene, where the contemponal activities in the promoter region of a gene, where the contemponal activities of the methylation level (DNA to mRNA). This sequence corresponds to an erbB2 gene PCR primer used in the method to silence corresponds to an erbB2 gene PCR primer used in the method to silence Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory; Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic; Leptin receptor related protein; OB-RGRP; leptin receptor; leptin-related disorders; osteoporosis; calcification; obesity; diabetes; anorexia; sexual maturity disorder; haematopoiesis; angiogenesis; thrombus formation; immunity; inflammation; fetal development; cancer; Gaps New oligonucleotides that inhibit expression of the leptin receptor related protein, useful for treatment and prevention of e.g. osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and ö 1.3%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 1.8e+02; tive 0; Mismatches 3; Indels Leptin receptor related protein, OB-RGRP, RT-PCR primer #1. Sequence 20 BP; 4 A; 7 C; 8 G; 1 T; 0 U; 0 Other; (AVET ) AVENTIS PHARMA SA. (INRM ) INSERM INST NAT SANTE & RECH MEDICALE. Couturier C, Uhlmann E; 840 AGGCCGGGGTGGATCCCTC 858 19 AGGCCTGGGTGCGTCCTC 1 ADR27673 standard; DNA; 14 BP. 10-FEB-2003; 2003FR-00001543 10-FEB-2003; 2003FR-00001543 human; RT-PCR; primer; ss. 04-NOV-2004 (first entry) Matches 16; Conservative WPI; 2004-595751/58. Best Local Similarity FR2850971-A1 Homo sapiens 13-AUG-2004. Jockers R, ADR27673; Query Match RESULT 349 A CAN THE WAY AND A CONTROL OF THE C 8888888888888888888888888888 셤 ઠે

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The present invention relates to a leptin receptor related protein (OB-RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises specifically with and inhibits the expression of ADR27652. The ON promotes expression of leptin receptors on the cell surface and may contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a criethyleneglycol residue at the 3'-end; Also claimed are interfering RNA triethyleneglycol residue at the 3'-end; Also claimed are interfering RNA (IRNA) of 15-25 in that hybridize specifically with ADR27672, and inhibit expression of OB-RGRP. Also claimed are fusion proteins (FPS) and their expression of OB-RGRP. Also claimed are fusion proteins (FPS) and their coding sequences comprising OB-RGRP or MY047 (thought to be a member of the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that is a donor or acceptor of energy e.g. luciferase or yellow fluorescent protein (YFP) for detecting compounds that modify the interaction between the leptin receptor and OB-RGRP proteins, which can be used to prevent or treat leptin-related disorders. ON, also related interfering RNA, are treat leptin-related disorders. ON, also related disorders, e.g. used for prevention and/or treatment of leptin-related disorders, e.g. calcification; obesity, diabetes; anoroxia; disorders of sexual maturity, haematopoiesis, angiogenesis, thrombus formation, regulation of immunity and inflammation, fetal development and cancer. The present sequence is a RT-PCR primer used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; intercellular adhesion molecule; rel A; tumour necrosis factor; rNF-alpha; respiratory synoytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restensis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse IL-5 hammerhead ribozyme target sequence (nt. position 1148).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14 BP; 3 A; 4 C; 6 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.3%; Score 14; DB 1; Le
100.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Prec. ... 0; Mismatches
                                       Disclosure; Page 23; 104pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-00201109.
94US-00218934.
94US-00222795.
94US-00224483.
94US-00227958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT54666 standard; RNA; 15 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95WO-IB000156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 CCGTGGCAGGAAGC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ccercecaecaace 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sest Local Similarity
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15-APR-1994;
15-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
22-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9523225-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-FEB-1995;
  angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-AUG-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAR-1994
04-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT54666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-5) mRNA at the nucleotide base position indicated in the DB line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the IL-5 target sequences and thereby inhibit IL-5 expression, making them useful for treating chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes and preventing the recruitment and activation of eosinophils. The ribozymes can allo be used to treat cosinophils (related to parasitic infection or with pulmonary infiltration) and L-tryptophan-associated eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
                                                                                                                                                                                                                                                                                                                                                                     Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Tracz D, 'Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 2483.
                                                                                                                                                                                                                                                                                                                                                                  Dudycz LW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.3%; Score 14; DB 1; Length 15; 12.9%; Pred. No. 1.8e+02; ve 8; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                  Chowrira B, Direnzo A, Draper KG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 2 A; 2 C; 2 G; 0 T; 9 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 221; 407pp; English
94US-00245736.
94US-00291932.
94US-00291433.
94US-0029620.
94US-0029520.
94US-00305000.
94US-00311486.
94US-00311749.
94US-00311749.
94US-00311749.
94US-00311749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ63871 standard; RNA; 15 BP
                                                                                                                                                                                                                                                   94US-00345516.
                                                                                                                                                                                                                                                                                                    95US-00380734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 TGACTTTTCTTATG 136
                                                                                                                                                                                                                                                                                                                                   (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 UGACUUUUCUUAUG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-351090/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  Stinchcomb DT,
                                                                                                                          23-SEP-1994;
23-SEP-1994;
28-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAR-2000
                                                                                            02-SEP-1994
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                                                                               19-AUG-1994
                                                                                                                                                                        03-OCT-1994
07-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 351
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The present sequence represents the preferred target sequence of an enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves can be the patieits of virus (HCV) RNA sequence at the base position given in the descriptor line. The HCV sequence was screened for optimal ribozyme target sites using a computer folding algorithm and regions of the mRNA which did not form secondary folding structures and contained potential cibozyme cleavage sites were identified. Ribozymes were synthedised to target these sites and their activities optimised by either varying the carget these sites and their activities optimised by either varying the carget the binding arms or by modification to prevent degradation by nucleases. The ribozymes of the invention inhibit gene expression and/or viral replication, and are used to treat diseases associated with Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular carcinoma. The ribozymes may be used in combination with interferon to treat HCV infection, other infectious diseases, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enzymatic nucleic acid, RNA cleavage, Hepatitis C virus infection; HCV ribozyme; HCV expression, HCV replication, cirrhosis; virucide; liver failure, hepatocellular carcinoma; HCV infection; drug therapy; type I interferon; interferon alpha; interferon beta; cytostatic; interferon gamma; consensus interferon; hepatotropic; antiinflammatory; substrate; hammerhead ribozyme; HH ribozyme; 88.
                                                                                                                                                                                                                                                                                                                                                                                                Novel ribozymes for the treatment of diseases and conditions related to
cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus substrate #706 for HCV hammerhead ribozyme #706.
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                                                                                                                                                                                                                                                                                                                           Macejak D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15 BP; 4 A; 1 C; 5 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3%; Score 14; DB 1; 171.4%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                           Pavco PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                           Roberts E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 73; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                             98US-0083217P.
98US-0100842P.
99US-00257608.
99US-00274553.
                                                                                                                                                             99WO-US009027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 TGTGATCAAATGGG 359
                                                                                                                                                                                                                                                                                       (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABX00924 standard; RNA; 15
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                                                                                                                                                                                                                                                                                                                           Blatt L, Mcswiggen JA,
                    autoimmune disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                   hepatitis C infection.
                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-062023/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sest Local Similarity
                                                    Hepatitis C virus.
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                                                                                          W09955847-A2
                                                                                                                                                             26-APR-1999;
                                                                                                                                                                                                 27-APR-1998;
18-SEP-1998;
                                                                                                                                                                                                                                    25-FEB-1999;
                                                                                                                                                                                                                                                   23-MAR-1999;
                                                                                                                           04-NOV-1999
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17-SEP-2002; 2002WO-IB004208.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9954500-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                The present invention relates to enzymatic nucleic acids which specifically cleave RNA derived from Hepatitis C virus (HCV). The enzymatic nucleic acid or ribozyme is in a harmerhead (HH) or hairpin (HP) motif where the binding arms comprise sequences complementary to one of the substrate sequences defined in the specification. The HCV intozymes are useful for modulating the expression and/or replication of HCV. They can be used to treat cirrhosis, liver fallure and/or replication of hepatocellular carcinoma. The HCV infection in conjunction with one or more a condition associated with HCV infection in conjunction with one or more conterted rung therapies, particularly type I interferon. The present sequence represents a substrate for a HCV harmerhead (HH) ribozyme. Note: Some of the sequence data for this patent did not form part of the printed specification. The complete sequence data for this patent was obtained in electronic format directly from the USPTO web site at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds.
                                                                                                                                                                                                              New ribozymes targeting RNA derived from hepatitis C virus inhibit viral replication and are useful to treat hepatitis C virus infections and cirrhosis, liver failure or hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                  Macejack D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.3%; Score 14; DB 1; Length 15; 71.4%; Pred. No. 1.80+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15 BP; 4 A; 1 C; 5 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                   Roberts B, Pavco PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 segdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                              Claim 1; Page 41; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABT39781 standard; DNA; 17 BP.
                                                  99US-00274553.
                                                                         99US-00274553.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 71.49
Matches 10; Conservative
                                                                                                                                                                   Blatt L, Mcswiggen JA,
                                                                                                         MCSWIGGEN J A.
ROBERTS B.
PAVCO P A.
                                                                                                         (MCSW/) MCSWIGGEN J
(ROBE/) ROBERTS B.
(PAVC/) PAVCO P A.
(MACE/) MACEJACK D.
                                                                                                                                                                                         WPI; 2002-617759/66.
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   US2002082225-A1.
                                                                                                BLATT L.
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                                                  23-MAR-1999;
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                          27-JUN-2002
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                                                                                                BLAT/)
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The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic of any of them, or the corresponding RNA. The novel isolated nucleic component of a gene chip, in vitro as (anti) sense reagents, and for component of a gene chip, in vitro as (anti) sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alatheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these chips. The nucleic acid sequences of the invention can be used in gene things. The nucleic acid sequences of the invention can be used in gene things.
                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy. This polynucleotide sequence represents a tumour suppression related human fukutin oligonucleotide of the invention
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100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 667; 720pp; French.
                                                                                                                                                                             Tuijnder M;
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                                                                                      (MOLE-) MOLECULAR ENGINES LAB
17-SEP-2001; 2001FR-00011978.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            and transfected cells.
                                                                                                                                                                                 relerman A, Amson R,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                        AA265654 to AA269578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AA269579 to AA27440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment.

N. B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3056, 3157, 3237, 3297 and 3357, are not actually given a sequence in the Sequence Listing from the
                                                                                                                                                                                                                    Novel biallelic markers used to construct a high density disequilibrium
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100.0%; Pred. No. 1.9e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                  Chumakov I;
                                                                                                                                                                                                                                                                                    Claim 8; Page 1415; 2745pp; English.
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                      98US-0082614P.
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98US-0109732P.
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                                                                                                                               Blumenfeld M,
                                                                                                                                                                                                                                             map of the human genome
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Best Local Similarity
Matches 14; Conserv
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                    21-APR-1998;
23-NOV-1998;
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                                                                                                                             Cohen D,
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AA265654 to AA269578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AA269579 to AA277440 represent amplification nucleotide sequences. AA269579 to AA277440 represent amplification have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and disgnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment.

N. B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3157, 3227, 3297 and
                                                           Novel biallelic markers used to construct a high density disequilibrium
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No. 2e+02;
0; Indels
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                                                                                                                                                   Claim 8; Page 1123; 2745pp; English
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100.0%; Pre
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98US-0109732P.
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Best Local Similarity 100.º
Matches 14; Conservative
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                                                                                          map of the human genome.
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WPI; 2000-013267/01.
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ö invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment.

N. B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3056, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the The invention relates to human HTREK2 polypeptides and nucleic acid molecules encoding such polypeptides. TREK2 polypeptides are useful in screening assays to identify compounds that may stimulate or inhibit their function or level of expression. Sequences of the invention are used to treat cancer, diabetes, asthma, pulmonary disease, cardiovascular diseases, inflammatory disease, renal disease, pain, psychiatric ö Human, hTREK2 protein, cancer; diabetes; pulmonary disease; asthma; cardiovascular disease; inflammatory disease; psychiatric disorder; renal disease; neurodegenerative disease; neurological disorder; Alzheimer's disease; depression; schizophrenia; stroke; vaccine; trauma; Novel human TREK2 (HTREK2) polypeptide and polynuclectide encoding it, useful for identifying agonists and antagonists in the treatment of diseases associated with a HTREK2 imbalance, such as diabetes, cancers Gaps ; 1.3%; Score 14; DB 1; Length 20; 100.0%; Pred. No. 2e+02; ative 0; Mismatches 0; Indels Sequence 20 BP; 2 A; 4 C; 4 G; 10 T; 0 U; 0 Other; Human TREK2 cDNA specific forward PCR primer. Example 1; Page 20; 29pp; English. (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC. AAD34452 standard; DNA; 20 BP 25-APR-2000; 2000GB-00010060. 01-JUN-2000; 2000GB-00013370. 24-APR-2001; 2001GB-00010129. 324 CTGTTATTCTTGCT 337 4 CIGITALICITECT 17 Ä (first entry) Query Match 1.3 Best Local Similarity 100. Matches 14; Conservative Duckworth pain; PCR; primer; ss. WPI; 2002-332557/37. present invention Homo sapiens. 16-JUL-2002 13-FEB-2002. GB2365010-A Chapman CG, AAD34452; asthma RESULT 357 AAD34452/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel antisense compound targeted to nucleic acid encoding Fas, Fas
ligand or Fas associated protein-1 is useful for inhibiting expression of
Fas, Fas ligand, or Fap-1 in cells or tissues, and for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, immunoguppressive, antiinflammatory, hepatotropic; cytostatic; vasotropic; hepatitis; cancer; allograft rejection; ds; Fas.
                                                                                                                                                     Gaps
disorders including depression and schizophrenia, neurodegenerative
              disease including Alzheimer's disease, stroke and head trauma and neurological disorders. They are also used as vaccines. The present sequence is human hTREK2 cDNA specific PCR primer
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                                                                                                                 1.3%; Score 14; DB 1; Length 20; 100.0%; Pred. No. 2e+02;
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                                                                                 Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                                               100.0%; Prec. ...
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                                                                                                                                                                                                                                                                                                                                                                                                             Human Fas target oligonucleotide #54.
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18-SEP-2000; 2000US-00665615.
                                                                                                                                                                                        114 CTATTGGACTGACT 127
                                                                                                                                                                                                                                                                                                            ABN79739 standard; DNA; 20
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                                                                                                                                                                                                                   19 CTATTGGACTGACT 6
                                                                                                                                                        14; Conservative
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                                                                                                                                       Local Similarity
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(MARC/) MARCUSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (WYAT/) WYATT J. (ZHAN/) ZHANG H.
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                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases (e.g. diabetic retinopathy); disorders associated with excessive bone resorption (e.g. osteoporosis); disorders dimmanalin oral cavity (e.g. gingivitis); and inflammatory skin disorders (e.g. psoriasis). The present DNA sequence represents an anticonnection.
                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense nucleic acid, ss, alpha-V integrin chain, antisense inhibition, cell adhesion modulation; platelet aggregation; immune function; tissue repair; cell proliferation; tumour invasion; cancer; gingivitis; chronic inflammatory disease; Chron's disease; rheumatoid arthritis; ocular neovascular disease; diabetic retinopathy; osteoporosis; excessive bone resorption; inflammatory skin disorder; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense nucleic acid against alpha V integrin for use in pharmaceutical compositions for the specific inhibition of the expression of alpha
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA sequence represents an antisense nucleic acid of the on used to inhibit alpha-V integrin expression
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1.3%; Score 14; DB 1; Length 20; 100.0%; Pred. No. 2e+02; ve 0; Mismatches 0; Indels
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    1.35,
100.08; Pr
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                                                                                                                                                                                                                                                    AAL42518 standard; DNA; 20 BP
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                                                                                          620 AGATGAGTTTTATT 633
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                                                   Conservative
                                                                                                                    18 AGATGAGTTTTATT
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                         Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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                                                                                                                                                                                                                                                                                                AAL42518
    Query Match
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the predisposition of appearance or inheritance of inverted nipples, where the nucleic acid is identical to the region of microsatellites 20200, SW2443, S0097, SW1010 or S0164 on chromosomes 6, 2, 4, 14, 14 and 3, respectively, in pigs, or homologous positions in the genomes of cher mammals. The nucleic acids can be used to select pets, breeding or farm animals that lack inverted nipples, particularly by genomic screening of many related mammals in a population. The present sequence is a PCR primer used in the exemplification of the invention to identify microsatellite markers associated with the inverted nipple phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining predisposition to inverted nipples useful e.g. for selecting breeding animals comprises detecting specific microsatellite markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to the use of a nucleic acid to determine
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                                                                                                                                                               Mammalian inverted nipple associated microsatellite PCR primer #82.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3%; Score 14; DB 1; Length 20; 00.0%; Pred. No. 2e+02; ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                      Inverted nipple; microsatellite; PCR; primer; 88; pig
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ACH00628 standard; DNA; 20
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                                                                                                              (first entry)
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Best Local Similarity 100.
Matches 14; Conservative
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ADH77414
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Query Match

Best Loca Matches

17 TTTCCTTATATT 4

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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                             The invention describes a compound 8-80 nucleobases in length targeted to, and which specifically hybridizes with a nucleic acid molecule encoding PTPN12 (protein tyrosine phosphatase, non-receptor type 12), and inhibits the expression of PTPN12. The compound, composition and methods are useful for treating a disease or condition associated with PTPN12, such as a hyperproliferative disorder, e.g. colon cancer, or a metabolic disorder. They are also useful in research and diagnostics for modulating the expression of PTPN12. This sequence represents a human protein tyrosine phosphatase, non-receptor type 12 (PTPN12) antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense therapy; human; Fas; Fas ligand; FasL; Apo-1L; CD95L; Fas associated protein 1; Fap-1; signal transduction; autoimmune disease; inflammatory disease; cancer; immunosuppressive; antiinflammatory; cytostatic; phosphorothioate; ss.
                                       /mod_base= OTHER
/note= "OTHER= Phosphorothioate backbone. All cytindine
                                                                                                                                                                                                                                                                                                                  for
                                                                                          /mod_base= OTHER
/note= "OTHER= 2'-0-methoxyethyl (2'-MOE) nucleotides"
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                      New antisense oligonucleotides targeted to a nucleic acid encoding protein tyrosine phosphatase, non-receptor type 12 (PTPN12) useful treating a disease associated with PTPN12, e.g. colon cancer.
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100.0%; Pred. No. 2e+02;
cive 0; Mismatches 0; Indels
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                                                           residues are 5-methoxycytidine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Fas cDNA, antisense oligonucleotide #75.
                                                                                                                                                                                                                                                                                                                                               Example 15; SEQ ID NO 55; 117pp; English
           location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADL27795 standard; DNA; 20 BP.
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                                                                                                                                                                                                                         17-JUN-2002; 2002US-00172911
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Best Local Similarity 100.
Matches 14; Conservative
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                              *tag=
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           Key
modified_base
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The present invention relates to antisense compounds targeted to nucleic acids encoding human Pas (also known as Apo-1 or CD95), Fas ligand (Fast, also Apo-1L and CD951), and Fas associated protein 1 (Fap-1). The antisense compound comprises an antisense oligonucleotide that specifically hybridises with one of the said nucleic acids and inhibits Fas, Fast or Fap-1 mediated signal transduction. The antisense oligonucleotide is a chimeric oligonucleotide. The antisense oligonucleotide comprises at least one modified internucleoside linkage, preferably a phosphorothioate linkage. It also comprises at least one modified mucleoside properties and linkage. It also comprises at least one modified mucleosides, preferably a 2-O-methoxyethyl (2-MOE) sugar moiety, The antisense oligonucleotide further comprises at least one modified nucleobase, preferably a 5-methylcytosine. The antisense oligonucleotide further comprises at least one modified ancleosase, preferably a 5-methylcytosine. The antisense oligonucleotide sassociated with overexpression of constitutive activation of Fas, Fast, or Fap-1. The present sequence represents an antisense oligonucleotide used in the examples of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunosuppressive; antiinflammatory; hepatotropic; virucide; cytostatic; antisense technology; Fas; Fas ligand; Fap-1; Fas associated disorder; Fap-1 associated disorder; ischaemia reperfusion injury; apoptosis; allograft; autoimmune disease; inflammatory disease; hepatitis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense oligonucleotides of 20-50 nucleobases, useful for treating autoimmune or inflammatory diseases, and cancer.
                                                                                                                 /mod_base= OTHER
/note= "This oligonucleotide has a phosphorothioate
backbone and 2'-methyoxyethyl (2'-MOE) wings at the 5'
and 3' ends, which are 5 nucleotides in length at each
end. All cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 9 A; 3 C; 0 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.3%; Score 14; DB 1;
100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Fas antisense oligonucleotide seqid 156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 18; SEQ ID NO 156; 76pp; English.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wyatt J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-SEP-2000; 2000US-00665615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADM53567 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ហ
                                                                                   *tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         620 AGATGAGTTTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dean NM, Marcusson EG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-050524/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention.
                                         modified base
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376
                                                                                                                                                 C-erb-B2 sense oligonucleotide
                    AAQ40912 standard; DNA; 17 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВР
                                                                                                                                                                                                                                                                                                                                92WO-GB002073.
                                                                                                                                                                                                                                                                                                                                                                    91GB-00023947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 GAGCCTGCGGCCTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ40911 standard; DNA; 17
                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1993-182253/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 15, Conserv
                                                                                                                                                                                                                                                                                                                                                                    12-NOV-1991;
                                                                                                                                                                                                                                                                                                                                10-NOV-1992;
                                                                                                                                                                                                                                                         WO9309813-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                            Epenetos AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9309813-A1
                                                                                                                                                                                                                                                                                            27-MAY-1993.
                                                                                          25-MAR-2003
07-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
07-SEP-1993
                                                                                                                                                                                                                     Synthetic.
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                                                        AAQ40912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ40911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ40911/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
     AAQ40912
                      용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes an antisense compound 8-30 or 8-50 nucleobases in length targeted to the 5'-untranslated region, translational start site, translational termination region or 3'-untranslated region of a nucleic acid molecule encoding Fas Igand or Fap-1. Also described are: a pharmaceutical composition comprising the anti-sense compound and a pharmaceutical carrier or diluent; a method of inhibiting the expression of Fas or Fap-1 in cells or tissues: treating an animal having a disease or condition associated with Fas or Fap-1; anda preventing allograft rejection, ischaemia reperfusion injury or apoptosis in an allograft celection, ischaemia reperfusion injury or apoptosis in an allograft celection, ischaemia reperfusion of pharmaceutical composition is useful in diagnosing, treating or preventing autoimmune or inflammancy disease, e.g. hepatitis, cancer, e.g. cancer of the colon, liver, lung or a lymphoma, apoptosis, allograft rejection, e.g. cardiac, renal, hepatic or a lymphoma pharmaceutical injury. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense compound targeted to nucleic acid molecule encoding Fas or Fap-1, useful in diagnosing, treating or preventing autoimmune or inflammatory disease, cancer, apoptosis, allograft rejection or ischemia reperfusion injury.
                                                                                                                        /mod_base= OTHER
/note= "OTHER= Phosphorothioate backbone. All cytidines
are 5-methylcytidines"
                                                                                                                                                                                              *tag= a
/mod_base= OTHER
/note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                             /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.3%; Score 14; DB 1; Length 20;
100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 9 A; 3 C; 0 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represents a human Fas antisense oligonucleotide
lymphoma; human; antisense oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 18; SEQ ID NO 156; 83pp; English.
                                                                   Location/Qualifiers
1. .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wyatt J,
                                                                                                                                                                                                                                                                      /*tag= c
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-APR-1999; 99US-00290640.
18-SEP-2000; 2000US-0065515.
09-MAR-2001; 2001US-00802669.
                                                                                                                                                                                                                                                                                                                                                                                                                     14-JUL-2003; 2003US-00619220
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                                                                                                         Ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dean NM, Marcusson EG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Щ
G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-180091/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEAN N M.
MARCUSSON 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WYATT J.
ZHANG H.
                                                                                                                                                                                                                                                                                                                                               US2004033979-A1
                                                                                    modified base
                                                                                                                                                                                                                                                     modified base
                                                                                                                                                                                 modified base
                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   19-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
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(DEAN/) I (MARC/) N (WYAT/) V (ZHAN/) 2

Query Match Matches

8

RESULT 364

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For the selective killing of SKBR3 cells the following radiolabelled cerb-B2 oligonucleotides were used: (1) the antisense oligonucleotide given in AAQ40911, complementary to the non-transcribed sequence at the 5' end of the gene; (2) the sense oligonucleotide given in AAQ40912, complementary to the transcribed sequence at the 5' end of the gene; (3) the random sequence given in AAQ40913, having the same base compsn. as the antisense oligonucleotide. (Updated on 25-MAR-2003 to correct PN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cpd. comprising anti-sense oligo:nucleotide and radioactive moiety - for
treating viral infection, sepsis, leukaemia and tumours.
Double; triple; helix; duplex; triplex; major groove; SKBR3 cell; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Double; triple; helix; duplex; triplex; major groove; SKBR3 cell; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.2%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 2e+02; Ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17 BP; 1 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                 (IMCR ) IMPERIAL CANCER RES TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C-erb-B2 antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 26; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92WO-GB002073.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAY-1993
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Gaps

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12-NOV-1991;

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The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNY) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT, and AAA1768 to AAA17685 to AAA1768 and AAA19087 to corresponding target sequences; AAA17685 to AAA18856 and AAA19087 to AAA18154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086 and AAA19155 to AAA19222 represent their corresponding target sequences;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors.
I, II and III genes. These primers were targetted 100 bp upstream
                                   and downstream of each gene. The amplified sequences were cloned and further amplified using the primers given in AAT05982-87. COX genes from normal individuals and patients with Alzheimer's disease were sequenced and compared. The COX subunit I and II genes were found to be mutated in patients with Alzheimer's disease (AD) and comparison between wildtype and mutations. Knowledge of these mutations allows the detection of the sporadic form of AD. Mutations within the COX I and II genes have also been found to segregate with diabetes mellitus. Oligomers which are antisense to the positions of mutations can be used in the therapy of AD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; veruca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Webor-Rendu syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                       1.2%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 2e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                              Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human TIE-2 substrate sequence SEQ ID NO:1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 56; Page 116; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jarvis T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                562 TGGGTTTTTTAATACCT 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US006507.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 TGGTTTTTCTAATACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA18772 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pavco PA, Roberts E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-591315/50.
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9950403-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA18772;
                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA18772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $$GGGGGGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                              For the selective killing of SKBR3 cells the following radiolabelled cerb-B2 oligonucleotides were used: (1) the antisense oligonucleotide given in AAQ40911, complementary to the non-transcribed sequence at the 5, end of the gene; (2) the sense oligonucleotide given in AAQ40912, complementary to the transcribed sequence at the 5, end of the gene; and (3) the random sequence given in AAQ40913, having the same base compsn. as the antisense oligonucleotide. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mutant mitochondrial cytochrome C oxidase genes - useful for generating probes for diagnosing and treating e.g. Alzheimer's disease and new cell lines for screening for drugs.
                                                                                                                                                                                                                                           Cpd. comprising anti-sense oligo:nucleotide and radioactive moiety - for treating viral infection, sepsis, leukaemia and tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; mitochondrial cytochrome C oxidase; COX; subunit I; subunit II;
subunit III; mutation; Alzheimer's disease; AD; sporadic form;
diabetes mellitus; IDDM; detection; PCR; amplify; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AAT05976-81 are primers which were used in the amplification of the human mitochondrial cytochrome C oxidase (COX)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.8; DB 1; Length 17;
Pred. No. 2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 4 A; 8 C; 4 G; 1 T; 0 U; 0 Other;
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                                                                                                 (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                     Example 3; Page 26; 43pp; English.
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95US-00397808
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                                                91GB-00023947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.2%;
Best Local Similarity 88.2%;
Matches 15; Conservative
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                                                                                                                                                                                                  WPI; 1993-182253/22.
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Mcswiggen JA;

WO9526973-A1

Synthetic.

31-MAY-1996

AAT05984;

AAT05984,

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30-MAR-1995; 30-MAR-1994; 03-MAR-1995;

12-OCT-1995

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AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme sequences for integrin alpha 6 subunit, and AAA20362 to AAA2160 and AAA21689 to AAA21689 represent their corresponding target sequences.

AAA21896 to AAA21475 and AAA2342 to AAA23342 represent ribozyme sequence for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to AAA2342 represent ribozyme sequence for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT, integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are specially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verrues vulgaris, syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, and other syndrome, and diseases related to the levels of ARNT, Tie-2, and other syndromes and diseases related to the levels of ARNT, Tie-2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.2%; Score 13.8; DB 1; Length 17; 76.5%; Pred. No. 2e+02; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     integrin subunit alpha-6, or integrin subunit beta-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hammerhead ribozyme substrate #1736.
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Best Local Similarity
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AC AAF0422
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DT 16-FEB.
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DY RIBOZYI
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HOMO 8:
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HOMO 8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                     Gaps
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             Length 17;
                                     Indela
          Score 13.8; DB 1;
Pred. No. 2e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                  Hammerhead ribozyme substrate #2184.
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            1.2%;
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                                                               396 ITTICCTTACAATICAA
                                                                                       TTTTCCTTACAACTCCA
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                                     Conservative
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                         interferon alpha; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 15; Conserv
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                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                              RESULT 369
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Matches
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Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; notropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inozyme; G-dleaver; amberzyme; zinzyme; lymphoma; leukaemia; b-cell lymphoma; non-Hodgkin's lymphoma; MEL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cenebracycherapy-induced neuropathy; amyotrophic lateral sclerosis; chemocherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; parkingon's disease; ataxia; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease
Human NOGO Amberzyme #239.
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sapiens Synthetic. Homo

16-AUG-2001.

09-FEB-2001; 2001WO-US004273

11-FEB-2000; 2000US-0181797P. 28-FEB-2000; 2000US-0185516P. 06-MAR-2000; 2000US-0187128P.

RIBOZYME PHARM INC MCSWIGGEN J. RIBO-) BLAT/)

Chowrira BM; Mcswiggen J, Blatt L,

CHOWRIRA B M.

WPI; 2001-607195/69.

Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury

Claim 88; Page 136; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NGGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acid cleaving an RNA molecule DNAzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) proposessing an NCH motif). The CD20-targetting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg^2+. The CD20-targetting nucleic acid is used to cleave CC therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-creat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-creat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-creat lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, low-grade or follicular non-created may be contacted with a cell to reduce NOGO gene in the presence of a divalent cation that is preferably Mg^2+. Furthermore, the createring nucleic acid may be contacted with a cell to reduce NOGO activity of the creating nucleic acid may be contacted with a cell to reduce NOGO activity of the concleic acid may be contacted with a cell to reduce NOGO activity of the concleic acid may be contacted with a cell to reduce NOGO activity of the concleic acid may be contacted with a cell to reduce NOGO activity of the concleic acid may be contacted with a cell to reduce NOGO activity of the concleic acid may be contacted with a cell to reduce NOGO activity of the concleic acid may be contacted with a cell to reduce NOGO activity of the concleic acid may be contacted with a cell to reduce NOGO activity of the concleic acid may become of a gease, activity and cerebrovascular accident comprise at axia, multiple aclerosis (MS). Parkinson's disease, mu

BP.

AAF69029 standard; DNA; 17

RESULT 372 AAF69029/C ID AAF6903

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                                                                                                                                                                                                                                                                                                                                                            Mitochondria; cytochrome C oxidase; COX; Alzheimer's disease; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Targeting conjugate molecule to mitochondria having defective cytochrome C oxidase activity for diagnosing Alzheimer's disease, involves contacting mitochondria with a conjugate of targeting molecule and toxin.
states which respond to the modulation of NOGO expression. The present
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                                                                                                      Gaps
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                                                                      Score 13.8; DB 1; Length 17;
Pred. No. 2e+02;
0; Mismatches 2; Indels
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Pred. No. 2e+02;
0; Mismatches 2; Indels
              sequence is an amberzyme molecule of the invention
                                           Sequence 17 BP; 11 A; 2 C; 2 G; 0 T; 2 U; 0 Other;
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                                                                                                     0;
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                                                                                                                                     429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.2%;
                                                                          1.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-00219842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTTTTTCTAATACCTT
                                                                                                                                       413 GGGTTTTTCCTTATATT
                                                                                                                                                                 17 GAGTTTTTCCTTATTT
                                                                                                                                                                                                                                            AAF69066 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.2'
                                                                                                                                                                                                                                                                                                    12-APR-2001 (first entry)
                                                                          Query Match
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herrnstadt C, Parker WD;
                                                                                                                                                                                                                                                                                                                                  COXII PCR primer #13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-136875/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MITO-) MITOKOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       US6171859-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JAN-2001.
                                                                                                                                                                                                                                                                          AAF69066;
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                                                                                                                                                                                                               RESULT 371
                                                                                                                                                                                                                                AAF69066/
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Homo
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                                                                                                                                                                                                                                                                            The present invention relates to a method for selectively accumulating a mitochondrial disabling or destructive amount of a conjugate molecule in mitochondria having defective cytochrome C oxidase (COX) activity or displaying increased membrane potential. The method involves contacting mitochondria with a conjugate molecule comprising a targeting molecule accomjugated to a toxin, where the conjugate or targeting molecule socingated to a toxin, where the conjugate or targeting molecule accumulates in the mitochondria. The method is useful for diagnosis of Alzheimer's disease (AD), especially sporadic AD. The present sequence is a PCR primer used in the method of the present invention
                                                         Mitochondria; cytochrome C oxidase; COX; Alzheimer's disease; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitochondria; cytochrome C oxidase; COX; Alzheimer's disease; PCR primer;
                                                                                                                                                                                                                          Targeting conjugate molecule to mitochondria having defective cytochrome C oxidase activity for diagnosing Alzheimer's disease, involves contacting mitochondria with a conjugate of targeting molecule and toxin.
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                   Score 13.8; DB 1; Length 17;
Pred. No. 2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                             Example 2; Col 39; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                      562 TGGGTTTTTAATACCT 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-00413740.
                                                                                                                                       95US-00413740
                                                                                                                                                        94US-00219842
                                                                                                                                                                                                                                                                                                                                                                                                                                 17 TGGTTTTTCTAATACCT
                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                          WPI; 2001-136875/14.
                                         COXII PCR primer #5
                                                                                                                                                                        (MITO-) MITOKOR
                                                                                                                                                                                          Herrnstadt C,
                                                                                    Homo sapiens
                                                                                                                                      30-MAR-1995;
                                                                                                                                                        30-MAR-1994;
                         12-APR-2001
                                                                                                    US6171859-B1
                                                                                                                      09-JAN-2001
         AAF69029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 373
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The present invention relates to a method for selectively accumulating a mitochondrial disabling or destructive amount of a conjugate molecule in mitochondria having defective oyrochrome C oxidase (COX) activity or displaying increased membrane potential. The method involves contacting mitochondria with a conjugate molecule comprising a targeting molecule conjugated to a toxin, where the conjugate or targeting molecule selected accumulates in the mitochondria. The method is useful for diagnosis of Alzheimer's disease (AD), especially sporadic AD. The present sequence is a PCR primer used in the method of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondria; cytochrome C oxidase; COX; Alzheimer's disease; PCR primer;
                                                                                                                                                                                                                                                 Targeting conjugate molecule to mitochondria having defective cytochrome C oxidase activity for diagnosing Alzheimer's disease, involves contacting mitochondria with a conjugate of targeting molecule and toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Targeting conjugate molecule to mitochondria having defective cytochrome C oxidase activity for diagnosing Alzheimer's disease, involves contacting mitochondria with a conjugate of targeting molecule and toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a method for selectively accumulating a mitochondrial disabling or destructive amount of a conjugate molecule in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.2%; Score 13.8; DB:
88.2%; Pred. No. 2e+02;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Col 41-42; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Col 41-42; 88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
94US-00219842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGTTTTTCTAATACCT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-00413740.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           562 TGGGTTTTTAATACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF69064 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-APR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                            Parker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COXII PCR primer #11.
                                                                                                                                                                                     WPI; 2001-136875/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 15; Conserv
                                                            (MITO-) MITOKOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MITO-) MITOKOR
                                                                                                                            Herrnstadt C,
30-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
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Fri Aug 19 11:00:00 2005

ВР

ABL46970 standard; RNA; 17

ABL46970

ABL46970;

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The present invention relates to a method for selectively accumulating a mitochondrial disabling or destructive amount of a conjugate molecule in mitochondria having defective ortochrome c oxidase (COX) activity or displaying increased membrane potential. The method involves contacting mitochondria with a conjugate molecule comprising a targeting molecule conjugated to a toxin, where the conjugate or targeting molecule selected accumulates in the mitochondria. The method is useful for diagnosis of Alzheimer's disease (AD), especially sporadic AD. The present sequence is a PCR primer used in the method of the present invention
                                                                                                                                                                                                                ö
mitochondria having defective cytochrome C oxidase (COX) activity or displaying increased membrane potential. The method involves contacting mitochondria with a conjugate molecule comprising a targeting molecule conjugated to a toxin, where the conjugate or targeting molecule selected accumulates in the mitochondria. The method is useful for diagnosis of Alzheimer's disease (AD), especially sporadic AD. The present sequence is a PCR primer used in the method of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondria; cytochrome C oxidase; COX; Alzheimer's disease; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Targeting conjugate molecule to mitochondria having defective cytochrome C oxidase activity for diagnosing Alzheimer's disease, involves contacting mitochondria with a conjugate of targeting molecule and toxin.
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                  ;
0
                                                                                                                                                                               Score 13.8; DB 1; Length 17;
Pred. No. 2e+02;
                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                              Seguence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Col 38; 88pp; English.
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0
                                                                                                                                                                                                                                                     579
                                                                                                                                                                                                                                                                                                                                                                            BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-00219842
                                                                                                                                                                               1.2%;
Local Similarity 88.2%;
Les 15; Conservative
                                                                                                                                                                                                                                                                                      17 GGTTTTTCTAATACCTT
                                                                                                                                                                                                                                                                                                                                                                            AAF69018 standard; DNA; 17
                                                                                                                                                                                                                                                     563 GGGTTTTTTAATACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parker WD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-136875/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COXII PCR primer #3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herrnstadt C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US6171859-B1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                               AAF69018;
                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
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Human; inflammatory bowel disease 1 protein; IBD1; IBD1prox; intestinal inflammatory disease; apoptosis; NF-kappa B; cancer; inflammatory disease; immune disease; cryptogenetic inflammation; hemorrhagic rectocolitis; Crohn's disease; Blau syndrome; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to oligonucleotides that downregulate the expression of human Grb2-related with Insert Domain (GRID) gene. GRID is a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful for modulating the expression of GRID, to treat conditions such as tissue/graft rejection and leukaemia. The oligonucleotides can also be administered in conjunction with other therapies such as radiation, chemotherapy and cyclosporin treatment. The present oligonucleotide was used to illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer for studying biallelic polymorphic markers in the IBD1 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                            Human, Grb2-related with Insert Domain; GRID; T-cell; co-stimulatory adaptor protein; tissue rejection; graft rejection; leukaemia; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                               Ellis JH;
                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid(s) for regulating the Grb2-related with Insert [
[D] gene comprises using antisense and enzymatic nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13.8; DB 1; Length 17; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                               Hamblin PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 BP; 2 A; 2 C; 9 G; 0 T; 4 U; 0 Other;
                                                                         Human GRID zinzyme substrate oligonucleotide #54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                               Mcswiggen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                         (GRID) gene comprises using antisense as molecules such as hammerhead ribozymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 72; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 TCAGTGGGGCTATTGGA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17
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                                                                                                                                                                                                                                                           23-FEB-2001; 2001WO-US005957.
                                                                                                                                                                                                                                                                                      24-FEB-2000; 2000US-0184594P.
                                                                                                                                                                                                                                                                                                                                                                  Von Carlowitz I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 UCAGUGGGGCUGUGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI65652 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                     RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                    (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-550088/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                WO200162911-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JAN-2002
                                                                                                                                                                                                                              30-AUG-2001
                                            27-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                  Jarvis T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI65652;
                                                                                                                                                                                                                                                                                                                       (RIBO-)
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Gaps

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1.2%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 2e+02; tive 0; Mismatches 2; Indels

TGGGTTTTTTAATACCT 578

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Conservative

Query Match Best Local Similarity Matches 15; Conserv

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                                                                                                                                                                                                                                                                          primers AAI65647-78 were used to characterise biallelic polymorphic markers in the IBD1 gene region. The IBD1 gene encodes an inflammatory bowel disease 1 (IBD1) polypebtide, which is associated with intestinal inflammatory disease. The specification also describes a polypeptide which is in proximity to IBD1, and is designated IBD1prox. The IBD1 gene is probably involved in regulation of apoptosis and activation of NF-kappa B. The IBD1 and IBD1prox polymucleotides are is useful as source of probes and primers, as source of (anti) sense oligonuclectides, for recombinant production of polypeptides, and in screening for interactive compounds. The polypeptides are used to raise specific antibodies which useful for diagnostic detection or purification of IBD1 and IBD1prox polymucleotides and polypeptides are useful for creatment and prevention of inflammatory and/or immune diseases or cancer, where associated with mutations in genes corresponding to IBD1 and IBD1prox, especially cryptogenetic inflammation of the intestines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                       New human nucleic acids associated with intestinal inflammatory disease, useful for diagnosis, prognosis and control of these diseases, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (hemorrhagic rectocolitis, Crohn's disease and Blau syndrome)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.2%; Score 13.8; DB 1; Length 17;
88.2%; Pred. No. 2e+02;
ive 0; Mismatches 2; Indels
                                                                                                                                                         Chamaillard M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 3 A; 10 C; 2 G; 2 T; 0 U; 0 Other;
                                                                                                                                                         Lesage S,
                                                                                                                                                                                                                                                       Example 4; Page 85; 97pp; French.
                                                                                                                                                        Zouali M,
                                                                                                                                 (DAUS-) FOND DAUSSET-CEPH JEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 GCCATCTCCCCCATCCC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCCATCTCCCCAAGCCC 17
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                                                                                 27-MAR-2000; 2000FR-00003832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-2001; 2001WO-US016981.
                                                                                                         27-MAR-2000; 2000FR-00003832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Les 15; Conservative
                                                                                                                                                       Thomas G,
                                                                                                                                                                               WPI; 2001-608364/70
                                                                                                                                                                                                                             related proteins.
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            Homo sapiens.
                                   FR2806739-A1.
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                                                          28-SEP-2001
                                                                                                                                                       Hugot JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABN06757;
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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 strongly and read as probes to detect, characterise and quantify hGDMLP-1 protein substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunospens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption indisation, as the responsible of the harden captures encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed protein and but was obtained in electronic format directly from MIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2563.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 5 A; 2 C; 9 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK, Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 6749; 214pp; English
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                                                                                               2001WO-US000662.
2001WO-US000663.
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2000US-0236359P
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ji Y, Penn SG,
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                                                                                                                              30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
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30-JAN-2001;
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Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.

Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2564.

(first entry)

29-MAY-2002

ABN02572;

ABN02572 standard; DNA; 17 BP.

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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids in samples, as amplification substrates, to nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP-proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production and skeletal muscle disorders. hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1 in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence on this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip. wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins,
Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide, for raising antibodies that recognize hGDMLP-1 prote or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                   muscle, myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shannon ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR,
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                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US000663.
30-JAN-2001; 2001WO-US000664.
30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000665.
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2001WO-US000670.
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                                                                                                                                                                                                           25-MAY-2001; 2001WO-US016981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ji Y, Penn SG,
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                                                                                                                            WO200192524-A2.
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                                                                                    Homo sapiens.
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2001WO-US000663. 2001WO-US000663. 2001WO-US000664. 2000GB-00024263. 2001WO-US000661.

> 30-JAN-2001; 30-JAN-2001; 30-JAN-2001; 30-JAN-2001;

25-MAY-2001; 2001WO-US016981

WO200192524-A2.

06-DEC-2001

Homo sapiens.

2000US-0234687P 2000US-0236359P

26-MAY-2000; 27-SEP-2000; 04-OCT-2000; 30-JAN-2001;

21-SEP-2000;

2001WO-US000665. 2001WO-US000666. 2001WO-US000667.

30-JAN-2001;

2001WO-US000669. 2001WO-US000670. 2001WO-US000668

30-JAN-2001; 30-JAN-2001; 05-FEB-2001;

30-JAN-2001;

2001US-0266860P

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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 uncleic acids in sample, as amplification substrates, to nucleic acids in sample, as amplification substrates, to hGDMLP-1 uncleic acids in sample, as amplification substrates, to protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as concentration and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The polymucleotide sequence senceding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart captumence in the expression of hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGMDMLP-1 sequence in the exemplification of the present invention. N. B. Chimble-1 sequence data for this patent did not form part of the printed specific attor, but was obtained in electronic format directly from WIPO at they wipo int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser
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Gaps

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1.2%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 2e+02; ative 0; Mismatches 2; Indels

GCAGCTGCCACCTTATG 761

745 17

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Conservative

Query Match Best Local Similarity Matches 15; Conserv

Best Loca Matches

Shannon ME;

Chen W,

Hanzel DK, Rank DR,

Ji Y, Penn SG,

Gu Y,

(AEOM-) AEOMICA INC.

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Gaps

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protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL Mast two loaforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a roll similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mapped to human chromosome 10912.1. HTPL and its coding sequence are mapped to human chromosome 10912.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placente, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for
                                                                                                                                                                                                                                                                                                                                                                                            Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
human testis expressed Patched like protein; testis; adrenal; liver;
male germ cell development; bone marrow; brain; kidney; lung; placenta;
prostate; skeletal muscle; colon; male infertility; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention relates to human testis expressed Patched like
                                 Score 13.8; DB 1; Length 17; Pred. No. 2e+02;
                                                                        2; Indels
Sequence 17 BP; 4 A; 5 C; 7 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                         Human HTPL scanning oligonucleotide SEQ ID 4243
                                                    2e+02;
                                                                      0; Mismatches
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                                                                                                             744 GGCAGCTGCCACCTTAT 760
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2001WO-US000665.
2001WO-US000667.
2001WO-US000668.
2001US-00864761.
                                                                                                                                                                                                                                            ABV82997 standard; DNA; 17 BP
                                 1.2%;
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                                                      Local Similarity 88.2
1es 15; Conservative
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                                   Query Match
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                                                                                                                                                                                                      RESULT 381
                                                                        Matches
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The invention relates to a nucleic acid molecule (1) which down regulates expression of an Ets-related gene (RRG). (1) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration,
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male infertility and cancer. The present oligonucleotide was used in an example from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neovasculār glaucoma; myopic degenerātion; arthritis; verruca vulgaris; angicipitoma of tuberous sclerosis; port-wine stain; wound healing; sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polynucleotide which down regulates expression of Ets-related gen useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antitarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphome; Ewing's sarcome; melanome; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration;
                                                                                                                                          Gaps
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                                                                                                Score 13.8; DB 1; Length 17;
Pred. No. 2e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ERG Amberzyme target sequence Seq ID No 2055.
                                                          0 U; 0 Other;
                                                            G; 10 T;
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                                                                                                  1.2%;
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                                                            Sequence 17 BP; 3 A; 1 C; 3
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                                                                                                                                                                                                                        1 AGATTATGTTTCTTGTT
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                                                                                              Query Match
Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                ABK19408;
                                                                                                                                                                                                                                                                                     RESULT 382
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Gaps

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Indels

5;

Mismatches

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Conservative

15;

Matches

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2e+02;

Pred. No.

88.2%;

Best Local Similarity

Fri Aug 19 11:00:00 2005

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The invention relates to a typing kit for judging human leukocyte antigen (HLA) genotype of a sample by hybridising a substrate on which 10-24 base oligonucleotides (ABL30512-ABL31809) originating in the sequences of genes e.g. belonging to HLA class I antigens on human genome and containing gene polymorphisms as alloantigens have been immobilised as primers for amplification of cleaved nucleic acids relating to gene polymorphisms. The method is useful for judging HLA genotypes of individuals by determining immunogenetic differences before transplanting between them, providing genetic information to decide compatibility of organ and tissue for transplantation e.g. of bone marrow, kidney, liver, pancreas, langerhans islet in pancreas and cornea, susceptibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of individuals e.g. by determining immunogenetic differences when transplanting between them.
ERG gene, by contacting (I) with RNA, in the presence of a divalent cation such as Mg2+. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes. ABK17354-ABK22719 represent nucleic acids, including antisense and enzymatic nucleic acid molecules which regulate expression of ERG, and related PCR primers of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nishida M;
                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA; genotype; polymorphism;
genetic disease; ss.
                                                                                                                                                                                                                                  1.2%; Score 13.8; DB 1; Length 17; 70.6%; Pred. No. 2e+02; ve 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis of genetic diseases and identifying individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human HLA genotyping oligonucleotide SEQ ID NO 894.
                                                                                                                                                                                              Sequence 17 BP; 4 A; 3 C; 6 G; 0 T; 4 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Page 262; 345pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; human leukocyte antigen;
immunogenetic; transplantation;
                                                                                                                                                                                                                                                                                                               916
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                                                                                                                                                                                                                                                        70.6%;
                                                                                                                                                                                                                                                                                                               960 GGACCCAGGACATTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL31405 standard; DNA; 17
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                                                                                                                                                                                                                                                      Best Local Similarity 70.6 Matches 12; Conservative
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                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human;
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 383
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the present and diagnosis of Alzheimer's disease (AD). The method comprises treatment and diagnosis of Alzheimer's disease (AD). The method comprises the use of genetic mutations in the human mitochondrial cytochrome coxidase (COX) gene and their segregation with AD. Alze disclosed are antisense sequences specific to mutant human cytochrome coxidase genes that are designed to bind and inhibit transcription or translation of the carget mutant COX genes without inhibiting transcription or translation of wild-type cytochrome coxidase genes. Also disclosed are probes for detecting a disease state associated with one or more mutations in the mitochondrial COX genes, and a kit comprising a probe for detection of an alzheimer's disease genotype which is complementary to the sense or antisense strands of a mitochondrial COX gene. Definitive diagnosis of Alzheimer's disease can currently only be accomplished by pathological examination at autopsy, the new method provides a non-invasive diagnostic that is reliable at or before the earliest manifestations of AD symptoms. There is at present no effective therapy for AD other than certain compliative treatments. The new therapeutic compositions and methods provide an effective therapy that addresses the primary cause of AD. The present sequence represents a primer for the human mitochondrial COX present sequence represents a primer for the human mitochondrial COX
                                                                                                                                                                                                                                                                                           Alzheimer's disease, AD; human; mitochondrial cytochrome c oxidase; COX; segregation; nootropic; neuroprotective; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Compositions and methods for the treatment and diagnosis of Alzheimer's disease using nucleic acids related in sequence to (mutants of) the cytochrome c oxidase gene.
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88.2%; Pred. No. 2e+02;
iive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                        Human mitochondrial COX gene primer #9.
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420
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95US-00413740.
99US-00448312.
                                      17
                                                                                                                                       BP
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                                                                                                                                   ADA49961 standard; DNA; 17
404 ACAATTCAAGGGTTTTT
                              1 ACAATTACAGGGTTTTT
                                                                                                                                                                                                                     (first entry)
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Best Local Similarity
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30-MAR-1995;
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                                                                                                    RESULT 38
ADA49961/
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DB 1; Length 17;

1.2%; Score 13.8;

Query Match

Seguence 17 BP; 5 A; 2 C; 3 G; 7 T; 0 U; 0 Other;

ADA49972,

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The present invention relates to compositions and method for the treatment and diagnosis of Alzheimer's disease (AD). The method comprises the use of genetic mutations in the human mitochondrial cytochrome coxidase (COX) gene and their segregation with AD. Also disclosed are antisense sequences specific to mutant human cytochrome coxidase genes cartisense sequences specific to mutant thuman cytochrome coxidase genes cartisense sequences specific to mutant thuman cytochrome coxidase genes cartisted coxidase genes. Also disclosed are probes for target mutant COX genes without inhibiting transcription or translation of the carget mutant COX genes without inhibiting transcription or translation of the cartism a disease state associated with one or more mutations in the mitochondrial COX genes, and a kit comprising a probe for detection of an Alzheimer's disease genotype which is complementary to the sense or antisense strands of a mitochondrial COX gene. Definitive disagnosis of Alzheimer's disease can currently only be accomplished by pathological examination at autopsy, the new method provides a non-invasive diagnostic that is reliable at or before the earliest manifestations of AD symptoms. There is at present no effective therapy for AD other than certain call addresses the primary cause of AD. The provide an effective therapy that addresses the primary cause of AD. The
                                                                                                                                                                                                                                                                                              Alzheimer's disease; AD; human; mitochondrial cytochrome c oxidase; COX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compositions and methods for the treatment and diagnosis of Alzheimer's disease using nucleic acids related in sequence to (mutants of) the
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                                                                                                                                                                                                                                                                                                                    segregation; nootropic; neuroprotective; primer; ss.
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                                                                                                                                                                                                                                                     Human mitochondrial COX gene primer #55
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                                                                                                                              ADA50007 standard; DNA; 17 BP
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95US-00413740.
99US-00448312.
17 TGGTTTTTCTAATACCT 1
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                                                                                                                                                                                                                (first entry)
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23-NOV-1999;
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The present invention relates to compositions and method for the treatment and diagnosis of Alzheimer's disease (AD). The method comprises the use of genetic mutations in the human mitochondrial cytochrome coxidase (CCX) gene and their segregation with AD. Also disclosed are antisense sequences specific to mutant human cytochrome coxidase genes that are designed to bind and inhibit transcription or translation of the target mutant COX genes without inhibiting transcription or translation of wild-type cytochrome coxidase genes. Also disclosed are probes for detecting a disease state associated with one or more mutations in the mitochondrial COX genes, and a kit comprising a probe for detection of an Alzheimer's disease genotype which is complementary to the sense or antisense strands of a mitochondrial COX gene. Definitive diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alzheimer's disease can currently only be accomplished by pathological examination at autopsy, the new method provides a non-invasive diagnostic that is reliable at or before the earliest manifestations of AD symptoms. There is at present no effective therapy for AD other than certain palliative treatments. The new therapeutic compositions and methods provide an effective therapy that addresses the primary cause of AD. The present sequence represents a primer for the human mitochondrial COX
                                                                                                                                            Alzheimer's disease; AD; human; mitochondrial cytochrome c oxidase; COX; segregation; nootropic; neuroprotective; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compositions and methods for the treatment and diagnosis of Alzheimer's disease using nucleic acids related in sequence to (mutants of) the
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0; Mismatches
                                                                                                             Human mitochondrial COX gene primer #20.
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95US-00413740.
99US-00448312.
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ADA49972 standard; DNA; 17 BP
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                                                                        (first entry)
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23-NOV-1999;
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                                    ADA49972;
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ID ADAS00
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579

563 GGGTTTTTTAATACCTT 17 GGTTTTTCTAATACCTT

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88.2%;

Conservative

Best Local Similarity Matches 15; Conserv

Query Match

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Human mitochondrial COX gene primer #54
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ADA50271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to compositions and method for the treatment and diagnosis of Alzheimer's disease (AD). The method comprises the autations in the human mitochondrial cytochrome coxidase (COX) gene and their segretation with AD. Also disclosed are antisense sequences specific to mutant human cytochrome coxidase genes that are designed to bind and inhibit ing transcription or translation of the target mutant COX genes without inhibiting transcription or translation of the target mutant COX genes that a sesociated with one or more mutations in the mitochondrial COX genes, and a kit comprising a probe for detection of an also and a kit comprising a probe for detection of an alzaeimer's disease genotype which is complementary to the sense or antisense strands of a mitochondrial COX gene. Definitive diagnostic continuation at autopsy, the new method provides a non-invasive diagnostic that is reliable at or before the earliest manifestations of AD symptoms. There is at present no effective therapy for AD other than certain the reliable at the completion and method and method and the compositions and method and method and the completions and method and method and contains and method and contains and method and contains and method and contains and contains and method and contains and contains
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                                                                                                       Alzheimer's disease; AD; human; mitochondrial cytochrome c oxidase; COX;
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                                                                                                                       segregation; nootropic; neuroprotective; primer; ss.
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                                                                     Human mitochondrial COX gene primer #57.
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95US-00413740.
99US-00448312.
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Matches 15; Conserv
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30-MAR-1995;
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     ADAS0009;
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The present invention relates to compositions and method for the treatment and diagnosis of Alzheimer's disease (AD). The method comprises the use of genetic mutations in the human mitochondrial cytochrome coxidase (COX) gene and their segregation with AD. Also disclosed are antisense sequences specific to mutant human cytochrome coxidase genes that are designed to bind and inhibit transcription or translation of the target mutant COX genes without inhibiting transcription or translation of the carget mutant COX genes without inhibiting transcription or translation of wild-type cytochrome coxidase genes. Also disclosed are probes for detecting a disease state associated with one or more mutations in the conticendorial COX genes, and a kit comprising a probe for detection of an altoheimer's disease genotype which is complementary to the sense or Alzheimer's disease can currently only be accomplished by pathological commination at autopsy, the new method provides a non-invasive diagnostic that is reliable at or before the earliest manifestations of AD symptoms. There is at present no effective therapy for AD other than certain cylliative treatments. The new therapeutic compositions and methods present sequence represents a primer for the human mitochondrial COX present sequence represents a primer for the human mitochondrial COX
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Alzheimer's disease; AD; human; mitochondrial cytochrome c oxidase; COX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compositions and methods for the treatment and diagnosis of Alzheimer's disease using nucleic acids related in sequence to (mutants of) the cytochrome c oxidase gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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Pred. No. 2e+02;
0; Mismatches 2; Indels
                                      segregation; nootropic; neuroprotective; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 25; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             562 TGGGTTTTTAATACCT 578
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95US-00413740.
99US-00448312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regririrciaaracci
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nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herrnstadt C, Ghosh SS;
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                                                                                                                                                                                             US2003087858-A1
                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-1994;
30-MAR-1995;
23-NOV-1999;
                                                                                                                        Homo sapiens.
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This invention relates to a method for determining whether a patient will show a hypersensitivity, or similar, reaction to abacavir by typing the patient for presence of the 57.1 ancestral haplotype of the Major Histocompatibility Complex (MrC). The ancestral haplotype is defined by presence of the human leukcoyte antigen (HLA) subtypes HLA=B*5701, C4A6, HLA-DR7 and HLA-DQ3. Human immunodeficiency virus (HIV) is the actiological agent of a complex disease that includes progressive destruction of the immune system (acquired immune deficiency syndrome, AIDS) and degeneration of the peripheral nervous system. It is known that come antiviral compounds which act as inhibitors of HIV replication are effective agents in the treatment of AIDS. Treatment with an antiviral to a person with hypersensitivity may lead to a range of ailments and occasionally death. Patients who have the 57.1 ancestral haplotype are at nucleoside reverse transcriptase inhibitor (NRT) antiretroviral drug often used to treat HIV and AIDS. The identification method of the Invention may be useful for identifying patients who need to be excluded from treatment with abacavir. The present sequence is that of a human sequencing and PCR amplification primer which was used for identifying the present sequence or absence of the 57.1 ancestral haplotype of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
              immune system; acquired immune deficiency syndrome; AIDS; seripheral nervous system; antiviral compound; HIV replication inhibitor; antiviral; nucleoside reverse transcriptase inhibitor; NRTI; antiviral drug; abacavir; human; sequencing primer; primer; PCR; ss;
4LA-B*5701; C4A6; HLA-DR7; HLA-DQ3; Human immunodeficiency virus; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Method for the identification of subjects hypersensitive to abacavir, useful for excluding patients from treatment, comprises detecting the presence of the 57.1 ancestral haplotype.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antisense oligonucleotide; neurite growth inhibitor; NOGO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 5 A; 5 C; 5 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3xample 2; Page 21; 43pp; English
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                                                                                                                                                                                                                                                                                                                                          (EPIP-) EPIPOP PTY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-697530/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                             WO2003068985-A1.
                                                                                                                                       Homo sapiens.
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The invention comprises nucleic acids (e.g. antisense oligonucleotides)

that down regulate the expression or inhibit the function of a receptor

that down regulate the expression or inhibit the function of a receptor

(or a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),

consistent on are useful for treating: exebrovascular accident, central

nervous system (CMS) injury, spinal cord injury, cancer (e.g. melanoma,

lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,

restenosis or asthma), crohn's disease, diabetes, obesity, autoimmune

disease, lupus, multiple sclerosis, transplant/graft rejection,

conditions (e.g. asthma, allergic rhinitis or acpoic dermatitis). The

nucleic acids of the invention are also useful for down-regulating the

expression of a target gene and as a diagnostic tool to examine genetic

drifts and mutations within diseased cells or to detect the presence of a

target RNA in a cell. The present RNA sequence represents a human NOGO

receptor inozyme substrate sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel enzymatic nucleic acid that down-regulates expression of neurite growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or protein kinase PKR genes, for treating cancer and inflammatory disease.
           protein kinase PKR; cerebrovascular accident; central nervous system injury; CNS injury; spinal cord injury; cancer; melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis; restenosis; asthma; Crohn's disease; diabetes; obesity; autorimmune disease; lupus; multiple sclerosis; transplant rejection; graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis; allergy; asthma; allergic rhinitis; atopic dermatitis;
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prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
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); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; SEQ ID NO 217; 317pp; English.
                                                                                                                                                  NOGO receptor inozyme; substrate; ds.
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29-MAY-2001; 2001US-0294412P.
28-AUG-2001; 2001US-0315315P.
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nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-058513/05
                                                                                                                                                                                                                             WO200281628-A2
                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                17-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention comprises nucleic acids (e.g. antisense oligonucleotides)
that down regulate the expression or inhibit the function of a receptor
that down regulate the expression or inhibit the function of a receptor
(Brappa Kinase (RKK), or protein kinase PKR. The nucleic acids of the
invention are useful for treating: cerebrovascular accident, central
nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
Lymphoma or gliomal, inflammatory disease (e.g. rheumatoid arthritis,
restencis or asthma), Crohn's disease, diabetes, obesity, autoimmune
disease, lupus, multiple sclerosis, transplant/graft rejection,
conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
nucleic acids of the invention are also useful for down-regulating the
expression of a target gene and as a diagnostic tool to examine genetic
chifts and mutations within diseased calls or to detect the presence of
target RNA in a cell. The present RNA sequence represents a human NOGO
receptor amberzyme substrate sequence.
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                                                                                                                                                                                                                                                                                                                                                                          Novel enzymatic nucleic acid that down-regulates expression of neurite growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or protein kinase PKR genes, for treating cancer and inflammatory disease.
                                           rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; 88; GRID; Grb2-related with insert domain; hammerhead ribozyme;
prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK; protein kinase PKR; cerebrovascular accident; central nervous system injury; CNS injury; spinal cord injury; cancer; melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis restenosis; asthma; Crohn's disease; diabetes; obesity; autoimmune disease; lupus; multiple sclerosis; transplant rejection; graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis; allergy; asthma; allergic rhinitis; atopic dermatitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.2%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 2e+02;
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                                                                                                                                                                                                                                                                                                                          Haeberli P, Mcswiggen J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; SEQ ID NO 888; 317pp; English.
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29-MAY-2001; 2001US-0294412P.
28-AUG-2001; 2001US-0315315P.
                                                                                                                                                                                                                    03-APR-2002; 2002WO-US010512.
                                                                                                                                                                                                                                                                                                 (RIBO-) RIBOZYME PHARM INC.
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                                                                                                                                                                                                                                                                                                                          Chowrira B,
                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-058513/05.
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Best Local Similarity
                                                                                                                                                                WO200281628-A2.
                                                                                                                                       Unidentified.
                                                                                                                                                                                           17-OCT-2002,
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                                                                                                                                                                                                                                                                                                                            Blatt L,
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADM54293
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The invention relates to a nucleic acid molecule that down-regulates cayression of Grb2-related with insert domain (GRID) gene, e.g. a cayression of Grb2-related with insert domain (GRID) gene, e.g. a nammerhead ribozyme, NGH ribozyme, G-cleaver ribozyme, Zinzyme, DNAzyme, anderzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell including the novel nucleic acid molecule, reducing GRID activity in a cell by contacting the cell with the novel nucleic acid molecule, resorging the cell with the novel nucleic acid molecule, an expression certeating the cell with the novel nucleic acid molecule, an expression vector comprising a nucleic acid sequences (encoding at least the novel nucleic acid molecule in a manner that allows its expression), a concleic acid molecule in a manner that allows its expression), a caid molecule that cleaves RNA derived from a GRID gene. The nucleic acid molecule for treating a condition associated with the level of molecule is useful for treating a condition associated with the level of GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is a target region for the enzymatic nucleic acides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecule that down-regulates expression of Grb2-related with insert domain (GRID) gene, useful for treating a condition associated with the level of GRID, e.g. tissue/graft rejection and
NCH ribozyme; G-cleaver ribozyme; Zinzyme; DNAzyme; amberzyme; Inozyme;
hairpin ribozyme; tissue rejection; graft rejection; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; ds; breast cancer; human; ER+ breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 2 A; 2 C; 9 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; SEQ ID NO 603; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCAGTGGGGCTATTGGA 121
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                                                                                                                                                                                                                                                                                                                                                                                             10-FEB-2000; 2000US-0181594P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        JARVIS T.
CARLOWITZ I V.
MCSWIGGEN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HAMB/) HAMBLIN P A. (ELLI/) ELLIS J H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-829646/77.
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                                                                                                                                                                                  JS2003134806-A1
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                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (JARV/)
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                                                                                                                                                                                               The invention relates to a composition which contains at least one vector (B) containing a nucleic acid (I) associated with breast cancer. The vector (B), also polypeptides (II) encoded by (I), are used for treatment of breast cancer. Arrays based on (I), (II), or their fragments, and (II) especific antibodies (Ab) are used to predict characteristics (e.g. invasiveness or stage) of breast cancer, and (I), or its fragments, are used to modulate characteristics of such cells; to identify breast cancer genes and to detect breast cancer (by detecting polymorphic nucleic acid or its products). The present sequence represents a human ER+ breast cancer differentially expressed sequence.
                                                                                                                                       Vector containing nucleic acid associated with breast cancer, useful for treating, diagnosing and characterizing breast cancer, also related polypeptides and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                нимап; вв; probe; myosin-like protein-l; hGDMLP-l;
hGDMLP-l agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
skeletal muscle function.
                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                 1.2%; Score 13.8; DB 1; Length 17;
88.2%; Pred. No. 2e+02;
cive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                              Sequence 17 BP; 7 A; 6 C; 2 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                               Claim 1; SEQ ID NO 270; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human GDMLP-1 probe SEQ ID NO:6749.
                                                                                                                                                                                                                                                                                                                                                                        898 GACCAAGAGCCTCAACA 914
                                                                                                                                                                                                                                                                                                                                                                                            GATCAAGACCCTCAACA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                             ACN69847 standard; DNA; 17 BP
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30-JAN-2001; 2001WO-US000664.
30-JAN-2001; 2001WO-US000665.
                                      08-JAN-2003; 2003US-00339782.
                                                         09-JAN-2002; 2002US-0348053P.
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2001WO-US000661.
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                                                                             (LYNX-) LYNX THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-2004 (first entry)
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.27
Best Local Si Conservative
                                                                                                 Goodman LJ, Bowen BA,
                                                                                                                    WPI; 2004-069003/07
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US2003166026-A1
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21-SEP-2000; 2
27-SEP-2000; 2
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30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-NOV-2003;
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                   04-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACN69847;
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 394
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The invention relates to a novel polypeptide (I) comprising a sequence (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully defined in the specification, a fragment of at least 8 amino acids of (S1), 95% deviation from (S1) which are conservative substitutions, and 55% identity to (S1). A polypeptide of the invention acts as a agonist or antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A pharmaceutical composition of the invention is useful for treating or preventing a disorder associated with decreased expression or activity of hGDMLP-1, such as a disorder of heart and/or skeletal muscle function. The present sequence represents a 17-mer nucleotide, used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel myosin-like protein-1, useful for treating or preventing disorder associated with decreased expression or activity of human genome-derived myosin-like protein-1 such as disorder of heart and/or skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
                                                                                                                                                                                                                                                                                                                                                                                                              Shannon MB;
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88.2%; Pred. No. 2e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention for scanning the sequence represented in ACN63103
                                                                                                                                                                                                                                                                                                                                                                                                           Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 BP; 5 A; 2 C; 9 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                           Hanzel DK, Rank D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 6749; Opp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            836 AGGAAGGCCGGGGTGGA 852
2001MO-US000667.
2001MO-US000668.
2001MO-US000669.
2001MO-US00670.
2001US-0266860P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACN65662 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-DEC-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.2
Matches 15; Conservative
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skeletal muscle function.
                                                                                                                                                                                                                                                                                                                                                                                                           Ji Y, Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-533378/51.
                                                                                                                                                                                                                                                                                                                                                        SHANNON M E.
                                                                                                                                                                                                                                          PENN S G.
HANZEL D K.
RANK D.
CHEN W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2004137589-A1
                                                  30-JAN-2001; 2
30-JAN-2001; 2
05-FEB-2001; 2
25-MAY-2001; 2
     30-JAN-2001;
30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                            (CHEN/)
(SHAN/)
                                                                                                                                                                                                                                          (PENN/)
(HANZ/)
(RANK/)
                                                                                                                                                                                       (GUYY/)
                                                                                                                                                                                                                                                                                                                                                                                                           Gu Y,
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ACN65662/c
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                                                                                                                                                                                                                                                                                         Novel myosin-like protein-1, useful for treating or preventing disorder associated with decreased expression or activity of human genome-derived myosin-like protein-1 such as disorder of heart and/or skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; 88; probe; myosin-like protein-1; hGDMLP-1;
hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
skeletal muscle function.
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1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                   Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 4 A; 5 C; 7 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                   Rank D,
                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 2564; Opp; English.
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                                                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         744 GGCAGCTGCCACCTTAT 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACN65661 standard; DNA; 17 BP
                                                                                2001WO-US000666.
2001WO-US000667.
2001WO-US000668.
                                                                                                             30-JAN-2001; 2001WO-US000669
30-JAN-2001; 2001WO-US000670.
05-FEB-2001; 2001US-0266660P.
25-MAY-2001; 2001US-00866108
                               2001WO-US000661
                                                   2001WO-US000663.
2001WO-US000664.
2001WO-US000665.
                                         2001WO-US000662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCAGCTGCCGCCTTCT
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                                                                                                                                                                                                                                                    Ji Y, Penn SG,
                                                                                                                                                                                                                                                                        WPI; 2004-533378/51.
                                                                                                                                                               GU Y.
JI Y.
PENN S G.
HANZEL D K.
RANK D.
CHEN W.
                                                                                                                                                                                                                                SHANNON M E.
                                                   30-JAN-2001; 2
30-JAN-2001; 2
30-JAN-2001; 2
30-JAN-2001; 2
                                                                                           30-JAN-2001; 2
30-JAN-2001; 2
30-JAN-2001; 2
                                         30-JAN-2001;
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                              30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                           function.
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(PENN/)
                                                                                                                                                                                                          (RANK/)
(CHEN/)
                                                                                                                                                                                                                                SHAN/)
                                                                                                                                                                    (GUXX/)
                                                                                                                                                                                                  (HANZ/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel myosin-like protein-1, useful for treating or preventing disorder associated with decreased expression or activity of human genome-derived myosin-like protein-1 such as disorder of heart and/or skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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88.2%; Pred. No. 2e+02;
rative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 4 A; 5 C; 7 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanzel DK, Rank D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 2563; Opp; English.
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2001WO-US000664.
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2001WO-US000668.
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2000US-0236359P.
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                                                                                  2003US-00723361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-NOV-1998 (first entry)
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les 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ji Y, Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHANNON M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-533378/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GU Y.
JI Y.
PENN S G.
HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RANK D.
CHEN W.
US2004137589-A1
                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
                                                                                                                                                                                                                                                                             30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
                                                                                     26-NOV-2003;
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                                                                                                                                                                                                                  30-JAN-2001;
30-JAN-2001;
                                                                                                                                                      21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                              04-OCT-2000;
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                                          15-JUL-2004
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(CHEN/)
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ID AAV446
XX
AC AAV446
XX
DT 24-NOV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Method for treating disease associated with altered UCP-2 expression - by administering agent which enhances or inhibits UCP-2 activity, effectively to treat obesity, diabetes, fever, hyperthermia, cachexia
                                           Uncoupling protein-2; UCP2 gene; human; respiration; thermogenesis; obesity; hyperinsulinaemia; glucose intolerance; diabetes; syndrome X; hypothermia; wasting; cachexia; anorexia; inflammation; fever; hyperthermia; gene therapy; diagnosis; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis E virus; HEV; binding partner; virus; US-HEV infection; vaccine; passive immunisation; PCR primer; ss.
               Human uncoupling protein-2 UCP2 gene reverse primer hUCP2g.e6rl.
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                                                                                                                                                                                                                                                                                                                                                                       Collins SA, Warden CH, Seldin MF, Ricquier D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.2%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 2e+02; ve 0; Mismatches 2; Indels
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hes 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 BP; 5 A; 1 C; 10 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                     (UYDU-) UNIV DUKE.
(REGC ) UNIV CALIFORNIA.
(CNRS ) CENT NAT RECH SCI.
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nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis E virus.
                                                                                                                                             Homo sapiens
                                                                                                                                                                           WO9831396-A1
                                                                                                                                                                                                                                           22-APR-1997;
                                                                                                                                                                                                                                                                           15-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                        Bouilland F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-1999
                                                                                                                                                                                                           23-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                         Surwit RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                             Synthetic
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AAZ00111
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hz-1 pagl promoter; persistence-associated gene 1; insect cell; constitutive expression promoter; direct repeat; ss.
                                                                                                                                             Mushahwar IK;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13.8; DB 1; Length 18;
Pred. No. 2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                              Detection of United States isolates of hepatitis E virus
                                                                                                                                                                                                                                                                                                                                                                                      present sequence represents a HEV specific primer
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 BP; 6 A; 8 C; 2 G; 2 T; 0 U; 0 Other;
                                                                                                                                           Dawson GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hz-1 Pagl gene direct repeat sequence.
                                                                                                                                           Desai SM,
                                                                                                                                                                                                                         Example 2; Page 141; 260pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1035 TAAACATCACACCCAAC 1051
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95US-0005128P.
                                                                                       97US-0061199P
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Best Local Similarity 88.2
Local Similarity 88.2
Local Similarity
Conservative
                                                                                                                                           Erker JC,
                                                                                                                                                                     WPI; 1999-288017/24
                                                                                                                 LAB.
                                                                                                                 (ABBO ) ABBOTT
                                                                                                                                             Schlauder GG,
                                                              15-OCT-1998;
                                                                                        15-OCT-1997;
            WO9919732-A1
                                     22-APR-1999
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Homo sapiens
                                                                                       WO9954500-A2
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23-NOV-1998;
                                    15;
                                                              10-SEP-2001
                                                                                          28-OCT-1999
                                                                                                             Cohen D,
                                                          AAZ71685;
                                Query Match
                                                  RESULT 400
                                  Best Loca
Matches
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differential efficacious responses to and side effects from
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                                                                                                                                                                                                                                                                                                                                                     ö
                                                                          This sequence represents a direct repeat from the Hz-1 persistence-associated gene 1 (Hz-1 pag1). The invention relates to the Hz-1 pag1 promoter. The pag1 gene promoter is useful in insect calls for driving constitutive expression of e.g. genes encoding foreign proteins. The promoter of the pag1 gene is constitutively expressed and stronger than that of the polyhedrin gene in insect calls, enabling it to express foreign genes more strongly e.g. lacZ and luciferase, in addition to which it can be expressed more prominently as a short promoter. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human biallelic marker upstream amplification primer SEQ ID NO:6041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
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0
                                                                                                                                                                                                                                                                                                             1.2%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                         Sequence 18 BP; 11 A; 2 C; 2 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                     2;
        HZ-1 virus persistence-associated gene promoter
                                                                                                                                                                                                                                                                                                                               Pred. No. 2e+02;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Page 1519; 2745pp; English.
                                              Example 1; Fig 3c; 56pp; English
                                                                                                                                                                                                                                                                                                                                                                                             582
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                                                                                                                                                                                                                                                                                                                                                                                               566 TTTTTTAATACCTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ71685 standard; DNA; 18
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                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                   Local Similarity
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ARZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nuclectide sequences. AAZ69579 to AAZ7740 represent amplification.

C primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the climater action of a disease as well as other treatment. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and a propert invention a sequence in the Sequence Listing from the
                                                                                                                                                                                                                                                                 ö
pharmaceutical agents acting on a disease as well as other treatment. N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human biallelic marker downstream amplification primer SEQ ID NO:11352.
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
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                                                                                                                                                                                                      1.2%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 2e+02;
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                                                                                                                                            Sequence 18 BP; 6 A; 9 C; 0 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                 ed. No. 2e+0
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 2650; 2745pp; English
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                                                                                                                                                                                                                                                                                                                              942 AATCTGAAGCCCCACTC 958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ76996 standard; DNA; 18
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                                                                                                                                                                                                                                           Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                              present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-OCT-1999.
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                                                                                                                                                                                                                   Query Match
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N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel biallelic markers used to construct a high density disequilibrium
                                         Gaps
                                                                                                                                                                                                                                                                                                              Human biallelic marker upstream amplification primer SEQ ID NO:4732
                                                                                                                                                                                                                                                                                                                                             Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
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1.2%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 2e+02; ive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 1240; 2745pp; English.
                                                                      204 CCCCCATCCCCCATTC 220
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                                                                                                          18 ccrccarccccarcrc 2
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                                                                                                                                                                                                    AAZ70376 standard; DNA; 18
                                                                                                                                                                                                                                                                            (first entry)
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cohen D, Blumenfeld M,
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Best Local Similarity
Matches 15; Conserv
 Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis; ss
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23-NOV-1998;
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                                                                                                                                                                                                                                      AAZ70376;
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Gap vector for Bscherichia coli stop codon assay used for assaying

Disclosure; Page 19; 33pp; Korean. heterozygous truncating mutation.

(KWAN-) KWANGMYUNG SUNGAE MEDICAL FOUND.

WPI; 2001-495301/54.

99KR-00031647.

02-AUG-1999; 02-AUG-1999;

05-MAR-2001

Escherichia coli; stop codon assay;

PCR primer; gap vector; truncating mutation; ss.

CR2001016649-A.

Synthetic.

PCR primer BV-b5.

BP.

ABL54891 standard; DNA; 18

RESULT 4 ABL54891

(first entry)

31-MAY-2002

ABL54891;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention. The invention relates to agap vector (GV) for assaying Escherichia coli (B.coli) stop codon. The invention also relates to a method for assaying heteroxygous truncating mutation using the GV comprising heteroxygous truncating mutation using the GV comprising the following steps: (1) multiplying exon fragments showing truncating mutation by polymerse chain reaction (PCR) and cloning the exon fragments with a plasmid for B. coli having a low copy number; (2) using the plasmid having cloned exon gene as a template and performing PCR with a primer having 50-200 bp of 5' and 3' terminals of the exon gene to make a gap vector for B. coli stop codon assay; (3) multiplying the same genetic fragment as the multiplied exon fragment through RT-PCR or PCR using RNA obtained from a sample to be measured or cDNA as a cor PCR using RNA obtained from a sample to be measured or cDNA as a complate; and (4) transforming the gap vector obtained from step (2) and the genetic fragment obtained from step (3) into B. coli at the same time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primer used within the scope of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.2%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human progesterone receptor PCR primer SEQ ID NO:277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1000 CACATGAAAGTTTGAGA
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es 15; Conserv
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Gaps

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905 AGCCTCAACATTTCCTA 921

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Conservative

17 AGCCTCAGCATTTCATA 1

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The present invention describes a method for determining the methylation status of CpG dinucleotides within the genes for oestrogen receptor, p21, p27, p16, progesterone receptor, myoglobin, pend, cdC2, c-eral2, p53 and/or CEA, which comprises contacting the target nucleic acid with a creagent that distinguishes between methylated and non-methylated CpG dinucleotides, and determining from the methylation status of 6 the CpG positions the presence of a colon cancer. A set of oligomers or peptide nucleic acid (PNA)-oligomers can be used as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNP) of a corresponding genomic DNA by analysis of a chemically pretreated genomic DNA is useful for the determination of the methylation status of a corresponding genomic DNA and pretreated genomic DNA are also useful for the characterisation, classification, diagnosis and differentiation of colon call provider and pretracted genomic DNA and differentiation of colon call providers and pretracted genomic DNA and site of colon characterisation, classification, diagnosis and differentiation of colon call provider and pretracted genomic DNA represent sequences call provider and pretracted genomic DNA represent sequences
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                                                                                                                                                                                                                                                                                                                                                         Determining methylation status of CpG dinucleotides using modified genomic sequences, oligonucleotides and/or PNA-oligomers, useful in the characterization, grading, staging and/or diagnosis of colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 26; Page 171; 219pp; English.
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                                                                                                                                                           09-AUG-2002; 2002WO-EP008939.
                                                                                                                                                                                                  09-AUG-2001; 2001DE-01039283.
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Matches 15; Conservative
                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                 Distler J, Model F,
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                      sapiens.
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                                     Synthetic.
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The present invention describes a method for determining the methylation status of CpG dinucleotides within the genes for oestrogen receptor, p21, p27, p16, progesterone receptor, myoglobin, pena, cdc2, c-erB2, p53 and/or CEA, which comprises contacting the target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides, and determining from the methylation status of the CpG constitions the presence of a colon cancer. A set of oligomers or peptide nucleic acid (PNA)-oligomers can be used as probes for determining the curresponding genomic DNA by analysis of a chemically pretreated commic DNA. The pretreated genomic DNA is useful for the determination of the methylation status of a corresponding genomic DNA and/or detection of the methylation classification, diagnosis and differentiation of colon cell proliferative disorders. ACF62275 to ACF63278 represent sequences used in the exemplification of the present invention
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Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; gene therapy; diagnostic marker; pharmaceutical; 88; PCR; primer.
                                                                                                                                                                    Determining methylation status of CpG dinucleotides using modified genomic sequences, oligonucleotides and/or PNA-oligomers, useful in the characterization, grading, staging and/or diagnosis of colon cancer.
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88.2%; Pred. No. 2e+02;
ative 0; Mismatches
                                                                                                                                                                                                                                         Claim 26; Page 170; 219pp; English.
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                                                                                                            Taubert H;
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             09-AUG-2002; 2002WO-EP008939.
                                            09-AUG-2001; 2001DE-01039283
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Seki N, Yoshikawa T,
                                                                                                            Model F,
                                                                            (EPIG-) EPIGENOMICS
                                                                                                                                          WPI; 2003-256600/25.
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les 15; Conser
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                                                                                                            Distler J,
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                                                                                                                                                                                                                                                                                               ö
                                                                                               The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a method of genetically screening for detecting thereditary hearing-loss. The method comprises detecting a nucleic acid from a connexin 26 (Cx26), a mitochondrial gene and/or a Cytomegalovirus (CMV) gene by hybridisation and/or PCR. The methods of the invention are represents a primer used in the isolation of DNA encoding the human connexin 26 (Cx26) mutant Cx26 235 Del.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetically screening for detecting hereditary hearing loss by detecting connexin 26, a mitochondrial or Cytomegalovirus nucleic acids by hybridization and/or PCR.
                                                                                                                                                                                                                                                                                              Gaps
                       New polynucleotides and polypeptides are useful in gene therapy, developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hereditary hearing loss, connexin 26, Cx26, mitochondrial gene, Cytomegalovirus gene; CMV, human; PCR; primer; 88; mutant.
                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human connexin gene 26 Cx26 235 Del mutant primer seg id 10.
                                                                                                                                                                                                                                                                   1.2%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 2e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                           Sequence 18 BP; 9 A; 7 C; 1 G; 1 T; 0 U; 0 Other;
                                                                          Example 8; SEQ ID NO 5064; 305pp; English.
                                                                                                                                                                                                                   oligonucleotide used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; SEQ ID NO 10; 22pp; English.
                                                                                                                                                                                                                                                                                                                     TGGAATTGTTGTTCTG 311
                                                                                                                                                                                                                                                                                                                                                                                                             ВР
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                                                                                                                                                                                                                                                                                                                                                                                                           ADJ65208 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                            15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DOBR/) DOBROWOLSKI S F. (LINZ/) LIN Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dobrowolski SF, Lin Z;
 WPI; 2003-723558/69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-213937/20.
                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2004038266-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Нощо варіепв.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ65208;
                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ss; cytostatic; gene therapy; vaccine; non-small cell lung cancer; NSCLC; diagnosis; cancer; URLC1; antisense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing, preventing and treating non-small cell lung cancer (NSCLC) comprises determining an expression level of an NSCLC-associated gene in
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                                           DB 1; Length 18;
                                                                                               Indels
Sequence 18 BP; 3 A; 11 C; 1 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human NSCLC gene antisense-S oligonucleotide #39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 BP; 5 A; 7 C; 0 G; 6 T; 0 U; 0 Other;
                                         1.2%; Score 13.8; DB 1
88.2%; Pred. No. 2e+02;
iive 0; Mismatches
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                                                                                                                                             196 GGCCATCTCCCCCATCC 212
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                                                                                                                                                                                                                                                                                                                     BP
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28-FEB-2003; 2003US-0451374P.
28-APR-2003; 2003US-0466100P.
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ID ADN35818 standard; DNA; 18
                                                                                                                                                                            1 CCCCATCTCCCACATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGAGGAAATGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-2004 (first entry)
                                                                     Local Similarity 88.2
nes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Daigo Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-330206/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-APR-2004.
                                                                                                                                                                                                                                                                                                                                                                      ADN35818;
                                              Query Match
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                                                                                                                                                                                                                                                                    RESULT 408
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Matches
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RESULT 409

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The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDKI, PCNA and Cyclin B1. Representative examples of ribozyme recognition sites are given in AAA82215 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in
                                                   Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                         New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13.8; DB 1; Length 19;
Pred. No. 2.18+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19 BP; 10 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                      Robbins JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 62; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Welch PJ, Barber JR,
                 cdk8 ribozyme binding site #173.
                                                                                                                                                                                                                                                                                                                      Barber JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cdk6 ribozyme binding site #123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415 GITTITCCTTATATITG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВР.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.2%;
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                                                                                                                                                                                                        99WO-US028772.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTTTCCATATACTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restenosis treatment
                                                                                                                                                                                                                                                                                                                      Welch PJ,
                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-412314/35.
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                                                                                                                                                                                                                                                                                  (IMMU-) IMMUSOL INC.
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Best Local Similarity
                                                                                                                               WO200032765-A2.
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                                                                                                                                                                                                        06-DEC-1999;
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                                                                                           Mammalia
                                                                                                                                                                                                                                                                                                                        Tritz R,
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AAA83063/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel method for predicting the responsiveness of a subject with a cell proliferative disorder of the breast tissues to a therapy comprising analysing the methylation pattern of a target nucleic acid by contacting at least one of the target nucleic acids in a biological sample obtained from the subject prior to or during treatment. The method of the invention has cytostatic activity, and may have a use the property. The set of oligonactic activity, and may have a use the oligoners are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) within the sequences. The methods, nucleic acid, oligonucleotide, and kit are useful for the creatment, characterisation, classification and/or differentiation, of breast cell proliferative disorders. The method is also useful for predicting the responsiveness of a subject with a cell proliferative is used in the breast tissues to a therapy. The present sequence is used in the breast.
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disorder, useful for treating or differentiating breast cell
proliferative disorders comprises analyzing methylation pattern of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Model F;
Marx A;
                                                                                                                                                                                      ss; cell proliferative disorder; breast; methylation; cytostatic; gene therapy; single nucleotide polymorphism; SNP.
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Schmitt M, Look MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
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                                                                                                                                                   Oligonucleotide of the invention SEQ ID NO:1135.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koenig T,
Schmitt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 GAGGATTATGGCGTTTA 168
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07-JAN-2003; 2003DE-01000096.
17-APR-2003; 2003DE-01017955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic DNA from the subject
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Conservative
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                                     ADS90119 standard; DNA; 18
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                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rujan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-348468/32
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Matches 15; Conser
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                                                                                                                                                                                                                                                  Unidentified.
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Nimmrich I,
                                                                                                               18-NOV-2004
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                                                                             ADS90119;
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of the
                                                                                              The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCKN and Cyclin B1.

Representative examples of ribozyme recognition sites are given in AA884315 to AA868797. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention specifically claims AAH56368 to AAH56832 which are antisense oligonucleotides to nucleotide sequences encoding groß. More generally, antisense compounds (1) comprising antisense oligonucleotides of 5-50 bases targeted to a nucleotide sequence encoding großL (heat shock protein (HSP) 60) (GL) and groß (HSP10) (GS) gene from a microorganism, where the antisense compound is complementary to GL or GS of a microorganism and specifically hybridises with and inhibits the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth; microorganism; Bscherichia coli; Streptococcus pneumoniae; diagnosis; Streptococcus pyogenes; sphylococcus aureus; Pseudomonas aeruginosa; antibacterial; antiviral; antiproliferative; antisense therapy;
                         cleaves
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes groEL antisense oligonucleotide SEQ ID NO:354.
                      New hairpin and hammerhead ribozyme for inhibiting restenosis, cleavor RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1 PCNA and Cyclin B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel antisense compounds targeting nucleic acid encoding groEL or gene of microorganism, which hybridize with and inhibit expression genes, useful to inhibit growth of microorganism having the genes.
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                                                                                                                                                                                                                                       Score 13.8; DB 1; Length 19;
Pred. No. 2.1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                               Seguence 19 BP; 4 A; 4 C; 4 G; 7 T; 0 U; 0 Other;
                                                                         Disclosure; Page 56; 109pp; English
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                                                                                                                                                                                                                                                                                         603 AAGACTTCATAAGTAGG 619
                                                                                                                                                                                                                                                                                                                                                                                AAH56706 standard; DNA; 19 BP
                                                                                                                                                                                                                                       1.2%;
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                                                                                                                                                                                                                                                                                                             19 AACACTTCAGAAGTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     microbial infection; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wright JA, Young AH,
                                                                                                                                                                                        restenosis treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-355633/37.
WPI; 2000-412314/35
                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                        AAH56706:
                                                                                                                                                                                                                                       Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                        RESULT 412
                                                                                                                                                                                                                                                                  Matches
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antiproliferative activities, and can be used in antisense therapy and for inhibition of expression of großS or großL. (I) are useful for inhibition of expression of Groß in cells or tissues in vitro. (I) are useful for also useful for inhibiting the growth of a microorganism, or inhibiting the growth of a microorganism, or inhibiting the growth of a microorganism, or inhibiting the expression of GL or GS gene in a microorganism (a bacterial cell or a control baving an expression of GL or GS gene which involves administering to the microorganism or to a cell infected with the microorganism, (I). (I) are also useful for treating a mammalian pathological condition mediated by the microorganisms which involves identifying a eukaryotic organism chaving a pathological condition mediated by microorganisms having a GL or GS gene and administering (I) such that the growth of microorganism is their compounds are utilised for diagnostics, to completed. The antisense compounds are utilised for diagnostics, to compense the antisense compounds are utilised for diagnostics, conclusively markers. Additions in humans. They are also useful as molecular weight markers. Additions in humans. They are also useful as molecular weight markers for groß sequences which are used in the represent crepresent invention. Addition can also depresent exemplification of the present invention in the present invention
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expression of GL or GS, is claimed. (I) have antibacterial, antiviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 19 BP; 8 A; 2 C; 2 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 13.8; DB 1;
Pred. No. 2.1e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.2%;
88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     567 TTTTTAATACCTTTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 TTTTAAAACCTTTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH58225 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tritz R;
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nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200130362-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH58225;
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                                                 The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme [1] which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule [11] comprising a promoter operally linked to a nucleic acid segment encoding [1]. (1) can have antipsoriatic, dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling, cepthalmological, vulnerary, keratolytic and virucide activities, and claves RNA encoding cytokine involved in inflammation. (1) can be used in gene therapy. (1) and (11) are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, aquamous or basal cell carcinoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, virreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing carring such as keloid, adhesion and hypertrophic or hypertrophic burn car. AAHSTST7 to AAHSC2099 represent sequences used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.8; DB 1; Length 19;
Pred. No. 2.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of the present invention
   Example 1; Page 119; 408pp; English
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88.2%;
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Best Local Similarity 88.2
Matches 15; Conservative
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The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme [1] which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (WMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule [11] comprising a promoter operably linked to a nucleic acid segment encoding [1]. [1] can have antipsoriatic, dermatcological, cytostatic, antiseborrheic, antidiabetic, antisickling, dermatcological, vulnerary, keratolytic and virucide activities, and cleaves RNA encoding cytokine involved in inflammation. [1] can be used in gene therapy. [1] and [1] are useful for treating proliferative skin diseases such as postiasis, atopic dermatitis, actinic keratosis, aquamous or basal cell carcinoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, virreoretinopathy, sickle cell retinopathy, etchnopathy, sickle cell retinopathy, of prematurity and retinal detachment, and for treating and preventing cararing such as keloid, adhesion and hypertrophic or hypertrophic burn and second in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
metalloproteinases, growth factors and cell-cycle dependent kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a protein derived from Pyrococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13.8; DB 1; Length 19;
Pred. No. 2.1e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19 BP; 10 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the present invention
                                                                                        Example 1; Page 147; 408pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.4.
Best Local Similarity 18.4.
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200109348-A1.
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furiosus having thermophilic glucoamylase activity. Also described are:

(i) a nucleic acid encoding the protein; (ii) a nucleic acid hybridisable
with any of the above nucleic acids under stringent conditions and
concoding a protein with thermophilic glucoamylase activity; (iii) a
recombinant DNA contains the nucleic acid; (iv) a transformant which is
cransformed with the recombinant DNA; (v) a process for producing the
transformed with the recombinant bolor collecting the protein that
has thermophilic glucoamylase activity from the cultured material; and
(vi) a process for producing glucose by the action of the above protein
con the alpha-1,4 linkage in a D-glucopyranose polymer to produce free
glucose, or oligosaccharides, or cyclodextrin. The proteins are
applicable in efficient utilisation of biomass e.g. in decomposing starch
to produce glucose or oligosaccharides or cyclodextrins. Such proteins
can be produced by genetic engineering at low cost. The present sequence
represents a PCR primer for a Pyrococcus furiosus protein having
thermophilic glucoamylase activity, which is used in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA interference; short interfering nucleic acid; siNA; short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miknA; short hairpin RNA; shRNA; expression modulation; gene therapy; prog screening; diagnosis; therapeutic target identification; pharmacogenomics; gene function analysis; gene mapping; cancer; proliferative disease; restenosis; polycystic kidney disease; inflammatory disease; allergic disease; autoimmune disease; transplant rejection; cytostatic; vasotropic; nephrotropic; antiinflammatory; antiallergic; immunosuppressive; human; insulin-like growth factor 1 receptor; IGF-IR; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                     1.2%; Score 13.8; DB 1; Length 19; 88.2%; Pred. No. 2.1e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                  Sequence 19 BP; 3 A; 4 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human IGF-1R siNA lower strand, SEQ ID NO:499.
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06-JUN-2002; 2002US-0386782P.
29-AUG-2002; 2002US-0406784P.
05-SEP-2002; 2002US-0408378P.
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                                                                                                                                                                                                                                                                                                                                                                                                                         88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 88.2
nes 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-721691/68.
                                                                                                                                                                                                                                                                                                                            present invention
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ADF31834
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New short interfering nucleic acid, useful e.g. for treatment and

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The invention relates to short interfering nucleic acids (siNA) which downregulate expression of the human insulin-like growth factor 1

C creceptor (IGF-IR) gene by RNA interference. The siNAs may or may not comprise ribonuclectides and may be double or single stranded. They comprise sense and antisense regions, or alternatively are assembled from a sense oligonuclectide and an antisense oligonucleotide. Specifically, the siNAs include short interfering RNA (siRNA), double. Stranded RNA, micro-RNA (miRNA) and short hairpin RNA (siRNA). The siNAs can be unmodified or chemically modified, can contain decoxyribonucleotides, and can be chemically synthesised, expressed from a vector or enzymatically synthesised. The invention also relates to kits for the in vitro or in vivo delivery of siNA; conjugates and/or complexes of siNA; and vectors that express siNA. The siNAs are used to modulate expression of the IGF-IR gene in cells, tissue explants or organisms of sinA; and vectors the express siNA. The siNAs are used to modulate expression of the IGF-IR gene in cells, tissue explants or organisms concerned to a variety of conditions. They may be used for treating cancer and other proliferative diseases (e.g., restenosis and polycystic diseases and transplant rejection. The siNAs are also useful for drug cancer and other proliferative diseases (iscuedate) and validation, genetic engineering, pharmacogenomics, studying gene function, and gene cancer the lower strand of a human IGF-IR-targeted double-stranded constrained a human IGF-IR-targeted double-stranded
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diagnosis of cancer , downregulates expression of the insulin-like growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 13.8; DB 1; Length 19;
Pred. No. 2.1e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19 BP; 3 A; 3 C; 11 G; 0 T; 2 U; 0 Other;
                                                                  Example 3; SEQ ID NO 499; 147pp; English
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11-MAR-2002; 2002US-0363124P.
06-JUN-2002; 2002US-0386782P.
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                         factor-1 receptor gene.
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The invention relates to short interfering nucleic acids (siNA) which comparison of the human insulin-like growth factor 1 creeptor (IGF-IR) gene by RNA interference. The siNAs may or may not comprise ribonucleotides and may be double or single stranded. They comprise ribonucleotides and antisense regions, or alternatively are further comprise sense and antisense regions, or alternatively are sesembled from a sense oligonucleotide and an antisense oligonucleotide. Specifically, the siNAs include short interfering RNA (siRNA), doublect stranded RNA, micro-RNA (miRNA) and short hairpin RNA (siRNA). The siNAs can be unmodified or chemically modified, can contain contain an enzymatically synthesised. The invention also relates to kits of the in vitro or in vivo delivery of siNA; conjugates and/or complexes of siNA; and vectors that express siNA. The siNAs and can do modulate capression of the IGF-IR gene in cells, tissue explants or organisms of cancer and other proliferative diseases (e.g., restenosis and polycystic kidney disease), inflammatory and/or allergic diseases, autoimmune concerning, disease), inflammatory and/or allergic diseases, autoimmune conserving, diseases and transplant rejection. The siNAs are also useful for drug cancer and other proliferative diseases (e.g., restenosis and polycystic denesing, disease), inflammacogenomics, studying gene function, and gene conservation, is identical to the IGF-IR transcript strand of a human IGF-IR-targeted double-stranded size and the identical polymorphisms). The present sequence conservative in the identical polymorphisms. The represent sequence of the identical polymorphisms of the identical polymorphisms of a human identical representation and validation.
                                                                                                                                                                                                                                            New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer, downregulates expression of the insulin-like growth
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primer; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     siNA, which is identical to the IGF-1R transcript target sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 BP; 2 A; 11 C; 3 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                        Example 3; SEQ ID NO 222; 147pp; English.
                                                                                                                                                           Chowrira B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 CGGGCCGTGGCAGGAAG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADF88498 standard; DNA; 19 BP
                  05-SEP-2002; 2002US-0408378P.
09-SEP-2002; 2002US-0409293P.
15-JAN-2003; 2003US-0440129P.
2002US-0406784P.
                                                                                                                                                         Beigelman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                               (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Conservative
                                                                                                                                                                                                                                                                                                factor-1 receptor gene.
                                                                                                                                                                                                      WPI; 2003-721691/68.
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                           Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 418
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The invention relates to a novel polynucleotide isolated and purified from a human gene having any one of 935 fully defined sequences as given in specification, or a sequence having a base substitution. The invention further relates to: an oligonucleotide containing single nucleotide polymorphisms; a PCR primer set chosen from the combination of two DNA primer set chosen from the combination of two DNA regentification; a labelling probe containing the SNP containing oligo; and a microarray equipped with the SNP containing oligo. The isolated human gene of the invention is useful for detecting the single nucleotide olymorphisms in human gene. The isolated human gene is also effect to a medical agent. The isolated human gene is also effective in detecting single nucleotide obolymorphisms in a human gene. This polymorleotide sequence represents one of the PCR primers used in the single nucleotide polymorphism cone of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza minuta Pi9 locus nucleotide binding site (NBS) gene PCR primer #63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2 and NBS3, useful for producing plants resistant to Magnaporthe grisea
                                                                                                                         Novel polynucleotide useful for detecting single nucleotide polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice blast; plant breeding; transgenic plant; PCR; primer; BS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19 BP; 3 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                               claim 2; SEQ ID NO 2081; 704pp; Japanese.
                                                               (KAGA-) KAGAKU GLJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            750 TGCCACCTTATGCAGTG 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
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01-FEB-2002; 2002US-0353304P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-JAN-2003; 2003US-00352179.
12-FEB-2002; 2002JP-00034717
                              12-FEB-2002; 2002JP-00034717
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                                                                                                WPI; 2003-820454/77
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Best Local Similarity
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(LIUG/) LIU G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang G, Liu G;
                                                                                                                                                   in human gene
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Sequence 19 BP; 4 A; 4 C; 6 G; 0 T; 5 U; 0 Other;
                                         Query Match
Best Local Similarity
Matches 11; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel small interfering RNA (siRNA) polynucleotides capable of interfering with expression of a polypeptide having protein-tyrosine-phosphatase (PTP) activity. The products of the invention have cytostatic, immunomodulator, antimicrobial, antifical manatory, antidiabetic and anorectic activity. The methods and compositions of the present invention are useful for treating diseases or conditions associated with aberrant expression or activity of the protein tyrosine phosphatase, such as cancer, autoimmune diseases, infection, inflammation, diabetes and obseity. This sequence represents a siRNA directed against dual specificity phosphatase (DSP) expression.
                                                                                          The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Manaporthe grises in plant breeding programs. The present DNA sequence represents a PCR primer for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated small interfering RNA (siRNA) polynucleotide useful for treating diseases with aberrant activity of the protein tyrosine phosphatase, such as cancer, autoimmune disease, infection, inflammation, diabetes and obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           small interfering RNA; siRNA; protein-tyrosine-phosphatase; PTP;
cytostatic; immunomodulator; antimicrobial; antimiflammatory;
antidiabetic; anorectic; cancer; autoimmune disease; infection;
inflammation; diabetes; obesity; RNA interference; gene silencing; ss.
                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                            Sequence 19 BP; 14 A; 3 C; 1 G; 1 T; 0 U; 0 Other;
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                                                 Disclosure; SEQ ID NO 63; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 600; 392pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lewis SP, Tonks NK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCPTP associated siRNA hTCPTP1.5 #2.
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(COLD-) COLD SPRING HARBOR LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 GGTTTTTTTTTTT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAY-2003; 2003WO-US016632.
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14-APR-2003; 2003US-0462942P.
                                                                                                                                                                                                              the Oryza minuta Pi9 locus.
                                                                                                                                                                                                                                                                                                                                                                                                        414 GGTTTTTCCTTATATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADN75775 standard; RNA; 19
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                                                                                                                                                                                                                                                                                                                                                       15; Conservative
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                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAY-2002;
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    infection
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                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated small interfering RNA (siRNA) polynucleotide useful for treating diseases with aberrant activity of the protein tyrosine phosphatase, such as cancer, autoimmune disease, infection, inflammation,
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                                                            Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      small interfering RNA; siRNA; protein-tyrosine-phosphatase; PTP;
cycostatic; immunomodulator; antimicrobial; antihifammatory;
antidiabetic; anorectic; cancer; autoimmune disease; infection;
inflammation; diabetes; obesity; RNA interference; gene silencing;
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18.2%; Pred. No. 2.18+02;
ve 0; Mismatches 2; Indels
   Length 19;
                                                            Indels
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1.2%; Score 13.8; DB 1; 64.7%; Pred. No. 2.1e+02; ative 4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Meng T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klinghoffer R, Lewis SP, Tonks NK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ICPTP associated siRNA hTCPTP1.5 #1.
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(COLD-) COLD SPRING HARBOR LAB.
                                                                                                                      343 GGCTGTGATCAAATGGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 GGCTGTGATCAAATGGG 359
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14-APR-2003; 2003US-0462942P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 88.2
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diabetes and obesity.
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Mus musculus.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting sequence of RNA interference useful for synthesizing siRNA, by detecting regions in sequence fulfilling specific criteria such as base at 3' terminal is adenine, thymine or uracil, base at 5' terminal is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      short inhibitory RNA; siRNA; adipocyte; cell membrane; electroporating; permeabilised cell membrane; antidiabetic; anorectic; gene therapy; type II diabetes; insulin resistance; obesity; Myolc; ds; mouse; murine.
                                                                                                                                                             detection; RNA interference; siRNA; gene silencing; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse Myolc targeted short inhibitory RNA (siRNA) target DNA SeqID90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             corresponds to an RNA interference target sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.2%; Score 13.8; DB 1; Length 19; 88.2%; Pred. No. 2.1e+02; ative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 200; 325pp; Japanese.
                                                                                                                              RNA interference target sequence #186.
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                              ADQ27278 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                        21-NOV-2003; 2003WO-JP014893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tei K, Naito Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              guanine or cytosine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-487423/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                     (SAIG/) SAIGO K.
(TEIK/) TEI K.
(NAIT/) NAITO Y.
                                                                                                                                                                                                                                                                                                                                                                                        (NATO/) NATORI Y.
                                                                                                                                                                                                                                                      WO2004048566-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-SEP-2004
                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                    cytotoxicity
                                                                                                                                                                                                                                                                                        10-JUN-2004.
                                                                                                  26-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADP48850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saigo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                ADQ27278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 423
RESULT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP48850
ID ADP4
XX ADP4
XX ADP4
XX ADP4
XX BD2
XX BD2
XX ShOR
XX ShOR
XW PETW
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                                                                                                                                                                                                                                                            I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            short inhibitory RNA; siRNA; adipocyte; cell membrane; electroporating; permeabilised cell membrane; antidiabetic; anorectic; gene therapy; type II diabetes; insulin resistance; obesity; Myolc; ds; mouse; murine.
                                                                                                                                                                                                                                                         Introducing a nucleic acid into an adipocyte, useful for treating type diabetes, obesity or insulin resistance, comprises contacting an adipocyte having a cell membrane with a nucleic acid molecule, thus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse Myolc targeted short inhibitory RNA (siRNA) target DNA SeqID89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.2%; Score 13.8; DB 1; Length 19; 88.2%; Pred. No. 2.1e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19 BP; 3 A; 5 C; 3 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 90; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1097 TACCTGCTCATTTGTTT 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-DEC-2003; 2003WO-US039774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-DEC-2002; 2002US-0432427P.
                                                                                                      11-DEC-2003; 2003WO-US039774.
                                                                                                                                      11-DEC-2002; 2002US-0432427P.
                                                                                                                                                                                                    Jiang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYMA-) UNIV MASSACHUSETTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP48849 standard; DNA; 19
                                                                                                                                                                    (UYMA-) UNIV MASSACHUSETTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACCACCTCATTTGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 88.2
nes 15; Conservative
                                                                                                                                                                                                                                 WPI; 2004-468860/44.
                                                                                                                                                                                                    Czech MP, Zhou Q,
                                                                                                                                                                                                                                                                                                                   forming a mixture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004053103-A2
                                            WO2004053103-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUN-2004.
                                                                          24-JUN-2004
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                                                                                                                            This invention relates to a novel method of introducing a nucleic acid membrane and adipocyte which comprises contacting an adipocyte having a cell membrane with a nucleic acid molecule, thus forming a mixture and electroporating the mixture under conditions such that the cell membrane becomes permeablised, such that the nucleic acid is introduced into the adipocyte. The invention may be useful for the production of compounds with an antidiabetic or anorectic activity whilst the disclosed sequences may be useful for gene therapy. The methods are useful for treating type II diabetes, inaulin resistance or obesity. The present sequence is that of a region of a gene which may be targeted by short inhibitory RNA (siRNA) used with the method of the invention.
                                           Introducing a nucleic acid into an adipocyte, useful for treating type II diabetes, obesity or insulin resistance, comprises contacting an adipocyte having a cell membrane with a nucleic acid molecule, thus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a method for identifying a target cell or for allowing direct genetic analysis of target cell, the method involves in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying target cell for prenatal diagnosis, by in situ hybridizing target sequence in target cell with complementary labeled sequence and identifying target cell by detecting hybridized sequence by flow
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, PCR; primer, beta actin; molecular beacon;
target cell identification; prenatal diagnosis; cystic fibrosis;
chromosomal aberration; trisomy 21; Down's syndrome; 88.
                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                 1.2%; Score 13.8; DB 1; Length 19; 88.2%; Pred. No. 2.1e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                            Sequence 19 BP; 4 A; 5 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weidner J;
                                                                                                        Disclosure; SEQ ID NO 89; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 3/4; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                    1097 TACCTGCTCATTTGTTT 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human beta actin PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                            072/c
ABK15072 standard; DNA; 15 BP.
                                                                                                                                                                                                                                                                                                                                                                3 TACCACCTCATTTGTTT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JUL-2000; 2000EP-00115268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
Jiang
                                                                                                                                                                                                                                                                                                   Query Match 1.2
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PRAE-) PRAENADIA GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-156652/21.
                       WPI; 2004-468860/44.
Zhou Q,
                                                                                 forming a mixture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1172445-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wiebusch H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JAN-2002
Czech MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytometry
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK15072;
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 425
                                                                                                                                                                                                                                                                                                                                                                                                                          ABK15072,
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complementary labeled sequence, and identifying the target cell with a complementary labeled sequence, and identifying the target cell by a detecting the presence of a hybridised sequence by flow cyrometry. The method of the invention is useful for distinction of foetal and maternal cells and can be used in prenatal disgnosis for the detection of cystic fibrosis or chromosomal aberrations such as trisomy 21 (Down's syndrome). The method is also useful for the disgnosis of diseases which are due to or characterised by the transcription of genes which are not expressed in the wild type cell, or diseases characterised by the absence of altered expression or expression rates of certain genes or gene fragments. This method improves the identification of foetal cells within a maternal and companies and therefore enables the distinction between maternal and companies than common practices and increases the overall sampling rate of target cell within a blood sample. The method also allows simultaneous which can be combined with the detection of various genetic difference within the cells at once. The method also allows detection of rare conjunction with the primer represented in AbRASO71 as a control PCR and conjunction with the primer represented in AbRASO71 as a control PCR and conjunction with the primer represented in AbRASO71 as a control PCR and control and publication of the number of target cells used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease; anglogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15 BP; 1 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLMSY-encoding nucleotide #28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-2004 (first entry)
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Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-505179/47.
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(HAAL/) HAALAND P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003045973-A2.
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                        New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer; carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease;
                                                                                                                                                                                                                                                                                                                                                Gaps
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0
                                                                                                                                                                                                                                                                                                                 Score 13.4; DB 1; Length 15;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                  Sequence 15 BP; 5 A; 5 C; 1 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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   Disclosure; SEQ ID NO 81; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spargo CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BECT ) BECTON DICKINSON & CO. (HAAL/) HAALAND P D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLMSY-encoding nucleotide #20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJ82292 standard; DNA; 15 BP.
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                                                                                                                                                                                                                                                                                                                                                                                615 GTAGGAGATGAGTTT 629
                                                                                                                                                                                                                                                                                                                     Query Match
1.2%;
Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            15 GTAGGACATGAGTTT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                    14; Conservative
                                                                                                                                                                                                                                                        encoding the P3 peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-505179/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    angiogenesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ82292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 427
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The invention relates to an isolated peptide or polypeptide (I) of no more than about 50 amino acid residues which when contacted with cells in which a platelet-derived growth factor receptor (PDGF-R) is activated in an autocrine manner, inhibits the growth of these cells. The isolated

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The invention relates to an isolated peptide or polypeptide (I) of no more than about 50 amino acid residues which when contacted with cells in which a platelet-derived growth factor receptor (PDGF-N) is activated in an autocrine manner, inhibits the growth of these cells. The isolated peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-Lys (PI) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-Lys (P4) Phe-Phe-His-Pro-Val (P5). (I) is useful for inhibiting cell proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma, sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic)
peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-Lys-Lys-Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5). (I) is useful for inhibiting cell Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5). (I) is useful for inhibiting cell proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma, sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney, ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders. This sequence represents a possible nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease;
                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                       1.2%; Score 13.4; DB 1; Length 15; 93.3%; Pred. No. 2.2e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                               Sequence 15 BP; 6 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 85; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spargo CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLMSY-encoding nucleotide #32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BECT ) BECTON DICKINSON & CO. (HAAL/) HAALAND P D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-NOV-2001; 2001US-0333476P.
                                                                                                                                                                                                                                                                                                                                                                                                                         615 GTAGGAGATGAGTTT 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADJ82304 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                 Query Match 1.2
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                         encoding the P3 peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-505179/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                angiogenesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HER4; hammerhead ribozyme; Inozyme; zinzyme; DNAzyme; amberzyme; cancer; brain tumour; cytostatic; short interfering RNA; siRNA; RNA interference; prostate cancer; colorectal cancer; brain cancer; oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer; cervical cancer; head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma; multidrug resistant cancer.
ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders. This sequence represents a possible nucleotide encoding the P3 peptide.
                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                      DB 1; Length 15;
                                                                                                                                                                                                                                                                                                                                                            1; Indels
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                                                                                                                                                                                                                 Seguence 15 BP; 5 A; 5 C; 1 G; 4 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                   1.2%; Score 13.4; DB 1; 93.3%; Pred. No. 2.2e+02; tive 0; Mismatches 1
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ADG13597 standard; RNA; 15 BP
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04-DEC-1997; 97US-00985162.
2-SEP-1999; 99US-00401063.
03-MAY-2001; 2001US-00848754.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 GTACGAGATGAGTTT 1
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                                                                                                                                                                                                                                                                                                                                                            14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              615 GTAGGAGATGAGTTT
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                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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11D ADG1
12D Huma
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pCR primers AAH77878-79 were used to amplify cDNA encoding a human polypeptide, designated hB7-H2. The hB7-H2 polypeptide co-stimulates T cells. The hB7-H2 proteins and its variants are generally useful as immune response-stimulating therapeutice. For example, the polypeptides can be used for treatment of disease conditions characterized by immune used for treatment of disease conditions characterized by immune deficiencies. They may also be employed to increase immune immune deficiencies. They may also be employed to increase immune therefore are particularly useful when use of radiotherapy or immune used to treat conditions used to a certain conjunction with such therefore are particularly useful when given in conjunction with such therefore are particularly useful when given in conjunction with such used to treat conditions involving cellular immune responses, e.g., inflammatory conditions (such as, for example, those induced by infectious agents including Mycobacterium tuberculosis or M. leprae), or infectious agents including Mycobacterium tuberculosis or M. leprae), or
                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated DNA encoding a hB7-H2 polypeptide, useful for treating cancer, AIDS, or autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis or insulin-dependent diabetes mellitus).
    for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune diseases (e.g. rheumatoid arthritis), multiple sclerosis, or
                                                                                                                                          Gaps
target site. The present sequence is an BGFR/HER1-4 target sequence an siRNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR primer used to amplify cDNA encoding a human hB7-H2 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hB7-H2; T cell stimulator; immunosuppression; cancer; AIDS; congenital immune deficiency; cellular immune response; PCR primer; inflammatory condition; autoimmune disease; rheumatoid arthritis; inflammatory condition; autoimmune disease; rheumatoid arthritis; aultiple sclerosis; insulin-dependent diabetes mellitus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other pathologic cell-mediated responses such as those involved in
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                                                                                                   Length 15;
                                                                                                                                        Indels
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                                                                                                 Score 13.4; DB 1;
Pred. No. 2.2e+02;
                                                           Sequence 15 BP; 1 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
                                                                                                                                          Mismatches
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                                                                                                   1.2%;
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                                                                                                                                                                                 380 GCAGGCAATGCAGTC 394
                                                                                                                                                                                                                                                                                                                       AAH77878 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                          14; Conservative
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                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                  RESULT 430
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H. pylori strain J99 genome fragment SEQ ID NO:890.
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                                                                                       13-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                stroke in an individual compression remaining for an at-risk haplotype in the phosphodiesterase 4D (PDE4D) gene that is more frequently present in an individual susceptible to stroke (affected) compared to a healthy individual susceptible to a trisk haplotype increases risk of stroke significantly. The composition, methods and kit are useful for diagnosing, predicting of clinical course and treating stroke using polymorphisms in the PDE4D general and any also be used in identifying agents that enhance or inhibit PDE4D polypeptide expression or activity. The present sequence represents a fragment of H. pylori strain J99 genome which is not referred to at all in the main body of the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Diagnosing susceptibility to a stroke in an individual comprising screening for an at-risk haplotype in the phosphodiesterase 4D gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to a method of diagnosing susceptibility to a
                                                                                                                                                                                                                                                                                                                                                            Thorleifsson G;
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                Indels
                                                                                                                                                                            H. pylori strain J99 genome fragment SEQ ID NO:466.
                                                                                                                                                                                                                                                                                                                                                            Gretarsdottir S, Jonsdottir S, Reynisdottir ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16 BP; 2 A; 1 C; 6 G; 7 T; 0 U; 0 Other;
       93.3%; Pred. No. 2.3e+02;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 466; 574pp; English
                                                                                                                                                                                                    ds; stroke; phosphodiesterase 4D; PDE4D.
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                                                                                                                ADO49843 standard; DNA; 16 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      442 TGATTTTAGCTGGGA 456
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04-FEB-2002; 2002US-00067514.
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                                                                                                                                                                                                                                                                                                                                           (DECO-) DECODE GENETICS EHF.
                                        63
                                                    1 CCGCGGCCCAAGTTC 15
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                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Conservative
       Best Local Similarity 93.3
Matches 14; Conservative
                                       49 CCGCGCCCCAGTTC
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-374932/35.
                                                                                                                                                                                                                         Helicobacter pylori
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Matches 14; Conserv
                                                                                                                                                                                                                                             US2004091865-A1.
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                                                                                                                                      AD049843;
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                                                                                             RESULT 431
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The invention relates to a method of diagnosing susceptibility to a stroke in an individual comprising screening for an at-risk haplotype in the phosphodiesterase 4D (PDE4D) gene that is more frequently present in an individual susceptible to stroke (affected) compared to a healthy individual (control), where the at-risk haplotype increases risk of stroke significantly. The composition, methods and kit are useful for diagnosing, predicting of clinical course and treating stroke using polymorphisms in the PDB4D gene. These may also be used in identifying agents that enhance or inhibit PDE4D polypeptide expression or activity. The present sequence represents a fragment of H. pylori strain J99 genome which is not referred to at all in the main body of the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing susceptibility to a stroke in an individual comprising screening for an at-risk haplotype in the phosphodiesterase 4D gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thorleifsson G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gretarsdottir S, Jonsdottir S, Reynisdottir ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16 BP; 2 A; 1 C; 6 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 890; 574pp; English.
ds; stroke; phosphodiesterase 4D; PDE4D
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                                                                                                                                                                                                                                                       25-SEP-2002; 2002US-00255120.
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04-FEB-2002; 2002US-00067514.
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                                                                  Helicobacter pylori
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interferon alpha
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ID AAF
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AC AAF
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                                                                                                                                              The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRR-2 and/or the CAAT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoletin, granulocyte colony stimulating factor protein and interferon alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                               Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                     1.2%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 2.3e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                           Sequence 17 BP; 2 A; 3 C; 4 G; 8 T; 0 U; 0 Other;
              Mcswiggen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mcswiggen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hammerhead ribozyme substrate #2321.
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                                                                                                                       Claim 4; Page 98; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF04805 standard; DNA; 17 BP
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            Pavco P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                14; Conservative
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                                      WPI; 2000-647423/62.
            Zwick M,
                                                                                                                                                                                                                                                                                                                   Local Similarity
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            Blatt L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                                                               Gaps
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Pred. No. 2.3e+02;
0; Mismatches 1; Indels
                                          Query Match 1.2%; Score 13.4; DB 1; Length 17; Best Local Similarity 93.3%; Pred. No. 2.3e+02; Matches 14; Conservative 0; Mismatches 1; Indels
Sequence 17 BP; 2 A; 3 C; 4 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hammerhead ribozyme substrate #1735.
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                                                                                                                                               865
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Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                             851 GATCCCTCTTTGTGT
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Human; ss, antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inozyme; inozyme; inozyme; junghoma; lustyme; lymphoma; leukaemia; b-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphoma; leukaemia; human immunodeficiency virus; HTV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaemia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; cerebroterapy.induced neuropathy; amyotrophic lateral sclerosis; ALS; parkinson's disease; ataxia; Huntington's disease; creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
                                                                                                                                                                                                                                   The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TR-1, the GATA transcription factor gene, IRR-2 and/or the CAATH Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and
                                                                                                             Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
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                                       Mcswiggen J;
                                                                                                                                                                                                        Claim 37; Page 72; 164pp; English.
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28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
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                                         Pavco P,
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(BLAT/) BLATT L.
(MCSW/) MCSWIGGEN J.
(CHOW/) CHOWRIRA B M.
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(RIBO-) RIBOZYME PHARM INC
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                                                                                WPI; 2000-647423/62.
                                           Zwick M,
                                                                                                                                                                                                                                                                                                                                                                                                    interferon alpha
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                                             Blatt L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
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                                                                                                        Ribozyme; erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.
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1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 3 A; 6 C; 1 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                            Mcswiggen J;
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                                                                        Hammerhead ribozyme substrate #2183.
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                                (first entry)
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                                                                                                                                                                                Homo sapiens.
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                                16-FEB-2001
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RESULT 437 AAF02422

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The invention relates to a nucleic acid molecule which down regulates expression of a cutter of a cut molecule which down regulates expression of a neurite growth inhibitor gene (MoZO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a numberzyme (an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with an NCH motif) properson or an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a NGN with a relative collour the presence of a divalent cation that is preferably MG<sup>2</sup>+. Furthermore, it may be contacted with a call to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20: The treatment may further comprise the use of one or more the cation in particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, HUV (human immunodeficiency virus) associated will, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, implementation of a divalent cation that is preferably MG<sup>2</sup>+. Furthermore, the presence of a divalent cation that is preferably MG<sup>2</sup>+. Furthermore, the cargetting nucleic acid may be contacted with a cell to reduce NOGO gene in the presence of a divalent cation that is preferably MG<sup>2</sup>+. Furthermore, the call and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more central nervous system (CNS) injury and cereboxoscular accident (CVA, stroke), Allaneimer's disease, dementia, multiple sclerosis (MS), arkington's disease, central particular, thurington's disease, central particular dystrophy, and/or other neurodegenerative disease central response of the respection of the modular dystrophy, and/or other neurodegenerative of the present cation the 
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                                                                                                      Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence is an inozyme of the invention
Chowrira BM;
                                                                                                                                                                                                                                           Claim 88; Page 79; 200pp; English.
                                                                                                                                                                                           central nervous system injury.
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  Mcswiggen J,
                                                WPI; 2001-607195/69.
Blatt L,
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The invention relates to a nucleic acid molecule which down regulates expression of a cD20 gene and a nucleic acid molecule which down concreasing the systems of a neurite growth inhibitor gene (NG20). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids and NGH molecule possessing an NGH molif), a G-cleaver (cleaving RNA with a NRY motif) propersessing an NGH molif), a G-cleaver (cleaving RNA with a NRY motif) propersessing an NGH molif), a G-cleaver (cleaving RNA with a NGY motif). The CD20-targetting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably MG 2+.

Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more the reatment may further comprise the use of fone or more theory of the CD20. The treatment may further comprise to the use of fone or more cleavemin's lymphoma (NRL), bulky low-grade or follicular NHL, lymphocytic lymphoma (NCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, cleave MRL), immunocytoma (IMC), small B-cell lymphocytic lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma (IMC) are differency virus) associated with mattle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma (IMC) are differency of the nord of a divalent cation that is preferably MG<sup>2</sup>+. Furthermore, the presence of a divalent cation that is preferably MG<sup>2</sup>+. Furthermore, the concentral nervous system (CNC) arithory and creabency and treat a patient having a condition associated with the level of NOCO. The treatment may further comprise the use of one or more (CNA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy and/or other neurodegenerative disease central response the modular dystrophy, and/or other neurodegenerative disease centered a day of the cannere of a day an amherywhen molecular di
chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
Parkinson's disease; ataxia; Huntington's disease;
Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chowrira BM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    central nervous system injury.
                                                                                                                                                                                                                                                                                                                              28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
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MCSWIGGEN J.
CHOWRIRA B M.
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                                                                                                 Homo sapiens
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                                                                                                                    Synthetic.
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Query Match 1.2%; Score 13.4; DB 1; Length 17; Best Local Similarity 93.3%; Pred. No. 2.3e+02; Matches 14; Conservative 0; Mismatches 1; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOG0; hammerhead ribozyme; DNAzyme; inozyme; G-cleaver; amberzyme; inizyme; J-ymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphoma; leukaemia; human immunodeficiency virus; HTV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaemia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
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                                                                                                                                                                                   ABK00819 standard; RNA; 17 BP
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28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
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           GTTTTCCTTATTT
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                                                                                                                                                                                                                                                                                                                                                                                                         Human NOGO Inozyme #89
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CHOWRIRA B M.
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presence of a divalent cation that is preferably Mg^2+. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (MS), parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, staxia, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present
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2001WO-US000669.
2001WO-US000670.
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30-JAN-2001; 2001WO-US000662.
30-JAN-2001; 2001WO-US000663.
30-JAN-2001; 2001WO-US000664.
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30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US000667.
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Matches 13; Conservative
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27-SEP-2000;
04-OCT-2000;
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                  The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterises and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunospens to raise antibodies that specifically recognise hGDMLP-1 proteins, as specifically of hGDMLP proteins, as specific biomolecule and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed production.
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Disclosure; SEQ ID NO 6288; 214pp; English.
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ABN06295
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Thurster actual cards in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 provide initial substrates for the recombinant engineering of hGDMLP-1 provide initial substrates for the recombinant engineering of hGDMLP-1 proteins or polypeptides may be expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as specifically recognise hGDMLP-1 proteins, as specific and concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as concentration to production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The colorate associated with the expression of hGDMLP-1 in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the specification of the present invention. N.B.

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                                                                                                                                                                                                                                          New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
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                                                                            Shannon ME;
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                                                                                Chen W,
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                                                                                Hanzel DK, Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 6287; 214pp; English.
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                Ji Y, Penn SG,
(AEOM-) AEOMICA INC.
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The present sequence for this patent did not form part of the printed production, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                               New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
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                                                                                                                                                                                                                        Rank DR,
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                                                                                                                                                                                                                          Hanzel DK,
                             30-JAN-2001; 2001W0-US000663.
30-JAN-2001; 2001W0-US000664.
30-JAN-2001; 2001W0-US000665.
30-JAN-2001; 2001W0-US000666.
30-JAN-2001; 2001W0-US000667.
30-JAN-2001; 2001W0-US000668.
30-JAN-2001; 2001W0-US000669.
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ID ABN02575 standard; DNA; 17 BP.
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Best Local Similarity 93.39
Matches 14; Conservative
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                                                                                                                                                                                            (AEOM-) AEOMICA INC.
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The present invention describes a human genome-derived myosin-like concein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used as probes to detect, characterise and quantify nucleic acids can be used as probes to detect, characterise and quantify provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for protein variants having desired phenotypic improvements, and for caypressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as specifically recognise hGDMLP-1 proteins, as specifically recognise hGDMLP-1 proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therefore and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The polyuncleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart con and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B.

The sequence data for this patent did not form part of the printed form and shell and the present invention. The present captured in the analysis of the present invention. N.B.
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2001WO-US000669.
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                                                                                                                                                                                                                                                                                   2001WO-US000662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US000670
05-FEB-2001; 2001US-0266860P
                                                       25-MAY-2001; 2001WO-US016981
                                                                                                                                                                                                                     2000GB-00024263
                                                                                                                                                                                                                                                  2001WO-US000661
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Best Local Similarity 93.33
Matches 14, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AEOM-) AEOMICA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001;
                                                                                                                                                                                                                     04-OCT-2000;
                                                                                                                                                                                                                                                                                   30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                               10-JAN-2001;
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                                                                                                                                                                                          27-SEP-2000
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06-DEC-2001
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ID ABV8
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ABV82998 standard; DNA; 17 BP

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Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL.
                                                             Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
human testis expressed Patched like protein; testis; adrenal; liver;
male germ cell development; bone marrow; brain; kidney; lung; placenta;
prostate; skeletal muscle; colon; male infertility; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 3 A; 1 C; 2 G; 11 T; 0 U; 0 Other;
                                         Human HTPL scanning oligonucleotide SEQ ID 4245.
                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 620; 718pp; English.
                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000664.
30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000668.
33-JAN-2001; 2001WO-US000669.
09-OCT-2001; 2001WS-008699
                                                                                                                                                                                    28-JAN-2002; 2002EP-00001167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            example from the invention
                   03-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-676582/73.
                                                                                                                                                                                                                                                                                                           (AEOM-) AEOMICA INC
                                                                                                                     Homo sapiens
                                                                                                                                          EP1229046-A2
                                                                                                                                                                                                          30-JAN-2001;
                                                                                                                                                              07-AUG-2002
ABV82999;
                                                                                                                                                                                                                                                                                                                              Zhan J;
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The present invention relates to human testis expressed Patched like protein (HTPL, see ABN78759 to ABN7862 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall structure strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome 10pl2.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in the trapped to human chromosome 10pl2.1. HTPL and its creatment or prevention of useful for diagnosing a disorder caused by mutation in HTPL, and in the trapped to human disorders include disorders of testis, or adrenal, adult and feetal liver, bone marrow, brain, kidney, lung, placenta, prostate.

C skeletal muscle or colon function. HTPL proteins and nucleic acids are callingally useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an

; 0 1.2%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 2.3e+02; ive 0; Mismatches 1; Indels Matches 14; Conservative Query Match Best Local Similarity

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Gaps

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1.2%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 2.3e+02; ive 0; Mismatches 1; Indels

Best Local Similarity 93.3 Matches 14; Conservative

Query Match

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Gaps

689

675 ATTATGTTACTTGTT

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2 ATTATGTTTCTTGTT 16

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RESULT 446 ABV82998

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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two isoforms, with a few single base pair differences between the two of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall structure organisation with the Patched protein. The shares an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is minar chromosome loppiz.1. HTPL and its coding sequence are usepul for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful disapnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL.
                                                                                                                                                                          Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
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                                                                                                                                  Human HTPL scanning oligonucleotide SEQ ID 4244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 620; 718pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001WO-US000664.
2001WO-US000665.
2001WO-US000667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000668.
30-JAN-2001; 2001WO-US000669.
23-MAY-2001; 2001US-00864761.
09-OCT-2001; 2001US-0327898P.
                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JAN-2002; 2002EP-00001167
                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AEOM-) AEOMICA INC
                                                                                                                                                                                                                                                                                                                                         EP1229046-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001;
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                                                                                     03-JAN-2003
                                                                                                                                                                                                                                                                                              Homo sapiens
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                                          ABV82998;
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Gaps

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Indels

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Mismatches

5

Conservative

12;

Matches

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The invention relates to a nucleic acid molecule (I) which down regulates corporates and the state of an Eta-related gene (ERG). (I) is useful for treating corputations selected from cancer, lymphoma, Ewing's sarcoma, metanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, conditions selected from cancer, lymphoma, arthritis, psoriasis, verruca vulgaris, angiofibroma of tubercous sclerosis, port-wine stains, Sturge weber syndrome, Rippel-Trenaunay-Weber syndrome, Osler-Weber-rendu cyndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, to y contacting ocals of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more therapies conduction suitable for the treatment. Leukaemia or tumour conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or chemotherapy treatment. (I) is useful for reducing ERG activity in a coll by contacting (I) with RNA, in the presence of a divalent cation such as Mg2+. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to the presence of ERG RNA in a cell. (I) is useful for specifically trangeting genes that share homology with ERG gene or ERG fusion genes.

Changeting genes that share homology with ERG gene or ERG fusion genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polynucleotide which down regulates expression of Ets-related gene, useful for treating cancer. diahatic rationathy.
                                                                                                                                                                                                            Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cencer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous selerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzymatic nucleic acid molecules which regulate expression of ERG, and
                                                                                                                                                                        Human ERG hammerhead ribozyme target sequence, Seq ID No 1047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.4; DB 1; Length 17; Pred. No. 2.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 5 A; 4 C; 5 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mcswiggen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 77; 149pp; English.
                                       ABK18400 standard; RNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAY-2000; 2000US-00572021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAY-2001; 2001WO-US015866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Von Carlowitz I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RIBO-) RIBOZYME PHARM INC
(GLAX ) GLAXO GROUP LTD.
                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              related PCR primers of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-082995/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200188124-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                 09-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                       amberzyme.
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                                                                                      ABK18400;
RESULT 447
                  ABK18400
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Randi AM;

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The invention relates to a novel isolated 17 mer nucleic acid sequence, cgiven in the specification, a sequence containing at least 15 consecutive given in the specification, a sequence with, after Optimal andless to mucleotides from the 17 mer sequence, a sequence that alignment, at least 80 % identify to the 17 mer sequence, a sequence that optimizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated mucleic caids of the invention are useful as probes and primers for detecting, identifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti) sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, corrector or antibodies directed against the polypeptides are useful for vector or antibodies directed against the polypeptides are useful for cy preparation of pharmaceuticals for prevention and/or treatment of viral ciseases that are characterised by development of tumours or cell diseases that are characterised by development of tumours or cell corrections. Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for disposis and/or prognosis of these companients. The nucleic acid sequences of the invention can be used in gene therapy. This polymucleotide sequence represents a tumour suppression crelated human fukutin oligonucleotide of the invention
                                                                                                                                                                                                                                                                        Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isolated nucleic acid, useful for treating viral diseases associated tumors and cell degeneration, also related polypeptides, antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                      Jumour suppression related human fukutin oligo SEQ ID No 5370.
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93.3%; Pred. No. 2.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 661; 720pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuijnder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR ENGINES LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-SEP-2001; 2001FR-00011978.
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-2002; 2002WO-IB004208.
958 CTGGACCCAGGACAT 972
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                                                                                                                                ABT39733 standard; DNA; 17
                                                                                                                                                                                                        (first entry)
                       CUGGACUCAGGACAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and transfected cells.
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Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003025175-A2
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                        12-JUN-2003
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                                                                                                                                                                     ABT39733;
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1.2%;

Query Match Best Local Similarity

2 ATCTGTATACATATG 16

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given in the specification, a sequence containing at least 15 consecutive nuclectides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence that obtained to the model of the model 
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antibense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel isolated 17 mer nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumour suppression
                                                                                                                                                                                                                                                                                                                                                                                               Tumour suppression related human fukutin oligo SEQ ID No 1463.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy. This polynuclectide sequence represents a tumm related human fukutin oligonuclectide of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tuijnder M;
                                                                                                                                                                                                             ABT35826 standard; DNA; 17 BP.
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588 ATGTTCACTTTAAGA 602
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                                     17 ATGTTCACTTGAAGA
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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2, MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy, or in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23, MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids can also be used as probes to detect and characterize gross alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are useful in constructing microaarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as proteins. The present sequence was used to illustrate the invention.
                                                                                                                                                                                     Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MDZ3; MDZ4; MDZ1; chromosome 7q22.1;
chromosome 6p21.3-22; chromosome 16p11.2; chromosome 15q26.1; cancer;
developmental disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
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                                                                                                                                                 Human MDZ3 scanning oligonucleotide SEQ ID 766.
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                                   ADA99777 standard; DNA; 17
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Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                           20-NOV-2003
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                                                                         ADA99777;
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RESULT 450
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513 ATCTGTATACATGTG 527

14; Conservative

Matches

Query Match Best Local Similarity

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Gaps

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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ3, MDZ4, MDZ1, MDZ12. MDZ3 is proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is cancoded at chromosome 6p21.3-22.2, MDZ7 is encoded at chromosome 6p21.3-22.2, MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome 16p12. and MDZ12 is encoded at chromosome 16p12. and MDZ12 is encoded at chromosome 16p13. MDZ4, MDZ7, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy, or in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ1, or MDZ12, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease acids can also be used as probes to detect and characterize gross alterations in MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acids can also be used as probes to detect and characterize gross alterations in MDZ3, MDZ7, or MDZ12 genetic locus. The probes are proteins are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as
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                                                                                                                            Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ4; MDZ4; MDZ1; chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
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                                                                  Human MDZ3 scanning oligonucleotide SEQ ID 767.
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nes 14; Conservative
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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is proteins and their coding sequences: MDZ3, MDZ4, MDZ12. MDZ31s. MDZ4 is encoded at chromosome 6p12.3-22.2, MDZ4 is encoded at chromosome 6p11.2 and MDZ12 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome 16p12.3 and MDZ12 is encoded at chromosome 16p2.3 and manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ1, e.g. cancer or developmental disorders. The nucleic caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acids and slso be used as probes to detect and characterize gross alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV; RNA stability; RNA expression; RNA synthesis; antisense; enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
                                                                                                                                                                                                                                                                                                                                                   New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23, MD24, MD27 or MD212, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amberzyme, G-cleaver ribozyme, decoy molecule, aptamer;
HBV reverse transcriptase; Enhancer I region; viral replication;
degenerative, disease state; HBV infection; HCV infection; cirrhosis;
liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
virucide; antiinflammatory; substrate; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 7 A; 5 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 8; SEQ ID NO 768; 103pp; English.
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                                                                                                                                                         30-JUL-2002; 2002EP-00016874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCACAGACCAAGAG 906
                                                                                                                                                                                               02-AUG-2001; 2001US-00922181
                                                                                                                                                                                                                                                                              Gu Y, Nguyen C;
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developmental disorder; ss.
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                                                                                                                                                                                                                                      (AEOM-) AEOMICA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                         Homo sapiens
                                                                               EP1281758-A2
                                                                                                                      35-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes, Inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed in en uncleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds compounds and/or potential therapies directed against HBV, and compounds and mar/or potential for the treatment of degenerative and that modulate the expression and for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene carcinoma. The present sequence represents a substrate for one of the HBV ribozyme, inozyme, G-cleaver, zinzyme, DNAzyme or amberzyme sequences
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                                                                                                                                                                                                                                                                                      Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
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40.0%; Pred. No. 2.3e+02;
iive 8; Mismatches 1; Indels
                                                                                                                                                                                                                                    Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 4 A; 3 C; 2 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                    Mcswiggen J, Morrissey D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HBV G-cleaver substrate sequence #36.
                                                                                                                                                                                                                                                                                                                                 Example 1; Page 154; 387pp; English.
                                                                     08-JUN-2001; 2001US-00B77478.
08-JUN-2001; 2001US-0296876P.
24-OCT-2001; 2001US-0335059P.
05-DEC-2001; 2001US-0337055P.
                                        26-MAR-2002; 2002WO-US009187
                                                             2001US-00817879
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                                                                                                                           RIBOZYME PHARM INC
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Best Local Similarity 40.07
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Roberts E;
                                                                                                                                              MACEJAK D.
MCSWIGGEN J.
MORRISSEY D.
                                                                                                                                                                                                                                                                 WPI; 2003-229207/22
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DRAPER K.
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WO200281494-A1
                                                            26-MAR-2001;
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                   17-0CT-2002
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Draper K,
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(PAVC/) 1
(LEEP/) 1
(DRAP/) 1
(ROBE/) 1
                                                                                                                                     (BLAT/)
(MACE/)
(MCSW/)
                                                                                                                           (RIBO-)
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The present invention relates to nucleic acid molecules which modulate
the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
are nucleic acid decoy molecules and aptamers that bind to HBV reverse
transcriptase and/or HBV reverse transcriptase primer sequences, as well
as oligonucleotides that specifically bind the Enhancer I region of HBV
DNA. The nucleic acids may be used to modulate the expression of HBV
compounds and/or potential therapies directed against HBV, and compounds
that modulate the expression and/or replication of HCV. The compounds
that modulate the expression and/or replication of HCV. The compounds
char modulate the expression and/or replication of HCV. The compounds
char modulate the expression and/or replication of HCV. The compounds
char modulate the activated to HBV and HCV infection, replication and gene.

Compounds uch as cirthosis, liver failure, and hepatocellular
carcinoma. The present sequence represents a substrate for one of the HBV
carcinoma, inozyme, G-cleaver, zinzyme, DNAzyme or amberzyme sequences
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Nucleic acid molecule, Hepatitis C virus, HCV, Hepatitis B virus; HBV; RNA expaliity; RNA expression; RNA synthesis; antiennse; enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptemer; nozyme; amberzyme; deverse transcriptase; Enhancer I region; viral replication; degenerative; disease state; HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee
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40.0%; Pred. No. 2.3e+02;
ative 8; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mcswiggen J, Morrissey D, Pavco P,
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                                                                                                                                                                                                                                    virucide; antiinflammatory; substrate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 165; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disclosed in the present invention
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08-JUN-2001, 2001US-00877478.
08-JUN-2001, 2001US-0296876P.
24-OCT-2001, 2001US-0337055P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002; 2002WO-US009187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macejak D,
Roberts E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLATT L.
MACEJAK D.
MCSWIGGEN J.
MORRISSEY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-229207/22.
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                                                                                                                                                                                                                                                                                                  Hepatitis B virus.
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DRAPER K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROBERTS E
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                                                                                                                                                                                                                                                                                                                                                                      WO200281494-A1.
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Draper K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection.
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(LEEP/)
(DRAP/)
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                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine; tumour suppression; tumour reversion; apoptosis; virus resistance; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
                                                                                                                            Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine; tumour suppression; tumour reversion; apoptosis; virus resistance; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
                                                                                                       Murine oligonucleotide associated with tumour supression, SEQ ID 5707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine oligonucleotide associated with tumour supression, SEQ ID 1496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17 BP; 5 A; 3 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 698; 738pp; French
                                                                                                                                                                                                                                                                                                                               Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACC64249 standard; DNA; 17 BP.
                                   BP.
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                                                                                                                                                                                                                                                           17-SEP-2002; 2002WO-IB004210
                                   ACC68460 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 Actrcarcagragga 3
                                                                                (first entry)
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nes 14; Conservative
                                                                                                                                                                                                                                                                                                                               Telerman A, Amson R,
                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-333167/31.
                                                                                                                                                                 schizophrenia; ss
                                                                                                                                                                                                            WO2003025176-A2.
                                                                                                                                                                                        Mus musculus.
                                                                                01-JUL-2003
                                                                                                                                                                                                                                     27-MAR-2003.
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                                                          ACC68460;
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Matches
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            RESULT 455
                        ACC68460/
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The present invention relates to murine oligonuclectides (ACC62754-ACC68806), which are associated with tumour suppression, tumour reversion, apoptosis and virus resistence. The oligonuclectides are useful as (1) as probes and primers for detecting, identifying, quantifying and/or amplifying nucleic acid, e.g. as one component of a gene chip; in vitro as (anti) sense reagents; and (2) for production of recombinant polypeptides. The oligonuclectides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer; probe; tumour suppression; tumour reversion; apoptosis; virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specifically cancer but also Alzheimer's disease and schizophrenia
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0
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                                                                                                                                                                                                                                    17-SEP-2002; 2002WO-IB004210.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and transfected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                    Telerman A, Amson R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-333167/31.
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schizophrenia; ss.
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                                                                                                                  WO2003025176-A2.
                                                          Mus musculus.
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04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or cell degeneration (e.g. Alzheimer's disease or schizophrenia). Analysis of the expression of the nucleotides can be used for diagnosis and/or prognosis of these diseases. The nucleotides and polypeptides can
                                                                                                                                                                                                                                                                                                                                                  suppression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies (Ab) against the polypeptide are useful for prevention and/or treatment of viral infections or diseases characterized by development of tumours
                                                                               New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; angiomotin-like protein 1; AMLP1; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           also be used to screen for their specific interactive molecules, potentially useful for treating diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 1.2%; Score 13.4; DB 1; Length 17; al Similarity 93.3%; Pred. No. 2.3e+02; 14; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 6 A; 3 C; 3 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
                                                                                                                                                                Disclosure; Page 420; 771pp; French.
                   Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression of the nucleotides.
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                 Amson R,
                                                      WPI; 2003-441574/41.
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003037931-A2.
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                   Telerman A,
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                                                                                                       The present invention describes the human anglomotin-like protein 1 (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and compositions of the present invention can be used for treating or preventing a disorder associated with decreased or increased expression or activity of AMLP1. The present sequence represents a scanning oligonucleotide for human AMLP1b, which is used in an example from the present invention.
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New isolated nucleic acid molecule encoding a human angiomotin-like protein, useful for treating or preventing a disorder associated with decreased or increased expression or activity of AMLP1.
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                                                                                                                                                                                                                                                                            Sequence 17 BP; 8 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; SEQ ID NO 814; 172pp; English.
                                                                          Example 2; SEQ ID NO 813; 172pp; English
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 16 TCATTTTCCTTTCAA
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Tumour suppression/reversion associated nucleotide #5325.
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                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid molecule encoding a human angiomotin-like protein, useful for treating or preventing a disorder associated with decreased or increased expression or activity of AMLP1.
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                      Gaps
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     Length 17;
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                      1; Indels
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Pred. No. 2.3e+02;
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Best Local Similarity 93.3%;
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                                          393 TCATTTTCCTTACAA 407
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                                                                                                            ADC38463 standard; DNA; 17
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Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention.
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                                                                                                                                                                                                 AMLP1b; 88
                                                                                                                                                                                                                  Synthetic.
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fragments of at least 15 consecutive nucleotides of these nucleotides, a fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 8% identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides, or the complement, or corresponding RNA, of the nucleotides. The nucleotides are used as probes or primers for detecting, identifying, quantifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour suppression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as recombined models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies (Ab) against the polypeptide are useful for prevention and/or treatment of viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzhehamer's disease can be used for disponsis any siss of the expression of the nucleotides can be used for disponsis
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cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
primer; probe; tumour suppression; tumour reversion; apoptosis;
virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
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hes 14; Conservative
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primer; PCR; gene chip; antisense; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
                                                                                                                                                                                                                                                                                                                                in the phenomena of tumour suppression, tumour reversion, apoptosis and/or resistence to viruses. The invention may be useful for the and/or resistence to viruses. The invention may be useful for the nootropic or neuroleptic activity. The DNA sequences may be useful as probes and primers for detecting, indentifying, quantifying and/or amplifying nucleic acid, for example as one component of a gene chip, in vitro as antisense reagents and for production of recombinant polypeptides. The invention may therefore be useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. The present sequence is that of a nucleic acid sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                          New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
                                                                                                                                                                                                                                                                                                                     This invention relates to novel isolated nucleic acid sequences involved
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in the phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses. The invention may be useful for the development of compounds with a cytostatic, virucide, neuroprotective, nootropic or neuroleptic activity. The DNA sequences may be useful as probes and primers for detecting, indentifying, quantifying and/or amplifying nucleic acid, for example as one component of a gene chip, in vitro as antisense reagents and for production of recombinant vitro as antisense reagents and for production of recombinant pharmaceuticals for prevention may therefore be useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. The present sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
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17-SEP-2002; 2002WO-IB004523.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ATCTGCTGGGTTTT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      556 ATATGCTGGGTTTTT
                                                                                                                                                                                                                   relerman A, Amson R,
                                                                                                                                                                                                                                                                                        WPI; 2003-313354/30.
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Gaps

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Length 17; 1; Indels

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Sequence 17 BP; 6 A; 3 C; 3 G; 5 T; 0 U; 0 Other;
                          Claim 1; Page 752; 798pp; French.
                                                                                                                                                                                                                                  (LYNX-) LYNX THERAPEUTICS INC
                                                                                                                                                                                                                        09-JAN-2002; 2002US-0348053P.
                                                                                                     588 ATGTTCACTTTAAGA 602
                                                                                                                                                                                                               08-JAN-2003; 2003US-00339782
                                                                                                                                     ADL82512 standard; DNA; 17
                                                                                                             17 Argricacrigaaga 3
                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                           Bowen BA;
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                                     ведиенсе
                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                           Goodman LJ,
                                                                                                                                                        20-MAY-2004
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                                                                                                                                               ADL82512;
                                    This with
                                                                                                                            RESULT 465
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Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage; hepatitis B virus infection; hepatitis; hepatocellular carcinoma; cirrhosis; liver failure; lamivudine; interferon; genetic drift; virucide; hepatotropic; antiinflammatory; cytostatic.
                                                                                                                                                                                                                                                                                                                                                              Hepatitis B virus (HBV) RNA target sequence #1483.
        Query Match
1.2%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 2.38+02;
Matches 14; Conservative 0; Mismatches 1;
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07-FEB-1994; 94US-00193627.
08-NOV-1999; 99US-00436430.
20-MAR-2000; 2000US-00531025.
09-AUG-2000; 2000US-006358B5.
09-AUG-2000; 2000US-0063638B.
08-AUG-2000; 2000US-0063638F.
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                                                                                                602
                                                                                                                                  17 Argricacrigaaga 3
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                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                588 ATGTTCACTTTAAGA
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MCSWIGGEN J A.
MORRISSEY D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis B virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2004054156-A1.
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(MCSW/)
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                                                                                                                                                                                                    RESULT 466
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                                                                                                                                  셤
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                                                                                                                                                                                 The
                                    New nucleic acid sequences associated with tumor suppression, regression, apoptosis or virus resistance are useful to diagnose and treat viral disease, development of tumor cells and cell degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vector containing nucleic acid associated with breast cancer, useful for treating, diagnosing and characterizing breast cancer, also related polypeptides and antibodies.
                                                                                                                                                                                 with tumour suppression or regression, apoptosis or virus resistance. invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration
                                                                                                                                                                represents an isolated nucleic acid sequence associated
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human ER+ breast cancer differentially expressed sequence #482.
                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 1.2%; Score 13.4; DB 1; Length 17; Best Local Similarity 93.3%; Pred. No. 2.3e+02; Matches 14; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                Seguence 17 BP; 6 A; 3 C; 3 G; 5 T; 0 U; 0 Other;
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WPI; 2003-250498/25
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The invention relates to an enzymatic nucleic acid molecule that specifically cleaves RNA derived from hepatitis B virus (HBV) and comprising one or more binding arms, without requiring the presence of a useful for treating hepatitis B virus infection, hepatitis, hepatocellular carcinoma, cirrhosis and liver failure, either alone or in combination with other therapies such as lamivadine and interferons. The nucleic acids are useful as diagnostic tools to examine genetic drift and mutations within diseased cells, for detecting the presence of HBV RNA in a cell, for the study of RNA and for down-regulating gene expression of target genes in bacterial, fungal, viral, plant or mammalian cells. This sequence repersents an HBV RNA target sequence, used in the scope of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                          Novel enzymatic nucleic acid molecule such as DNAzymes and inozymes specifically cleaving RNA derived from hepatitis B virus and comprising one or more binding arms, useful for treating hepatitis and cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17 BP; 4 A; 3 C; 2 G; 0 T; 8 U; 0 Other;
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K, Blatt L, Mcswiggen JA, Morrissey
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 1483; 122pp; English
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No.

Pred. N

40.08;

Local Similarity

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The invention relates to an enzymatic nucleic acid molecule that specifically clasves RNA derived from hepatitis B virus (HBV) and comprising one or more binding arms, without requiring the presence of a 2.0H group within the molecule for activity. The nucleic acids are useful for treating hepatitis B virus infection, hepatitis, hepatocellular carcinoma, cirrhosis and liver failure, either alone or in combination with other therapies such as lamivudine and interferons. The nucleic acids are useful as diagnostic tools to examine genetic drift and mutations within diseased cells, for detecting the presence of HBV RNA in a cell, for the study of RNA and for down-regulating gene expression of target genes in bacterial, fungal, viral, plant or mammalian cells. This sequence represents an HBV RNA target sequence, used in the scope of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
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                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis B virus; HBV; 88; enzymatic nucleic acid; RNA cleavage; hepatitis B virus infection; hepatitis; hepatocallular carcinoma; cirrhosis; liver failure; lamivudine; interferon; genetic drift; virucide; hepatotropic; antiinflammatory; cytostatic.
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1.2%; Score 13.4; DB 1; Length 17;
40.0%; Pred. No. 2.3e+02;
tive 8; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis B virus (HBV) RNA target sequence #949.
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20-MAR-2000; 2000US-00531025.
09-AUG-2000; 2000US-00636385.
24-OCT-2000; 2000US-00696347.
08-JUN-2001; 2001US-00877478.
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                                                                                                                             569 TTTAATACCTTTATA 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                     Conservative
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MORRISSEY D.
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Query Match
Best Local Similarity
Matches 6; Conserv
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07-FEB-1994;
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(BLAT/)
                                                                                                                                                                                                                                                                                                        RESULT 467
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ADM5

ADM5

ADM5

ADM5

ADM5

ADM5

ADM5

ADM5

ADM7

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1.2%; Score 13.4; DB 1; Length 17;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel myosin-like protein-1, useful for treating or preventing disorder associated with decreased expression or activity of human genome-derived myosin-like protein-1 such as disorder of heart and/or skeletal muscle
                                                                                                                                                                                                                   ss; probe; myosin-like protein-1; hGDMLP-1;
-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
                    Gaps
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                    IndelB
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2.3e+02;
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                      Mismatches
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                                                                                                                                                                                                 Human GDMLP-1 probe SEQ ID NO:6289.
                    8,
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2000US-0236359P.
2000GB-00024263.
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2001WO-US000664.
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2001WO-US000666.
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2001US-0266860P
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2001WO-US000662
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                                                                                                                            ACN69387 standard; DNA; 17
                                                                                                                                                                          (first entry)
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hGDMLP-1 agonist hGDMLP aı
skeletal muscle function.
                                                          UNAAUGCCUUUAUAU
                                          570 TTAATACCTTTATAT
                    Conservative
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HANZEL D K.
RANK D.
CHEN W.
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05-FEB-2001;
25-MAY-2001;
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                                                                                                                                                                                                                                                                     Homo sapiens
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(RANK/)
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           Best Loc
Matches
                                                                                                      RESULT 468
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preventing a disorder associated with decreased expression or activity hGDWLP-1, such as a disorder of heart and/or skeletal muscle function. The present sequence represents a 17-mer nucleotide, used in the invention for scanning the sequence represented in ACN63103
                                                                                                                                                                                                                                                                                                                   se; probe; myosin-like protein-1; hGDMLP-1;
-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shannon ME
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                                                                                 Query Match 1.2%; Score 13.4; DB 1; Length 17; Best Local Similarity 93.3%; Pred. No. 2.3e+02; Matches 14; Conservative 0; Mismatches 1; Indels
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                                                              Sequence 17 BP; 1 A; 6 C; 8 G; 2 T; 0 U; 0 Other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                            Human GDMLP-1 probe SEQ ID NO:6288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US000663.
30-JAN-2001; 2001WO-US000664.
30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000669.
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2001WO-US000662.
2001WO-US000663.
2001WO-US000664.
2001WO-US000665.
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2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
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05-FEB-2001; 2001US-0266860P.
25-MAY-2001; 2001US-00866108.
                                                                                                                                                                                                                                                                                                                                                                                                                                          26-NOV-2003; 2003US-00723361
                                                                                                                                      21 CCGGGCCGTGGCAGG 35
                                                                                                                                                      CCGGGCTGTGGCAGG 15
                                                                                                                                                                                                                        ACN69386 standard; DNA; 17
                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                            skeletal muscle function.
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HANZEL D K.
RANK D.
CHEN W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHANNON M E.
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                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                    Human; se
hGDMLP-1
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(CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GUYY/)
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     The invention relates to a novel polypeptide (I) comprising a sequence (SI) of myosin-11ke protein-1 (hGDMLP-1) having 2568 amino acids fully defined in the specification, a fragment of at least 8 amino acids of (SI), 95% deviation from (SI) which are conservative substitutions, and satisfaction from (SI) hand are conservative substitutions, and antagonist to (BOMLP-1, or as an inhibitor of hGDMLP-1 activity. A pharmaceutical composition of the invention is useful for treating or preventing a disorder associated with decreased expression or activity of hGDMLP-1, such as a disorder of heart and/or skeletal muscle function. The present sequence represents a 17-mer nucleotide, used in the invention for scanning the sequence represented in ACN63103
                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ss; probe; myosin-like protein-1; hGDMLP-1;
hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
skeletal muscle function.
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                                                                                                                                                                 Sequence 17 BP; 1 A; 5 C; 9 G; 2 T; 0 U; 0 Other;
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30-JAN-2001; 2001WO-US000663.
30-JAN-2001; 2001WO-US000664.
30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000669.
30-JAN-2001; 2001WO-US000669.
30-JAN-2001; 2001WO-US000669.
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2001WO-US000661.
2001WO-US000662.
2001WO-US000663.
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                                                                                                                                                                                                        Local Similarity 93.3
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JI Y.
PENN S G.
HANZEL D I
RANK D.
CHEN W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-OCT-2000;
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(RANK/)
(CHEN/)
(SHAN/)
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Query Match
                                      (RANK/)
(CHEN/)
(SHAN/)
  (PENN/)
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                                                                                                                      Su Y,
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                                                                                                                                                                           The invention relates to a novel polypeptide (I) comprising a sequence (SI) of myosin-like protein-1 (hGDWLP-1) having 2568 amino acids fully defined in the specification, a fragment of at least 8 amino acids fully (SI), 95% deviation from (SI) which are conservative substitutions, and antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A pharmaceutical composition of the invention is useful for treating or preventing a disorder associated with decreased expression or activity of preventing a disorder of heart and/or skeletal muscle function. The present sequence represents a 17-mer nucleotide, used in the invention for scanning the sequence represented in ACN63103
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                                        Novel myosin-like protein-1, useful for treating or preventing disorder associated with decreased expression or activity of human genome-derived myosin-like protein-1 such as disorder of heart and/or skeletal muscle function.
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hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
skeletal muscle function.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.2%; Score 13.4; DB 1; Length 17; Best Local Similarity 93.3%; Pred. No. 2.3e+02; Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17 BP; 1 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
                                                                                                                                           Disclosure; SEQ ID NO 6287; Opp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-2000; 2000GB-00024263.
30-JAN-2001; 2001MO-US000661.
30-JAN-2001; 2001MO-US000663.
30-JAN-2001; 2001MO-US000663.
30-JAN-2001; 2001MO-US000664.
30-JAN-2001; 2001MO-US0006664.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 CCGGGCCGTGGCAGG 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Conservative
WPI; 2004-533378/51
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05-FEB-2001;
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                                                                                                                                                                                                                                                                                     Novel myosin-like protein-1, useful for treating or preventing disorder associated with decreased expression or activity of human genome-derived myosin-like protein-1 such as disorder of heart and/or skeletal muscle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                Shannon ME;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.2%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 2.3e+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVLQT1; KCNE1; long QT syndrome; LQT syndrome; minK antiarrhythmic; gene therapy; human; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Forward primer for amplifying human KVLQT1 exon 1.
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                                                                                                                                                                                Rank D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Splawski I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 2567; Opp; English.
                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sanguinetti MC,
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hes 14; Conservative
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                                                                                                                                                                                Ji Y, Penn SG,
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PENN S G.
HANZEL D K.
RANK D.
CHEN W.
                                                                                                                    SHANNON M E.
                                                                                                                                                                                                                                            WPI; 2004-533378/51.
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17-AUG-1998;
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                                                 The invention relates to KVLQT1 and KCNE1 genes, associated with long QT (LQT) syndrome. It provides a minK protein comprising a mutation which substitutes the wild type amino acids with Leu, Asp, Leu, His, Trp and Ala or Thr at residues 74,76,28,32,98 and 127 respectively. Screening KVLQT1 and KCNE1 is useful for identifying mutations for diagnosing and treating LQT. The ability to predict LQT enables physicians to prevent the diseases with medical therapy such as beta blocking agents and opts for better treatments. Sequences AAZ90707-Z90740 represent PCR primers for amplifying human KVLQT1 exons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human biallelic marker upstream amplification primer SEQ ID NO:5744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome, biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; gentotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
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                                                                                                                                                                                                                                                                                       1.2%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Page 1455; 2745pp; English.
                     Example 11; Page 70; 167pp; English.
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                   48 GCCGCGCCCCAGTT
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N. B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the
pharmaceutical agents acting on a disease as well as other treatment. N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel biallelic markers used to construct a high density disequilibrium
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                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
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                                                                                                                                                                                                                        1.2%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 2.4e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                                             Sequence 18 BP; 7 A; 0 C; 8 G; 3 T; 0 U; 0 Other;
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98US-0109732P.
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                                                                                                                                                                                                                                                                                             14; Conservative
                                                                                                                                                                                                                                                                                                                                              612 TAAGTAGGAGATGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-013267/01.
                                                                                                                                                                                                                                                            Local Similarity
                                                                                                  present invention
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23-NOV-1998;
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                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                             Matches
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Dog; genome; genomic marker; radiation hybrid map; identification; chromosome location; gene marker; polymorphic microsatellite marker; phenotype; behaviour; pedigree; ss.

Canis familiaris. WO200029615-A2.

Dog genomic marker oligonucleotide sequence SEQ ID NO:122.

09-OCT-2000 (first entry)

AAA66260;

AAA66260 standard; DNA; 18 BP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated mutant KVLQT1 nucleic acids, useful for developing products for the diagnosis, prevention and treatment of long QT syndrome.
                                                                                                                                                                                                                                                                                                                              KVLQT1; mutation; human; cardiac I(ks) potassium channel; KCNE1; ss;
cardiac arrhythmia; electrocardiogram; Long QT syndrome; gene therapy;
chromosome 11p15.5; PCR primer.
                     Gaps
                                                                                                                                                                                                                                                                                             Human long QT syndrome-associated KVLQT1 exon 1 forward primer #2.
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93.3%; Pred. No. 2.4e+02;
tive 0; Mismatches 1; Indels
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                                                                                                                                                                                  AAZ98939 standard; DNA; 18 BP
                                                     1060 CTTTCCAGTGGCTAA 1074
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                                                                          18 CTTACCAGTGGCTAA 4
                                                                                                                                                                                                                                                         (first entry)
Best Local Similarity 93.3
Matches 14; Conservative
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Burn TC, Splawski I;
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                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                             RESULT 475
AAZ98939
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New radiation hybrid map of the dog, Canine familiaris, genome, useful for e.g. identifying genes implicated in phenotypic and behavioral traits or in genetic diseases and for studying dog pedigrees.

(CNRS ) CNRS CENT NAT RECH SCI.

Galibert F, Andre C; WPI; 2000-387821/33.

98US-0108193P. 99WO-IB001907,

15-NOV-1999; 13-NOV-1998;

25-MAY-2000

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The present invention describes a radiation hybrid map of the dog (Canine familiaris) genome comprising the genome location of a marker selected from AAA66139 to AAA66942. The radiation hybrid map is useful for identifying and localising dog genes, since it covers approximately 80 % of the dog genome and provides a dense map integrating different types (i.e. Type I and Type II) of markers. The map and the dog genome markers responsible for phenotypic and behavioural traits in dogs, to identify morbid genes, to analyse diseases and identify implicated genes in such diseases and their alleles, and to study dog pedigrees. They may also be useful for isolating corresponding human gene sequences e.g. genes involved in genetic diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; KVLQT1; antiarrhythmic; cardiant; gene therapy; PCR primer; cardiac potassium channel; Jervell and Lange-Nielsen Syndrome; JLN; chromosome 11p15.5; long QT syndrome; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.2%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 2.4e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 4 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 58; 87pp; English.
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Matches 14; Conservative
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RESULT 477
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Gaps

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11 Similarity 93.3%; 14; Conservative (

Best Local Similarity Matches 14; Conserv

48 GCGCGCCCCAGIT 62 GCCGCGCCCCCAGTT 16

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Mutation analysis of NF1 gene by treating EBV transformed lymphoblastoid
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05-JUN-2000; 2000EP-00870122.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing primer
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                                                                                                                                                                                                                               KVLQT1 is a cardiac potassium channel and mutations in the KVLQT1 gene cause Jervell and Lange-Nielsen Syndrome (JLN). KVLQT1 maps to chromosome 11p15.5. The present invention relates to a mutant KVLQT1 coding sequence (see AAC89914). The mutant KVLQT1 coding sequence is useful in the diagnosis of long QT syndrome and in screening humans for the presence of KVLQT1 gene variants which cause JLN syndrome. The present sequence is a PCR primer used to amplify a KVLQT1 exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurofibromatosis type 1; NF1; peripheral blood lymphocyte; PBL; EBV; ss; Epstein-Barr virus; B-lymphoblastoid cell; phytohaemagglutinin; PHA; frame shift mutation; mis-sense mutation; silent mutation; PCR primer;
                                                                                                                                                                    DNA encoding for a mutant KVLQT1 which causes Jervell and Lange-Nielsen syndrome (JLN) when homozygous, useful for diagnosing long QT syndrome, or diagnosing or prognosing JLN.
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                                                                                                                                                                                                                                                                                                               Sequence 18 BP; 1 A; 10 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurofibromatosis (NF1) HA PCR primer #15.
                                                                                                                                                                                                                Example 5; Col 45-46; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS05095 standard; DNA; 18 BP
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05-JUN-2000; 2000EP-00870122.
                                                            98US-00135021
                                                                                97US-00874655
                                                                                         98US-0094477P
                                                                                                                                                                                                                                                                                                                                           Local Similarity 93.3%;
les 14; Conservative
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                                                                                                             (UTAH ) UNIV UTAH RES FOUND.
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                                                                                                                                Splawski I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Callens T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-300341/31.
                                                                                                                                                    WPI; 2001-060013/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequencing primer
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   Homo sapiens
                                                            17-AUG-1998;
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                                                                                13-JUN-1997;
                                                                                         29-JUL-1998;
                      US6150104-A.
                                                                                                                                  Keating MT,
                                         21-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS05095;
                                                                                                                                                                                                                                                                                                                                     Query Match
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ID AAS0
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The sequences represent neurofibromatosis type 1 (NF1) cDNA fragments and commandation analysis of the NF1 gene involves isolating extend for mutation analysis of the NF1 gene involves isolating peripheral blood lymphocytes (PBL) of a patient, establishing Epstein-CC Barr virus (EBV) transformed B-lymphoblastoid cell line with isolated Barr virus (EBV) transformed B-lymphoblastoid cell line with isolated Stimulation, treating the cell line or short-term culture with protein stimulation, treating the cell line or short-term culture with protein synthesis inhibitor and immediately extracting RNA from the cultures. The RNA is then amplified and peptide fragments are obtained by in vitro SNA is then amplified and peptide fragments. Nutation allysis of transcription/translation of amplified fragments. Nutation allysis of NF1 is used for detection of frame shift, mis-sense and silent mutations in various exons of the gene. This is useful in screening for NF1 mutations in young children who are often oligosymptomatic. Efficacy of a mutation is monitored in vitro using cell systems in which modulate nor systems of the sequences can be used to design defective NF1 gene is expressed. The sequences can be used to design drugs which modulate NF1 activity, by using knowledge of the structure of the NF1 protein and of specific defects of the various NF1 mutant the proteins. The method allows for reliable analysis of mutations that are difficult to detect due to unstable or wrong-spliced transcripts ö Neurofibromatosis type 1; NF1; peripheral blood lymphocyte; PBL; EBV; ss; Epstein-Barr virus; B-lymphoblastoid cell; phytohaemagglutinin; PHA; frame shift mutation; mis-sense mutation; silent mutation; PCR primer; Mutation analysis of NF1 gene by treating EBV transformed lymphoblastoid cell lines formed with lymphocytes of patient with protein synthesis inhibitor, and obtaining peptides by translating amplified RNA from cell Gaps ö 1.2%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 2.4e+02; rive 0; Mismatches 1; Indels Neurofibromatosis (NF1) genomic DNA sequencing primer #91. Sequence 18 BP; 10 A; 1 C; 4 G; 3 T; 0 U; 0 Other; Claim 9; Page 70; 102pp; English. AAS05039 standard; DNA; 18 BP. 430 07-SEP-2001 (first entry) Local Similarity 93.3 nes 14; Conservative TTTTCCTTATAGTT 416 TTTTTCCTTATATTT AAS05039; 18 Query Match RESULT 479 Matches

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The sequences represent neurofibromatosis type 1 (NF1) cDNA fragments and equencing primers for use in mutation analysis of NF1. A method for mutation analysis of the NF1 gene involves isolating certod for mutation analysis of the NF1 gene involves isolating particles. Perspheral blood lymphocytes (PBL) of a patient, establishing Epstein-Epsty transformed B-lymphoblastoid cell line with isolated PBL, or short-term culturing of PBL by phytohemagglutinin (PHA) stimulation, treating the cell line or short-term culture with protein synthesis inhibitor and immediately extracting RNA from the cultures. The RNA is then amplified and peptide fragments are obtained by in vitro transcription/translation of amplified fragments. Mutation analysis of NP1 is used for detection of frame shift, mis-sense and silent mutations in voung children who are often oligosymptomatic. Efficacy of a mutations in young children who are often oligosymptomatic. Efficacy of a clug or agent can be identified by a screening process in which modulation is expressed. The sequences can be used to design drugs which modulate NF1 activity, by using knowledge of the structure of the NF1 protein and of specific defects of the various NF1 mutant cross the NF1 protein and of specific defects of the various NF1 mutant cross that are difficult to detect due to unstable or wrong-spliced transcripts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing a DNA fingerprint of an individual by amplifying fragments containing a miniature inverted repeat transposable element is useful to detect polymorphisms and correlate genotype with phenotype particularly in maize.
cell lines formed with lymphocytes of patient with protein synthesis inhibitor, and obtaining peptides by translating amplified RNA from cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heartbreaker; Hbr; DNA fingerprint; phenotype; polymorphism;
miniature inverted repeat transposable element; MITE; molecular marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.2%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 2.4e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 BP; 10 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
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                                                                                 Claim 9; Page 64; 102pp; English.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR; primer; 88.
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                               PCR primers ABV72171-90 were used to amplify Heartbreaker (Hbr) loci from maize genomic DNA. The Hbr family of miniature inverted repeat transposable elements (MTTES) is useful to demonstrate the method of the invention. The specification describes a method for producing a DNA fingerprint of an individual. The method comprises generating restriction fragments to which an adaptor is ligated, amplifying fragments containing a MITE and resolving the amplified fragments. The presence of a certain amplified fragment is correlated to a phenotype. The method is used to characterize the DNA of an individual, to detect polymorphisms, to correlate presence of an amplified fragment with phenotype and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining the severity of arthritic conditions, e.g. rheumatoid arthritis, in a mammal or human by detecting whether a sample contains elevated levels of marker(s), e.g. CD21L polypeptides or lymphotoxin-beta polypeptides.
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                                                                                                                                                                                                                                                                                                                   1.2%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 2.4e+02; artive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arthritic condition, CD21L, lymphotoxin-beta polypeptide, chemoattractant; arthritis; PCR; primer; ss.
                                                                                                                                                                                                                                                                               Sequence 18 BP; 4 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer used to amplify a CD21L gene fragment.
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                                                                                                                                                                                                                                           generate a set of molecular markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 13; 27pp; English.
Example 1; Col 17; 37pp; English.
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Best Local Similarity 93.3
Matches 14; Conservative
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ADN35810 standard; DNA; 18 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a sample.
                                                                ADN35810;
              RESULT 483
                          ADN35810/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel inhibitor compound directed against the expressed proteins or the transcription product (mRNA) of a murine gene and/or its human orthologue and useful in the treatment of cancer. The compound of the invention demonstrates cytostatic and antiinflammatory activities and may be useful for the preparation of a therapeutic composition for the treatment of cancer, in particular for the treatment of solid tumours of the lung, colon, breast, prostate, ovary and pancreas, as well as leukaemia and lymphoma. Furthermore, the methods of the invention may be utilised to treat inflammatory disorders, as well as the invention and be accepted the invention may be utilised to treat inflammatory disorders, as well as the current sequence is that of the PCR primer of the invention which was used to amplify human PSK (prostate-derived STE20-like kinase) cDNA.
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                                                                                                                                                                                                                                                                                 inhibitor; cancer; cytostatic; antiinflammatory; solid lung tumour; colon; breast; prostate; ovary; pancreas; leukaemia; lymphoma; inflammatory disorder; gene therapy; antisense; RNA interference; PCR; primer; 88; human; PSK; prostate-derived STE20-like kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibitor compounds of expressed proteins of murine genes and/or their human orthologs, useful for treating inflammatory diseases and cancer disorders such as solid tumors, leukemias and lymphomas.
                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n 1.2%; Score 13.4; DB 1; Length 18; Similarity 93.3%; Pred. No. 2.4e+02; 14; Conservative 0; Mismatches 1; Indels
                          1.2%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 2.4e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martins CP, Mikkers HMM,
                                                                                                                                                                                                                                                        PCR primer used to amplify human PSK cDNA - SEQ ID 16.
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Sequence 18 BP; 3 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; SEQ ID NO 16; 280pp; English.
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                                                                                                                                                                              BP
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19-AUG-2002; 2002US-00224524.
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                                                                                   277 GGCATATTTCTTCAC 291
                                                                                                  1 GGCATGTTTCTTCAC 15
                                                                                                                                                                              ADK13869 standard; DNA; 18
                                                                                                                                                                                                                                   (first entry)
                      Query Match
Best Local Similarity 93.3<sup>4</sup>
....heg 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KYLI-) KYLIX BV.
                                                                                                                                                                                                                                                                                                                                                                                  WO2004012817-A2
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The invention relates to a method of diagnosing non-small cell lung cancer (NSCLC) or a predisposition to developing NSCLC in a subject by determining the expression level of a NSCLC-associated gene in a biological sample derived from the subject, where an increase or decrease of the level compared to a normal control level of the gene indicates that the subject suffers from or is at risk of developing NSCLC. The method is useful in diagnosing NSCLC or a predisposition to developing NSCLC in a subject. The compound, polyneucleotide and the encoded polypeptide and composition are useful in treating or preventing NSCLC. This sequence corresponds to an antisense oligonucleotide of genes that are differentially expressed in NSCLC cells.
                                                                                            ss; cytostatic; gene therapy; vaccine; non-small cell lung cancer; NSCLC; diagnosis; cancer; URLC1; antisense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing, preventing and treating non-small cell lung cancer (NSCLC) comprises determining an expression level of an NSCLC-associated gene in
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                                               Human NSCLC gene antisense-S oligonucleotide #35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 491; 394pp; English.
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28-FEB-2003; 2003US-0451374P.
28-APR-2003; 2003US-0466100P.
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Best Local Similarity 93.3
Matches 14; Conservative
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(first entry)
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CAGCCCAAGAGCCTC 1

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Fri Aug 19 11:00:00 2005

WO2004065959-A2.

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melanoma comprising detecting the presence or absence of one or more polymorphic variations associated with melanoma in a nucleic acid sample from a subject. Preventing melanoma in a subject comprises detecting the presence or absence of neor more polymorphic variations associated with melanoma in a nucleic acid sample from a subject; and administering a melanoma preventative to a subject in need thereof based upon the presence or absence of the one or more polymorphic variations in the nucleic acid sample. The preventative reduces ultraviolet (UV) light exposure to the subject. The methods, nucleic acids, proteins, and compositions are useful for treating melanoma. The present sequence represents a human cyclin-dependent kinase 10, CDK10, proximal SNP probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                apoptosis, cytostatic; antiinflammatory; antiasthmatic; respiratory; antirhemmatic; antiarthritic; gynaecological; cardiant; vasotropic; antipsoriatic; antiulcer; gastrointestinal; immunosuppressive; neuroprotective; cancer; autoimmune; neurodegenerative; inflammatory; asthma; chronic obstructive pulmonary disease; cystic fibrosis; myocardia inchritis; acute respiratory distress syndrome; preclampsia; myocardial ischaemia; reperfusion injury; psoriasis; bronchiolitis; Crohn's disease; ulcerative colitis; inflammatory bowel disease; 88;
melanoma associated polymorphic variation; SNP;
single nucleotide polymorphism; cyclin-dependent kinase 10; CDK10; probe.
                                                                                                                                                                                                                                                                                                                                                                                  Identifying a subject at risk of melanoma, useful for treating melanoma, comprises detecting the presence or absence of one or more polymorphic variations associated with melanoma in a nucleic acid sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method of identifying a subject at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.2%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 2.4e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR primer 2 used to amplify human Bcl2 cDNA.
                                                                                                                                                                                                                                                                                                          Kammerer SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quantitative PCR; QPCR; primer; human; Bcl2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Page 84; 295pp; English.
                                                                                                                                                                                                                                                                                                            Braun A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR05071 standard; DNA; 18 BP
                                                                                                                                                                                                          06-NOV-2002; 2002US-0424475P.
23-JUL-2003; 2003US-0489703P.
                                                                                                                                                                      06-NOV-2003; 2003WO-US035879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            702 TAGTCACGGTGCTCT 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 TAGTCAGGGTGCTCT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
                                                                                                                                                                                                                                                                    (SEQU-) SEQUENOM INC.
                                                                                                                                                                                                                                                                                                          Nelson MR,
                                                                                                                                                                                                                                                                                                                                                WPI; 2004-411721/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                          WO2004044164-A2.
                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-OCT-2004
                                                                                                                                27-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADR05071:
                                                                                                                                                                                                                                                                                                          Roth RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 485
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The invention relates to a novel method for identifying an agent that

modulates the function of an apoptosis-associated polypeptide,

particularly a kinase or GCFR (G-protein-coupled receptor). The method

comprises providing a sample containing an apoptosis-associated

polypeptide and a candidate agent and incubating under conditions to

polypeptide and a candidate agent and incubating under conditions to

polypeptide and a candidate agent to the polypeptide, measuring the

binding and comparing it with the binding of the polypeptide to a control

agent known not to bind to the polypeptide. The method of the invention

captured to antiathifammactory, antiasthmatic, respiratory,

antipsoriatic, antiulcer, gastrointestinal, immunosuppressive and

antipsoriatic, antiulcer, gastrointestinal, immunosuppressive and

cantipsoriatic, antiulcer, gastrointestinal, immunosuppressive and

carcar of the kidney, uterus, prostate, bladder, ovary, colon and breast,

leukaemias, sarcomas and myelomas. Purthermore, autoimmune,

cancer of the kidney, uterus, prostate, bladder, ovary, colon and breast,

leukaemias, asarcomas and myelomas. Purthermore, autoimmune,

cancer of the kidney, uterus, pulmonary disease, cystic fibrosis,

cantum, chronic obstructive pulmonary disease, cystic fibrosis,

rheumatoid arthritis, acute respiratory distress syndrome, preciampsia,

myocardial ischaemia, reperfusion injury, psoriasis,

crement sequence is that of a QPCR (quantitative PCR) primer of the

current sequence or absence of siRNAs (small interfering RNAs).
                                                                                                                                                                                                                                                                                                   Identifying a modulator of apoptogis-associated polypeptide function, useful for treating e.g., cancer, comprises incubating a sample containing an apoptosis-associated polypeptide and a candidate agent to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss; cell proliferative disorder; breast; methylation; cytostatic; gene therapy; single nucleotide polymorphism; SNP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.2%; Score 13.4; DB 1; Length 18; 33.3%; Pred. No. 2.4e+02; [ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 BP; 4 A; 10 C; 1 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 219; 230pp; English
                                                                                                                                                                                (EIRX-) EIRX THERAPEUTICS LTD
                                                                                                                                                                                                                        Seery L, Hayes I, Murphy F;
                                                                             23-JAN-2004; 2004WO-GB000271.
                                                                                                                      23-JAN-2003; 2003GB-00001566.
25-MAR-2003; 2003US-0457533P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.38;
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Matches 14; Conservative
                                                                                                                                                                                                                                                                 WPI; 2004-593556/57
                                                                                                                                                                                                                                                                                                                                                                      permit binding.
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                                      05-AUG-2004
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96US-0023424P.
96US-0027334P.
97US-0038685P.
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                                                       (MAGA-) MAGAININ PHARM INC
                                             UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                       CACTCTGGACCCTGG
                                                                                                                                                                                                                                                                                                                                                                                  14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       954 CACTCTGGACCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-405178/34.
                                                                                                               WPI; 1998-179058/16.
                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSA; human; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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09-SEP-1998;
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 22-AUG-1996;
            01-OCT-1996;
18-FEB-1997;
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                                                                               Wilson JM,
Zasloff M;
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                                               (UYPE-)
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                                                                                                                                                                                                                                                                           The invention relates to a novel method for predicting the responsiveness of a subject with a cell proliferative disorder of the breast tissues to a therapy comprising analysing the methylation pattern of a target nucleic acids in proliferating at least one of the target nucleic acids in a biological sample obtained from the subject prior to or during treatment. The method of the invention has cytostatic activity, and may have a use in gene therapy. The set of oligonucleotides comprising at least two of the oligomers are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNRs) within the sequences. The methods, nucleic acid, oligonucleotide, and kit are useful for the treatment, characterisation, classification and/or differentiation, of breast cell proliferative disorders. The method is also useful for predicting the responsiveness of a subject with a cell proliferative disorder of the breast tissues to a therapy. The present sequence is used
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                                                                                                                                                                                                  proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                Predicting responsiveness of a subject with breast cell proliferatidisorder, useful for treating or differentiating breast cell proliferative disorders comprises analyzing methylation pattern of
                                                                                                                                         Model F;
Marx A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antimicrobial peptide; cystic fibrosis; RT-PCR; emphysema; PCR; beta defensin-1; mbD-1; primer; amplification; ss.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.2%; Score 13.4; DB 1; Length 18; 33.3%; Pred. No. 2.4e+02; ve 0; Mismatches 1; Indels
                                                                                                                                         Martens J,
Look MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse beta defensin-1 gene specific forward primer 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 BP; 5 A; 0 C; 6 G; 7 T; 0 U; 0 Other;
                                                                                                                                          Maier S, M
Schmitt M,
                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 1300; 104pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                            in the exemplification of the invention.
                                                                                                                                          ΗÁ
                                                                                                                                            Koenig
Schmitt
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                                                                       01-OCT-2002; 2002DE-01045779.
07-JAN-2003; 2003DE-01000096.
17-APR-2003; 2003DE-01017955.
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                                                 01-OCT-2003; 2003WO-EP010881.
                                                                                                                                                                                                                                    genomic DNA from the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAGGAGATGAGATTT 17
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                            Harbeck N,
                                                                                                                      (EPIG-) EPIGENOMICS AG
                                                                                                                                                       Rujan T,
                                                                                                                                                                              WPI; 2004-348468/32
    WO2004035803-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-AUG-1997;
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                                                                                                                                            Foekens J,
Nimmrich I,
                              29-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV23538;
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The mouse beta defensin-1 (mbD-1) gene specific forward primer 2 was used with reverse primer 1 (AAV23539) or 2 (AAV23540) in a PCR reaction where mbD-1 cDNA (AAV23528) served as a template. The PCR product was used as a probe to isolate the mbD-1 genomic sequence from a mouse genomic library. The mbD-1 cDNA encodes for the mouse beta defensin-1 (AAW53857) peptide. The mbD-1 peptide was found to be highly salt sensitive and have antimicrobial properties. Expression of mbD-1 and its biological activity renders the mouse as at useful model to investigate the role of antimicrobial peptides in pulmonary microbial infections and in respiratory diseases
                                                                                                                                                           products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PG1 gene; biallelic marker; PCR primer; PG1-related biallelic marker; cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of a prostate cancer associated gene and biallelic markers derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                        New isolated mammalian beta defensin-1 gene(s) - used to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                          for treating microbial infections, e.g. respiratory conditions susceptible to microbial infection such as cystic fibrosis.
Anderson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.2%; Score 13.4; DB 1; Length 19; 93.3%; Pred. No. 2.4e+02; ative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19 BP; 2 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
   Stolzenberg ED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primer for PG1 biallelic marker 99-1481-285.
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                                                                                                                                                                                                                                                                                               Disclosure; Page 43; 79pp; English
      Goldman M, Bals R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
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Sequence 19 BP; 5 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

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The invention relates to a mammalian PG1 gene and protein, and a set of PG1 biallelic markers. The PG1 polymucleotide and biallelic markers are used in a hybridisation assay, a sequencing assay, or in an allelespecific amplification assay for determining the identity of a nucleotide at a PG1-related biallelic marker. The methods can be used to detect and to assess the risk of developing cancer or prostate cancer. Early-stage diagnosis of prostate cancer relies on prostate specific antigen (PSA) inability to discriminate between malignant and non-malignant affections of the organ. A need exists for both a reliable diagnostic procedure which would enable early-stage diagnosis, and for preventative and curative treatments of the disease. The PG1 gene can be used for detection of prostate cancer, and the risk of developing it in the future, and can also be used to determine therapies for the disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDKI, PCNA and Cyclin B1.
                                                                                                                                                                                                                                                                                                                          1.2%; Score 13.4; DB 1; Length 19; 93.3%; Pred, No. 2.4e+02; ttive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                             Sequence 19 BP; 2 A; 5 C; 5 G; 7 T; 0 U; 0 Other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 102; 109pp; English.
                              Claim 4; Page 351; 385pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA86085 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                        351 TCAAATGGGGAGCCT 365
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                                                                                                                                                                                                                                                                                                                                         Local Similarity 93.3
es 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tritz R, Welch PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-412314/35.
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                                                                                                                                                                                                                                                                                                                          Query Match
from it.
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                                                                                                                                                                                                                                                                                                                                                           Matches
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designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.

Representative examples of ribozyme recognition sites are given in AAA83415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment

The present invention relates to a hairpin or hammerhead ribozyme,

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W.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3157, 3277, 3297, and 3677, are not actually given a sequence in the Sequence Listing from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel biallelic markers used to construct a high density disequilibrium map of the human genome.
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                           Human biallelic marker upstream amplification primer SEQ ID NO:4387.
                                                                                                                                                                                                                                                                                                                                           Human genome, biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
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Length 19;
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                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 BP; 2 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Best Local Similarity 93.3%; Pred. No. 2.4e+02; Matches 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chumakov I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 1166; 2745pp; English
                                                                                                                                                                                                 AAZ70031 standard; DNA; 19 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-IB000822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0082614P
                                                                       238 CTATGACTCAGATGC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0109732P
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                                                                                                         2 crarcacrcadarde 16
                                                                                                                                                                                                                                                                       10-SEP-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cohen D, Blumenfeld M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-013267/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9954500-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-OCT-1999.
                                                                                                                                                                                                                                   AAZ70031;
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                                                                                                                                                              RESULT 490
AAZ70031/c
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polymerase III; holoenzyme; enzyme; thermophilic; replicase;

Thermus thermophilus.

WO200173052-A2

04-OCT-2001

primer; 88.

PCR S

Thermus thermophilus dnaQ gene PCR primer P133-A1237

(first entry)

11-MAR-2002

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AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ7440 represent amplification or primers for the biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the identification of the argets on and side effects from the pharmaceutical agents acting on a disease as well as other treatment. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                                                                               Human biallelic marker downstream amplification primer SEQ ID NO:11326.
                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.2%; Score 13.4; DB 1; Length 19; 93.3%; Pred. No. 2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chumakov 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 2645; 2745pp; English.
                                                                                                                                                                     AAZ76970 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0082614P.
98US-0109732P.
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                                                                                                                                                                                                                                                                                                          (first entry)
15 TCAAAAGGGGAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blumenfeld M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               map of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-013267/01.
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
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                                                                                                                                                                                                                                         AAZ76970;
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                                                                                                    RESULT 491
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Isolated DNA polymerase III holoenzyme subunits and accessory proteins useful for synthesizing DNA, e.g. in the polymerase chain reaction.

WPI; 2001-611633/70.

Mchenry CS;

28-MAR-2000; 2000US-0192736P.

(MCHE/) MCHENRY C S.

28-MAR-2001; 2001WO-US009950.

Example 14; Page 171; 249pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to DNA polymerase III holoenzyme subunits and accessory proteins and their coding sequences from Thermus in the various subunits may be useful in PCR assays and for synthesising DNA, since the subunits provide a thermophilic replicate capable of rapid replication and highly processive properties at elevated processive properties on the prior art that is limited by relatively non-processive repair-like DNA polymerases. The present sequence is a PCR primer, which was used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.2%; Score 13.4; DB 1; Length 19; 93.3%; Pred. No. 2.4e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19 BP; 3 A; 10 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cdc25 hs ribozyme binding site SEQ ID NO:3671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH61247 standard; DNA; 19 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sickle cell retinopathy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Conservative
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Matches 14; Conserv
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Gaps

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Indels

Mismatches

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Conservative

394 CATTITCCTTACAAT 408

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CATTIGCCTTACAAT

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ABA95463 standard; DNA; 19 BP.

RESULT 492

ABA95463;

ABA95463/ ID ABA9 XX AC ABA9

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Claim 4; Page 16; 528pp; Japanese.
     (RIKA ) RIKAGAKU KENKYUSHO.
(GENO-) GENOTEX YG.
                                                                          Arraying genome clones
                                                 WPI; 2002-144136/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADF85077;
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 용
                                                                                                                                                                                                                                            The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme (1) which cleaves RNA encoding a cytokine involved in inflammation, matrix metaloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid segment encoding (1). (1) can have antipsoriatic, ophthalmological, cytostatic, antiseborrheic, antidiabetic, antisickling, captualmological, vulnerary, keratolytic and virucide activities, and cleaves RNA encoding cytokine involved in inflammation. (1) can be used in gene therapy. (1) and (II) are useful for treating proliferative skin diseases such as psoriasis, atopic dermaticis, actinic keratosis, acquamquus or basal cell carcinoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, virreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing scarring such as keloid, adhesion and hypertrophic or hypertrophic burn carries. AMHSTOST to AAHSTOSD represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                       Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.2%; Score 13.4; DB 1; Length 19; 93.3%; Pred. No. 2.4e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human chromosome 1p36-35 PCR primer SEQ ID NO:584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 19 BP; 5 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exemplification of the present invention
                                                                                                                                                                                                                          3xample 1; Page 339; 408pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL43540 standard; DNA; 19 BP
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                                                26-OCT-2000; 2000WO-US029500
                                                                       26-OCT-1999; 99US-0161532P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 CTATGACTCAGATGC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTATCACTCAGATGC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 93.3
les 14; Conservative
                                                                                                                       Robbins JM, Tritz R;
                                                                                                (IMMU-) IMMUSOL INC.
                                                                                                                                                 WPI; 2001-300427/31.
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WO200130362-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromoso
PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                        03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL43540;
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The present invention describes a method of arraying genome clones. The method comprises: (a) clones of the genomic libraries contained in activated comprises: (a) clones of the genomic libraries contained in activated in each of the multiwell plates; (b) a primer designed based on the chromosome marker complished to the mixture to carry out an amplification reaction; (c) a signal corresponding to the marker is detected from the resultant camplified product to specify the discrimination Nos. of the multiwell plates containing the clones having said marker sequence; (d) the order of the maximum in the specified discrimination Nos. of the multiwell completes; (e) the clones in the multiwell plates of the specified discrimination Nos. to array the multiwell confercing discrimination Nos. are mixed respectively in each wells of longitudinal and lateral directions; (f) the mixed clones are cultured and the camplified products; (h) the clones in the multiwell plates are specified from the amplified by using the above primer; (g) signals care detected from the amplified products; (h) the clones are the multiwell plates are specified from the amplified by using the above primer; (g) signals care detected from the amplified by using the above primer; (g) reconstituted as the positions on the chromosome and arrayed. The mixroarray is useful for gene analysis; ABHASSSST to ABHASSSST capresent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634 represent PCR primers for human chromosome 21q22.1, which are specifically claimed for use in the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    short interfering nucleic acid; siNA; breakpoint cluster region; v-abl Abelson murine leukaemia viral oncogene homologue 1; BCR-ABL; cytostatic; leukaemia; lymphoma; human; ss; siRNA; ERG2; v-ets erythroblastosis virus E26 oncogene like (avian).
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2002US-0408378P.
2002US-0409293P.
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2002US-0386782P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406 AATTCAAGGGTTTTT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADF85077 standard; RNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2004 (first entry)
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Matches 14; Conservative
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05-SEP-2002;
09-SEP-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-FEB-2002;
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                                                                                                                                                            The invention relates to a novel double-stranded short interfering nucleic acid (siNA) that downregulates expression of the breakpoint cluster region-v-abl Abelson murine leukaemia viral oncogene homologue 1 (BCR-ABL) gene. The siNNA of the invention demonstrates cytostatic activity and may be useful for modulating expression of the BCR-ABL gene, as well as for treating leukaemia or lymphoma and in diagnosis, drug screening, target identification and validation, genetic engineering, gene function studies and gene mapping. The current sequence is that of the human ERGZ (v-ets erythroblastosis virus EZE oncogene like (avian))-targeted siRNA of the invention.
                                                                                                 double-stranded interfering nucleic acid, useful e.g. for treatment diagnosis of leukemia and lymphoma, downregulates the breakpoint
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  short interfering nucleic acid; siNA; breakpoint cluster region; v-abl Abelson murine leukaemia viral oncogene homologue 1; BCR-ABL; cytostatic; leukaemia; lymphoma; human; ss; siRNA; ERG2; v-ets erythroblastosis virus E26 oncogene like (avian).
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                                                                                                                                                                                                                                                                                     Sequence 19 BP; 7 A; 4 C; 5 G; 0 T; 3 U; 0 Other;
                                                                                                                                             Example 7; SEQ ID NO 1371; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ERG2-targeted siRNA - SEQ ID 1547.
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                                                          Chowrira B;
                                                                                                           and diagnosis of leukemia and lymphoma
cluster region-Abelson (BCR-ABL) gene.
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05-SEP-2002; 2002US-0408378P.
09-SEP-2002; 2002US-0409293P.
14-JAN-2003; 2003US-049029P.
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2002US-0386782P.
2002US-0404039P.
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                                                                                                                                                                                                                                                                                                                                                        958 CTGGACCCAGGACAT 972
   14-JAN-2003; 2003US-0439922P.
15-JAN-2003; 2003US-0440129P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ADF85253 standard; RNA; 19
                                                           Beigelman L,
                                     (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Best Local Similarity 80.0°
Matches 12; Conservative
                                                                                WPI; 2003-679889/64.
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05-SEP-2002;
09-SEP-2002;
14-JAN-2003;
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06-JUN-2002;
15-AUG-2002;
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                                                           Mcswiggen J,
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                                                                                                                                                                                                                    The invention relates to a novel double-stranded short interfering nucleic acid (siNA) that downregulates expression of the breakpoint cluster region-v-abl Abelson murine leukaemia viral oncogene homologue 1 (BRC-ABL) gene. The siRNA of the invention demonstrates cytostatic activity and may be useful for modulating expression of the BCR-ABL gene, as well as for treating leukaemia or lymphoma and in diagnosis, drug screening, target identification and validation, genetic engineering, gene function studies and gene mapping. The current sequence is that of the human ERC2 (v-ets erythroblascosis virus E26 oncogene like (avian))-targeted siRNA of the invention.
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                                               double-stranded interfering nucleic acid, useful e.g. for treatment diagnosis of leukemia and lymphoma, downregulates the breakpoint
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                                                                                                                                                                              Example 7; SEQ ID NO 1547; 197pp; English.
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                                                                                  and diagnosis of leukemia and lymphome
cluster region-Abelson (BCR-ABL) gene.
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(COLD-) COLD SPRING HARBOR LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAY-2002; 2002US-0383249P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGACCCAGGACAT 972
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WPI; 2003-679889/64.
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nes 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 497
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having protein-tyrosine-phosphatase (PTP) activity. The products of the invention have cytostatic, immunomodulator, antimicrobial, antiinflammatory, antidabetic and anorectic activity. The methods and compositions of the present invention are useful for treating diseases or conditions associated with aberrant expression or activity of the protein tyrosine phosphatase, such as cancer, autofimmune diseases, infection, inflammation, diabetes and obesity. This sequence represents a siRNA directed against dual specificity phosphatase (DSP) expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel small interfering RNA (siRNA) polynucleotides capable of interfering with expression of a polypeptide by a waying protein-tyrosine-phosphatese (PTP) activity. The products of the invention have cytostatic, immunomodulator, antimityr. The methods and thinflammatory, antidiabetic and anorectic activity. The methods and compositions of the present invention are useful for treating diseases or compositions associated with aberrant expression or activity of the protein tyrosine phosphatase, such aberrant expression activity of the protein tyrosine phosphatase, such as cancer, autoimmune diseases, infection, inflammation, diabetes and obesity. This sequence represents a siRNA directed against dual specificity phosphatase (DSP) expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated small interfering RNA (siRNA) polynucleotide useful for treating diseases with aberrant activity of the protein tyrosine phosphatase, such as cancer, autoimmune disease, infection, inflammation, diabetes and obssity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 small interfering RNA; siRNA; protein-tyrosine-phosphatase; PTP;
cytostatic; immunomodulator; antimicrobial; antiinflammatory;
antidiabetic; anorectic; cantucimmune disease; infection;
inflammation; diabetes; obesity; RNA interference; gene silencing; ss.
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                                                                                                                                                                                                                           Score 13.4; DB 1; Length 19;
Pred. No. 2.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                     Sequence 19 BP; 7 A; 5 C; 3 G; 0 T; 4 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CEPT-) CEPTYR INC.
(COLD-) COLD SPRING HARBOR LAB
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14-APR-2003; 2003US-0462942P.
                                                                                                                                                                                                                                                                                                             345 CTGTGATCAAATGGG 359
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                                                                                                                                                                                                                                                                   14; Conservative
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Best Local (
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The present invention relates to an analytical chip for simultaneous determination of one or more different bacterial 16S-rRNA in liquid determination of one or more bacterial 16S-rRNA, cample. The chip is useful for detecting one or more bacterial 16S-rRNA, derived from bacteria such as Achromobacter xylosoxidans, Acinetobacter chip such as Achromobacter xylosoxidans, Acinetobacter chip such adiobacter, Bacillus sp., Bacteroridas covatus, Campylobacter fetus, Citrobacter freundii, Enterococcus avium covatus, Campylobacter fetus, Citrobacter freundii, Enterococcus avium covatus, Campylobacter fetus, Citrobacter freundii, Enterococcus avium covatus, Catecophilus acidophilus, Legionella morbillorum, Gardnerella oxytoca catearrhalis, Wacobacterium avium, Neisseria cinerea, Nocardia sp., Cohrobactrum anthropi, Pasteurella multocida, Peptostreptococcus magnus corrobactrum anthropi, Sasteurella multocida, Peptostreptococcus magnus controbactrum anthropi, Sasteurella multocida, Peptostreptococcus magnus controbactrum anthropi, Pasteurella multocida, Peptostreptococcus magnus corrobactrum anthropi, Pasteurella multocida, Peptostreptococcus magnus controbactrum anthropi, Pasteurella multocida, Peptostreptococcus magnus controbactrum anthropi, Pasteurella multocida, Peptostreptococcus magnus controbactrum anthropi, Pasteurella sonnei, Veillonella parvula, Veillonella con sp. or Versinia enterocolitica. The chip is useful for detecting clinically relevant bacterial 16S-rRNA in a liquid sample, simultaneously and embles rapid, accurate, easy and reliable identification of bacteria by cannol a provided sample and also enables chemiliated cost, cannol which is produced at reduced cost, enables determination of 185-rRNA variation of a bacterium even in a complex biological sample. The chip variation of a bacterium even in a complex biological sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     analytical chip; bacterial 16S-rRNA; genotypic characterization; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in a sample with reduced experimental error and variation. The present
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Analytical chip useful for simultaneous determination of one or more different bacterial 16S-rRNA in liquid sample, comprising evanescent field measurement platform as solid carrier and several specific
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                                                 ö
    Length 19;
                                                 Indels
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  1.2%; Score 13.4; DB 1;
66.7%; Pred. No. 2.4e+02;
tive 4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                          Analytical probe chip of the invention #239.
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Ehrat M;
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                                                                                              CTGTGATCAAATGGG 359
                                                                                                                                      cueucaucauauece 16
                                                                                                                                                                                                                                                        ADO18480 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Francois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abel A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recognition elements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-375537/35.
Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004033720-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schrenzel J,
Kresbach GM,
                                                                                                                                                                                                                                                                                                                                                  15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                              345
                                                                                                                                                                                                                                                                                                     ADO18480;
                                                                                                                                                                                                           RESULT 499
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DB 1; Length 19;

1.2%; Score 13.4;

Query Match

Gaps

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Indels

7;

Mismatches

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14; Conservative

Matches

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The present invention relates to an analytical chip for simultaneous determination of one or more different bacterial 16S-rRNA in liquid determination of one or more different bacterial 16S-rRNA, early of the backerial such as Achromobacter xylosoxidans, Acromobacter baumannii, Actinomyces israelii, Aerococcus viridans, Aeromonas by Bacterial such as Achromobacter yalosoxidans, Bacherococcus viridans, Bacteridas of Covatus, Campylobacter fecus, Cirobacter Manna lentum, Gemella morbillorum, Gardnerella vaginalis, Cirobacterium nucleatum, Gemella morbillorum, Gardnerella vaginalis, Cirobacterium anticuenta, Hafnia alvei, Kingella sy. Klebsiella oxytoca catarrhalis, Mycobacterium avium, Neisseria cinerea, Nocardia sp., Corbrobactrum anticropi, Pasteurella multocida, Peptostreptococcus magnus ochrobactrum anticropi, Pasteurella sonnel, Veillonella parvula, Veillonella sp. or Yersinia enterocolitica. The chip enables determination of one or cinically relevant bacteria. The chip enables determination of bacteria by genotypic characterization in a provided sample and also enables chemitication of a bacterium even in a complex biological sample. The chip which is produced at reduced cost, enables determination of 165-rRNA in a sample with reduced experimental error and variation. The present in a sample with reduced experimental error and variation. The present corporation in a provide as an analytical chip.
                   ö
                                                                                                                                                                                                                                                                                                                                         analytical chip; bacterial 168-rRNA; genotypic characterization; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        different bacterial 16S-rRNA in liquid sample, comprising evanescent field measurement platform as solid carrier and several specific recognition elements.
                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Utinger D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Analytical chip useful for simultaneous determination of one or
                     ö
                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P, Charbonnier Y, Jacquet JG,
Ehrat M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 BP; 4 A; 4 C; 1 G; 10 T; 0 U; 0 Other;
   93.3%; Pred. No. 2.4e+02; ive 0; Mismatches 1.
                                                                                                                                                                                                                                                                                                       Analytical probe chip of the invention #332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 45; SEQ ID NO 332; 82pp; English
                                                                                                                                                                                               ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-SEP-2003; 2003WO-EP010626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-OCT-2002; 2002EP-00022631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYGE-) UNIV GENEVE HOPITAUX
                                                             480
                                                                                                 17
                                                                                                                                                                                             ADO18573 standard; DNA; 19
                                                                                                                                                                                                                                                                       (first entry)
                                                                                 GCACTTTATTCTTAT
                         14; Conservative
                                                             466 GCACTTTATTCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Francois l
Abel A, l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-375537/35.
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004033720-A2
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Kresbach GM,
                                                                                                                                                                                                                                                                       15-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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Score 13.4; DB 1; Length 19; Pred. No. 2.4e+02;

1.2%;

Query Match Best Local Similarity

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Interference RNA agent useful for treating dyslipidemias, coronary artery disease, diabetes, cancer or neurological disease, comprises sense sequence and antisense sequence which has specific modifications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sense sequence and an antisense sequence, where the sense sequences have one or more asymmetrical 2-0 alkyl modifications, the antisense sequences have sequences have one or more asymmetrical phosphorothioatte modifications and the antisense sequence targets a human gene sequence. Also described are: a pharmaceutical preparation comprising (1); reducing (M1) apoB-100 levels or glucose-6-phosphatase levels in a subject, producing (1); retablising (1), involves selecting a sequence with activity and introducing one or more asymmetrical modification in the sequence, where the modification decreases nuclease sensitivity while not decreasing its
                                                                                                                                                                                                                                                cytostatic; anticonvulsant; nostropic; muscula; anti-HIV;
RNA interference; iRNA; antisense technology; lipid metabolism;
coholesterol imbalance; dyslipidaemia hypercholesterolaemia;
coronary artery disease; CAD; coronary heart disease; CHD;
atherosclerosis; hepatic glucose production;
glucose-metabolism-related disorder; dlabetes; cancer; breast cancer; colon cancer; lung cancer; neurological disease; Huntington disease;
spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a RNA interference (iRNA) agent (I) comprising
                                                                                                                                                                                                                                   cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
                                                                                                                                                                                                    Human apolipoprotein B (ApoB) oligonucleotide seqid 3929.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 5; SEQ ID NO 3929; 378pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2003US-0454265P.
2003US-0454962P.
2003US-0455050P.
2003US-0462894P.
2003US-046565P.
2003US-046565P.
2003US-046565P.
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2003US-0510318P.
2003US-0518453P.
                                                                                                            BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAR-2004; 2004WO-US007070
466 GCACTTTATTCTGAT 480
                            17
                                                                                                              ADR79444 standard; DNA; 19
                                                                                                                                                                            (first entry)
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                              3 GCACTTTATTCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ALNY-) ALNYLAM PHARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-677362/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004080406-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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25-APR-2003;
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07-NOV-2003;
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                                                                                                                                                                                                                                             antilipemic;
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13-MAR-2003;
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                                                                                                                                                ADR79444;
                                                                                 RESULT
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activity; a kit comprising (I) and instruction for its use; and a device that can be dispense or administer a composition comprising (I). (I) is useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (MI) is useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (MI) is useful for reducing apoB-100 levels or glucose-6-phosphatase levels. The subject is suffering from a disorder characterised by elevated or cherwise unwanted expression of apol-100, elevated or otherwise unwanted levels of cholesterol, and/or disregulation of lipid metabolism. The disorder is chosen from the HDL/LDL cholesterol imbalance, disorder is chosen from the HDL/LDL cholesterol imbalance, bypercholesterolaemia, coronary artery disease (CAD), coronary heart disease (CHD) and atherosclerosis. (I) is administered to a subject to inhibit hepatic glucose production or for treating glucose-metabolism-related disorder e.g. diabetes or type-2 diabetes. (I) is useful for treating the diseases as mentioned above, cancer (e.g. breast, colon or lung cancer), neurological disease (e.g., Huntington disease or spinocerebellar ataxia) or viral disease (e.g., AlDS). This sequence represents a human apolipoprotein B (ApoB) antisense oligonucleotide that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic; cytostatic; anticonvulsant; nootropic; muscula; anti-HIV; RNA interference; iRNA; antisense technology; lipid metabolism; cholesterol imbalance; dyslipidaemia hypercholesterolaemia; coronary artery disease; CAD; coronary heart disease; CHD; atherosclerosis; hepatic glucose production; glucose-metabolism-related disorder; diabetes; cancer; breast cancer; olon cancer; lung cancer; aleurological disease; Huntington disease; spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                              1.2%; Score 13.4; DB 1; Length 19; 93.3%; Pred. No. 2.4e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human apolipoprotein B (ApoB) oligonucleotide segid 2294.
                                                                                                                                                                                                                                                                                                                                                                            Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR77809 standard; DNA; 19 BP
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2003US-0465802P.
2003US-0469612P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2003US-0454265P
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2003US-0510318P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-OCT-2003; 2003US-0510318P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             830 TGACCCAGGAAGGCC 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 reacreaseaasece 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004080406-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-APR-2003;
09-MAY-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 502
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sequence and an antisense sequence, where the sense sequences have one or more asymmetrical 2'-0 alkyl modifications, the antisense sequence and an antisense sequence, where the sense sequences have one or more asymmetrical phosphorothicate modifications and the antisense sequence targets a human gene sequence. Also described are: a pharmaceutical preparation comprising (1); reducing (M1) apoB-100 levels or glucose-6-phosphatase levels in a subject; producing (I); stronging one or more asymmetrical modification in the sequence, where introducing one or more asymmetrical modification in the sequence, where the modification decreases nuclease sensitivity while not decreasing its activity; a kit comprising (I) and instruction for its use; and a device that can be dispense or administer a composition comprising (I). (I) is useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1) consider the subject is suffering from a disorder characterised by elevated or otherwise unwanted expression of apoB-100, elevated or otherwise unwanted expression of apoB-100, elevated or otherwise unwanted concert is chosen from the HDL/LDL cholesterol imbalance, dyslipidaemias, hypercholestorolaemia, staffair-resistent conditions and attended concert is chosen from the HDL/LDL cholesterol imbalance, dyslipidaemias, hypercholestorolaemia, staffair-resistent conditions and anticoned above, cancer (e.g. breast, colon or inhibit hepatic glucose production or for treating glucose-metabolism.

The subject is disbetes or type-2 diabetes. (I) is useful for related disorder e.g. diabetes or type-2 diabetes. (I) is useful for related disorder e.g. diabetes or type-2 diabetes. (I) is useful for relating the diseases as mentioned above, cancer (e.g. breast, colon or lung cancer), neurological disease (e.g., AIDS). This sequence of processents a human apolipoprotein B (ApoB) antisace oligonucleotide that ö Interference RNA agent useful for treating dyslipidemias, coronary artery disease, diabetes, cancer or neurological disease, comprises sense sequence and antisense sequence which has specific modifications. The invention describes a RNA interference (iRNA) agent (I) comprising a Gaps Human herpes virus-6; HHV-6; multiple sclerosis; genetic marker; 38E; internal primer 38E6; diagnosis; ss. ö Query Match 1.2%; Score 13.4; DB 1; Length 19; Best Local Similarity 93.3%; Pred. No. 2.4e+02; Matches 14; Conservative 0; Mismatches 1; Indele HHV-6 associated MS genetic marker 38E internal primer 38E6 Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other; can be used to control ApoB gene expression. Example 5; SEQ ID NO 2294; 378pp; English AAQ91053 standard; DNA; 18 BP 94WO-US012655. 830 TGACCCAGGAAGGCC 844 2 reacreaceaacece 16 30-JAN-1996 (first entry) Manoharan M, Bumcrot D; (ALNY-) ALNYLAM PHARM. WPI; 2004-677362/66. 04-NOV-1994; WO9512313-A1 11-MAY-1995 Synthetic. AAQ91053; RESULT 503 AAQ91053, 셤 ઠ

Page 242

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18
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AAV48417/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Triplex forming oligomer binds to collagen gene promoter region - used to impede pathological fibrosis etc.
                                                                                                   Treatment of human herpes-virus-6-associated multiple sclerosis - using an antiviral agent, e.g. a nucleoside analogue, administered to the cerebrospinal fluid.
                                                                                                                                                                                                                                                                                                                                                                      Triplex; inhibition; collagen gene; promoter; pathological fibrosis; myocardial fibrosis; hypertensive heart disease; atherosclerosis; restenosis; liver cirrhosis; lung fibrosis; skin fibrosis; scleroderma; hypertrophic scar; burn injury; rat; polypurine; polypyrimidine; ss.
                                                                                                                                                         AAQ91052 and AAQ91053 are an internal primer pair for the human herpes virus-6 (HHV-6) associated multiple sclerosis (MS) genetic marker, 38E (AAQ91054). The primers can be used in the diagnosis of MS
                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                      Collagen gene promoter region binding oligomer Oligo 158 APS.
                                                                                                                                                                                                            Score 13.2; DB 1; Length 18;
Pred. No. 2.6e+02;
                                                                 Parker JD
                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/note= "Phosphorothioate linkages"
                                                                                                                                                                                            Sequence 18 BP; 7 A; 6 C; 3 G; 2 T; 0 U; 0 Other
                                                                  Brown JP,
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                                                                                                                                                                                                                             0; Mismatches
                                                                  Smith KT,
                                                                                                                                            Disclosure; Page 35; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kovacs A,
                                                                                                                                                                                                                                              130
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                                                                                                                                                                                                                                                                                                        BP.
       93US-00149176.
94US-00218029.
94US-00287942.
94US-00334482.
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96US-00712357.
                                                                                                                                                                                                             Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                              113 GCTATTGGACTGACTTTT
                                                                                                                                                                                                                                                             18 GCTGTTGGACTGGCATTT
                                                                                                                                                                                                                                                                                                        AAT60161 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                  Challoner PB,
                                                  (PATH-) PATHOGENESIS CORP.
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GUNT/) GUNTAKA R V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-202172/18.
                                                                                           WPI; 1995-215032/28.
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11-SEP-1996;
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         05-NOV-1993;
24-MAR-1994;
                        05-AUG-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-1997
                                                                   Burmer GC,
Nowinski RC;
                                                                                                                                                                                                                                                                                                                                        01-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                         AAT60161;
                                                                                                                                                                                                                                                                                         RESULT 504
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An oligomer has been produced which is capable of inhibiting expression of a collagen gene. The present sequence represents a specifically claimed oligomer Oligo 158 APS, which binds to the polypurine.

CC claimed oligomer region of the rat alphal(I) collagen gene promoter region. The oligomer may be used to impede pathological fibrosis which is associated with mycertanisty heart diseases, atherosclerosis, restenosis, liver cirrhosis, lung fibrosis, and skin fibrosis found in scleroderma, in hypertrophic scars and in skin fibrosis found in scleroderma, in hypertrophic scars and in skin collowing burn nigury. The oligomer inhibits sayression of a collagen collowing cligomer (TPO) which is targeted to a 30-mer polypurine corresponding to the noncoding strand of the promoter collowing oligomer (TPO) which is targeted to a 30-mer polypurine corresponding to the noncoding strand of the promoter colligonal physiological ph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta-1; TGF beta-1; antisense oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preparation of antisense oligo:nucleotide(s) which lack long runs of consecutive guanosine or inosine - and have specific ratio of residues able to form two or three hydrogen bonds, have greater activity and reduced toxicity, used therapeutically or to modulate growth of cells in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV48412-84 represent antisense oligonucleotides directed against transforming growth factor beta-1 (TGF beta-1). The oligonucleotides exemplify the invention. The specification describes oligonucleotides that contain 8-30 nucleotides, which contain at most 8 nucleotides that can each form three hydrogen bonds to cytosine; do not contain four
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transforming growth factor beta-1 antisense oligonucleotide N5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.2%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 2.6e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 BP; 6 A; 0 C; 12 G; 0 T; 0 U; 0 Other;
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Claim 18; Page 36; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 CICCCCCATCCCCCATIT 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV48417 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.2
Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-400910/35.
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consecutive cytosines; do not contain two sequences of three consecutive nucleotides each able to form three H-bonds to three consecutive cytosines, and the ratio between residues able to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The oligonucleotides are used to modulate expression of genes, particularly the genes for p53, ExbB-2, junb, TGF-beta 1 or beta 2 to control proliferation of primary cell cultures (e.g. bone marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The oligonucleotides can also be used to analyye function of proteins (by altering their expression or activity) and therapeutically, e.g. in cases of cancer or (targeting TGP) for stimulating the immune system The present invention describes Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and WISP-3 have homology to connective tissue growth factor (CTGR). Products from the present invention can be used to treat WISP-related disorders such as breast, ovarian, and colon cancer or melanoma. The products can be used to treat arteriosclerosis. The products can also be used to treat other diseases e.g. benign and malignant tumours, leukaemia and lymphoid WNT-1 induced secreted protein; WISP-1; WISP-3; CTGF; tumour; connective tissue growth factor; cancer; melanoma; arteriosclerosis; leukaemia; lymphoid malignancy; haematopoiesis-related disorder; tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion; kidney disorder; bone-related disorder; osteoporosis; trauma; burn; connective tissue disorder; catabolic state; inflammation; testicular-related disorder; anglogenesis; immunological disorder; ss. Gaps consecutive nucleotides able to form three H-bonds each to four ö Gurney AL, Hillan K, Lawrence DA; toy MA, Goddard A, Wood WI; New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 1.2%; Score 13.2; DB 1; Length 18; ilarity 83.3%; Pred. No. 2.6e+02; Conservative 0; Mismatches 3; Indels Seguence 18 BP; 2 A; 3 C; 12 G; 1 T; 0 U; 0 Other; Human WISP-2 PCR primer SEQ ID NO:131. Example 11; Page 272; 284pp; English. Roy MA, 196 CGCCATCTCCCCCATCCC 213 97US-0063704P. 98US-0073612P. 98US-0081695P. 18 ceccecricecearece 1 AAX76549 standard; DNA; 18 BP 98WO-US022991. (first entry) Botstein DA, Cohen RL, Levine AJ, Pennica D, (GETH ) GENENTECH INC. WPI; 1999-337420/28. Local Similarity nes 15; Conserv Homo sapiens. 29-OCT-1998, W09921998-A1 29-OCT-1997; 03-FEB-1998; 06-AUG-1999 14-APR-1998 06-MAY-1999 Synthetic AAX76549; Query Match RESULT 506 Matches 8888888888888888888 ઠ 용

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       plandular, macrophagal, epithelial, stronal, and blastocoelic disorders, haematopoiesis-related disorders, tissue-growth disorders, skin disorders, desmoplasia, fibrotic lesions, kidney disorders, skin disorders such as osteoporosis, transma such as burns, incisions, and other wounds, connective tissue disorders, catabolic states, testicular related disorders, and inflammatory, angiogenic and immunologic disorders including arteriosclerosis. The products can also be used for detection and diagnosis especially of individuals with neoplastic cell growth or proliferation. The products can be used in the production of transgenic or knock-out animals. Antibodies can be used to induce death in WISP-1, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides antisense compounds of 8-30 nucleotides that inhibit the expression of human Cellular Inhibitor of Apoptosis-1 (c-IAP-1). The antisense compounds may be used for diagnostics, therapeutics (for modulating the expression of c-IAP-1), prophylaxis (e.g. to prevent or delay infection, inflammation, or tumor formation), as research reagents (e.g. to distinguish between members of a biological pathway) and in kits. Sequences AAZ22150-189 represent phosphorothioate oligonucleotides used for antisense inhibition of cellular inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cellular Inhibitor of Apoptosis-1, antisense; diagnostic; therapeutic; c-IAP-1; prophylaxis; infection; inflammation; tumor formation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense compounds complementary to Cellular Inhibitor of Apoptosis-1 useful for e.g. diagnostics, therapeutics, and as research reagents.
                                                                                                                                                                                                                                                                                                                      Gaps
malignancies, neuronal, glial, astrocytal, hypothalamic and other
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                                                                                                                                                                                                                                                                               1.2%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 2.6e+02;
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Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human c-IAP-1 mRNA inhibiting antisense oligo ISIS #23361.
                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                            Sequence 18 BP; 6 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                            1 AGTCCAAGAGTCTCAGCA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
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                                                                                                                                                                                                                                                                                                                                                         897 AGACCAAGAGCCTCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ22179 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                         overexpressing cells
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nes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-NOV-1999
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209

192 TCCACGCCATCTCCCCCA

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The invention relates to a modified tRNA primer for reverse transcription of a Murine Leukaemia virus (MLV) retroviral transfer vector. The vector comprises (i) a retrovirus in which at least part of the genomic RNA sequences carrying information for the production of viral proteins have been replaced by one or more sequences carrying information to be the replaced by one or more sequences carrying information to be the replaced in a target cell chromosome, (ii) a primer binding site (PBS) which has been modified to a sequence that does not allow strong base consisting with the 3' end of any naturally occurring tRNA, and the three 5' nucleotides of the PBS are UGG, where the modified tRNA primer has been modified to allow strong base pairing with the PBS of the transfer vector. The retroviral vectors can used as antiviral agents. Such vectors can be directed against pathogenic viruses, e.g. HIV-1, or HIV-1, related to the type used for construction of the vector, thus having the same to the type used for construction of the vector, thus having the same construction of none place virus, or of virus spread. Only specialised packaging cells provided with appropriate artificial primers allow vector propagation. Sequences AAX2147-167 cepticalised with appropriate artificial primers allow vector propagation. Sequences AAX2147-167 cepticalised with appropriate artificial primers allow vector propagations of complex entry modified and cellation of complex entry modified and cellation of complex entry modified and cellation primers allow vector propagation. Sequences AAX2147-167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine leukaemia virus retroviral vector - whose transfer is dependent on the presence of specific \tauRNA-like primer.
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                                                                                                                                                                                                                                                                                                                                                                                    Murine Leukaemia virus; MLV; retroviral transfer vector; retrovirus; modified tRNA primer; antiviral agent; pathogenic; virus; HIV-1; HTLV-1; cellular tropism; murine; ss.
Gaps
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  Indels
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  3;
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  0; Mismatches
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                                           974 TTGATGAGATCCAAAGGA 991
                                                                                                                                                                                                 AAX22147 standard; tRNA; 18 BP.
                                                                                      18 Trgarcacarrcaaggra 1
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                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                    Murine tRNA gene fragment
    15; Conservative
                                                                                                                                                                                                                                                                                       (revised)
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PEDERSEN F S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOVMAND J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pedersen FS,
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(PEDE/) 1
(JORG/) 2
(LOVM/) 1
(DUCH/) 1
                                                                                                                                                          RESULT 508
      Matches
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transfer vector in which the genomic RNA sequences encoding viral proteins required in trans for MLV replication have been at least partly replaced by at least 1 sequence carrying information to be introduced into a target cell chromosome, where the primer binding site (PBS) has been modified to a sequence that does not allow strong base-pairing with the 3' end of any naturally occurring tRNA. The transfer vector can be used for gene therapy, e.g. for carrying antisense or ribozyme constructs targeted to the PBS of a pathogenic virus such as HIV or HTLV-I. The modified PBs reduces the risk of uncontrolled regeneration of whole virus by interaction of the vector with various engineered or endogenous cistor trans-acting components
                                                                                                                                                                                                           LRNA, transfer vector, viral protein; replication; primer binding site;
PBS; gene therapy; antisense; ribozyme; pathogenic; primer; tRNA-ala; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine leukaemia virus transfer vector - with modified primer binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Col 10; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  site requiring artificial primer.
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                         18
                                                                                                 ВЪ.
                                                                                                                                                                                      Mouse tRNA-Ala(g) primer tRNA
                                                                                                                                                                                                                                                                                                                                                95US-00525849.
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             1 UCCCCGGCAUCUCCACCA
                                                                                               AAX01825 standard; tRNA; 18
                                                                                                                                                         13-APR-1999 (first entry)
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Matches 12, Conservative
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                                                                                                                                                                                                                                                           Murine leukemia virus.
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PEDERSEN F S.
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                                                                                                                               AAX01825;
                                                                                                                                                                                                                                                                                                                                                                                                                         (LUND/)
(PEDE/)
(LOVM/)
(DUCH/)
                                                                                                                                                                                                                                                                                                                                                                                                          (JORG/)
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                                                                       RESULT 509
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Gaps

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Query Match
1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 12; Conservative 3; Mismatches 3; Indels

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18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a new tRNA primer for reverse transcribing a retroviral transfer vector comprising a primer binding site (PBS) that has been modified to a sequence that does not allow strong base pairing with the 3' end of any naturally occurring tRNA and comprises three 5' pairing with the modified PBS of a transfer vector; reverse transcribes the retroviral transfer vector which comprises a retrovirus in which at least part of the genomic RNA sequences necessary for production of viral proteins required in for retroviral replication have been replaced by sequences to be introduced in a target call chromosome; and has a PBS that has been modified to a sequence that does not allow strong base that has been modified to a sequence that does not allow strong base pairing with the 3' end of any naturally occurring tRNA and the three 5' nucleotides are UGG. The primer is used for reverse transcribing the retroviral vector comprising a retrovirus with infectivity for birds and channels in which a part of the genomic RNA sequences necessary for production of viral proteins required in trans for retroviral replication of viral proteins required in trans for retroviral replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                       New modified tRNA primer for reverse transcribing a retroviral transfer vector comprising a primer binding site modified to a sequence which does not allow strong base pairing with the 3' end in any occurring tRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to be introduced in a target cell represents a murine tRNA sequence used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                               tRNA primer; retroviral transfer vector; primer binding site; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genomic SNP allele specific oligonucleotide SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.2; DB 1; Length 18;
Pred. No. 2.6e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                            <u>ب</u>
                                                                                                                                                                                                                                                                            Jorgensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 BP; 3 A; 10 C; 2 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in the design of the primer of the invention
                                                                                                                                                                                                                                                                            Pedersen FS,
                      Murine Ala tRNA 3' nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Col 10; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 TCCACGCCATCTCCCCCA 209
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                                                                                                                                                                                                                                                                            Lund AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.2%;
                                                                                                                                          98US-00169248.
                                                                                                                                                                  95US-00525849.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 12, Conservative
                                                                                                                                                                                                     LOVMAND J.
PEDERSEN F S.
                                                                                                                                                                                                                            LUND A H.
JORGENSEN P.
                                                                                                                                                                                                                                                                                                  WPI; 2000-586220/55.
                                                                                                                                                                                                                                                                            Lovmand J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome. The
                                                                                                                                                                                                                                                     DUCH M.
                                                                                                                                           09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-2000
                                                                                                                                                                  08-SEP-1995;
                                                                                                                                                                              15-NOV-1996;
                                                                                            US6107478-A.
 20-FEB-2001
                                                                                                                     22-AUG-2000.
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                                                                                                                                                                                                    (LOVM/)
(PEDE/)
(LUND/)
(JORG/)
(DUCH/)
                                                                                                                                                                                                                                                                           Duch M,
                                                                      Mus sp.
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EXXXXEXE
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A method has been developed for detecting the presence or absence of a single nuclectide polymorphism (SNP) allele in a genomic Sample. The method comprises preparing a reduced complexity genome (RCG) from the genomic sample and analysing the RCG for the presence or absence of a SNP allele. The method can be used to characterise a tumour, to generate a genomic pattern for an individual genome or. to generate a genomic classification code for a genome. The method can be used to assess whether a subject is at risk for developing a disease or to identify a set of SNP alleles associated with a disease. The method can also be used to perform linkage analysis. AAA35941 represent sequences used in the exemplification of the present invention. AAA35948 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detection of single nucleotide polymorphisms in genomes by preparation and analysis of reduced complexity genomes, useful for genotyping, fingerprinting and determining allele frequency of SNPs.
Human, single nucleotide polymorphism; SNP; genotyping; DNA analysis;
allels epecific ollgonucleotide; ASO; reduced complexity genome; RCG;
genomic classification; identification; DNA fingerprinting;
tumour characterisation; hybridisation; BS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.2%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 2.6e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA36632 represent nucleotide sequences containing SNPs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 9 A; 0 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Charest A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Housman DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 53; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      568 TITIAATACCTTTATATA 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rrrraraccrrcaraa 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0101757P
                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US022283
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Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Landers JE, Jordan B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-293181/25
                                                                                                                                                                                                                                                               WO200018960-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                   24-SEP-1999;
                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                         06-APR-2000
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Sequence 18 BP; 2 A; 6 C; 2 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA08213;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                This sequence represents an oligomer which is capable of inhibiting the expression of the collagen gene. The oligomer is capable of binding to proteins, and is the major element of skin, bone, tendon, cartilage, blood vessels and teeth. The oligomers are useful for inhibiting a cell and causing an intracellular reaction to inhibit the gene expression of the collagen gene, comprising inserting the oligomers into a cell and causing an intracellular reaction to inhibit the gene expression. The collagen inhibitory oligomers of the invention are useful for treating pathological fibrosis associated with myocardial fibrosis in hypertensive heart disease, atheroscalensis, restenosis, liver cirrhosis, lung fibrosis, peritoneal fibrosis and skin fibrosis found in scleroderma, hypertrophic scars and burn injury
                                                                                        Inhibitors of collagen gene useful for treating fibrosis associated with atherosclerosis, restenosis, liver cirrhosis, lung and skin fibrosis, comprises oligomers capable of inhibiting collagen gene.
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytomegalovirus GlyB gene; detection oligonucleotide; detection; target-associated detectable structure; signal amplification; ss
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0
                                                                                                                                                                                                                                                                                                           1.2%; Score 13.2; DB 1; Length 18; 33.3%; Pred, No. 2.6e+02; ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                          Sequence 18 BP; 6 A; 0 C; 12 G; 0 T; 0 U; 0 Other;
                                                    Kandala J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CMV GlyB detection oligonucleotide SA-Bl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/note= "Biotinylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                      Kovacs A,
                                                                                                                                                                                                                                                                                                                                                       219
                                                                                                                                    Claim 19; Fig 8; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                 CTCCCCCTCCTTT 1
                                                                                                                                                                                                                                                                                                                                                                                                                            AAA97374 standard; DNA; 18 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-2000; 2000WO-GB000921
            98US-00130888
                                                                                                                                                                                                                                                                                                                       ilarity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                       202 CTCCCCCATCCCCCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oultram JD;
                                                    Weber KT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-638207/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human herpesvirus 5.
                                 (GUNT/) GUNTAKA R V.
                                                                        WPI; 2000-205739/18.
                                                                                                                                                                                                                                                                                                                       Local Similarity
ses 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200055365-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fulrooney C,
            07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2001
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                                                      Guntaka RV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                           18
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                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 513
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The invention relates to a novel method of detecting a target nucleic acid molecule. The method involves contacting a sample with a locator probe comprising a binding moiety specific for the target molecule and an amplification nucleic acid sequence. An amplification structure which is bound to the target molecule-locator probe complex is produced via amplification template (comprising, in the 5 to 3' direction, an extension nucleic asmple and locator probe using a single stranded amplification template (comprising, in the 5 to 3' direction, an extension nucleic acid sequence, a hybridisation nucleic acid sequence of capable of removing sufficient of the extension nucleic acid sequence of the amplification template when hybridised to the complementary strand to the amplification template to the complementary strand to of the amplification template to the complementary strand; After optionally repeating amplification of this structure, any additional correlated with the presence of a target molecules. The method is used to correlated with the presence of a target molecules. The method is used to amplification of the target acid detected, and the result of detect target molecules in a sample by using an enzymatically catalysed amplification of the target account of the amplification template and detectable structures. As a small ample to the amplification of the target acid sequence of a target detectable structures. As a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amplification rather than target amplification, thus overcoming contamination problems. It is an enzymatically catalysed process that actively assembles the signal generating structure rather than relying on the passive hybridisation-based methods of non-enzymatic methods such as bDNA. Unlike prior art techniques such as polymerase chain reaction (PCR), the method has the ability to address RNA and DNA targets with equal efficiency without pretreatments. The present sequence represents detection oligonucleotide, SA-BL, used with amplification template SA-EXI (AAA97373) in an exemplification of the invention to detect the CMV GlyB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                number of inexpensive components are utilised, the new method is more economical than previous methods. The method utilises signal amplification rather than terrat components.
Detecting a target molecule by enzymatically catalyzed amplification of target associated detectable structures comprises contacting a sample with a locator probe, amplifying the structure bound and detecting bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           target oligonucleotide CMV-002 (AAA97372)
                                                                                                                                                                                                                                                                                                                                       Example 5; Page 72; 75pp; English
                                                                                                                                                                                                                        locator probes.
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Gaps ö Length 18; 3; Indels 1.2%; Score 13.2; DB 1; 83.3%; Pred. No. 2.6e+02; ive 0; Mismatches 3; Conservative Local Similarity nes 15; Conserv Query Match

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1056 TTATCTTTCCAGTGGCTA 1073 1 TTCTCCTTCCAGTTGCTA 18 BP AAA08213 standard; tRNA; 18

vviral vector; antiviral; retrovirus; infection; primer binding site; human immunodeficiency virus; human T-cell lymphotropic virus-1; Murine tRNA oligonucleotide sequence SEQ ID NO:3. 98US-00169078 (first entry) Mus musculus 09-OCT-1998; US6037172-A. 14-MAR-2000 Retroviral HIV; 88.

95US-00525849

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                                                                                                                                                                                                                         The present invention describes a retroviral vector (I) comprising a retrovirus in which at least part of the genomic RNA sequences carrying information for the production of viral proteins required in trans for retroviral replication have been replaced by one or more sequences carrying information to be introduced in a target cell chromosome, where the primer binding site (PBS) has been modified to a sequence that does not allow strong base pairing with the 3'-end of any naturally occurring tRNA, and where the three 5'-nucleotides of the PBS are UGG. (I) are potentially useful as antiviral agents, e.g. against human immunodeficiency virus or human 1'-cell lymphotropic virus-1. (I) depends on a specifically engineered tRNA-like primer for reverse transcription, so only special packaging cells, containing an artificial primer, can support vector propagation. This reduces the risk of uncontrolled regeneration of complete virus if (I) interacts with engineered or endogenous cis- or trans-acting components, particularly transfection efficiency is reduced by a factor of 100000 in normal packaging cells. (I) can be derived from pathogenic viruses of the same type as used for vector construction, i.e. they have the same host range and cell tropism, but the modified PBS means that antiviral activity would not be directed against the vector's own cis-acting elements. The present sequence is murine tRNA sequence, which is used in the exemplification of the present and the present in the exemplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                              Retroviral vector for gene transfer, useful as antiviral agent, has a primer binding site modified to prevent base pairing with natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human biallelic marker upstream amplification primer SEQ ID NO:5708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.2%; Score 13.2; DB 1; Length 18; 65.7%; Pred. No. 2.6e+02; ve 3; Mismatches 3; Indels
                                                                                           Pedersen FS, Duch M, Jorgensen P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 BP; 3 A; 10 C; 2 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                 Disclosure; Col 10; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 TCCACGCCATCTCCCCCA 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the present invention
                                                                                           Lovmand J,
              PEDERSEN F S.
                                                     JORGENSEN P.
                                                                                                                     WPI; 2000-282226/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 12; Conserv
                          LUND A H.
LOVMAND J.
                                                                DUCH M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis; ss
                                                                                                                                                                          transfer RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9954500-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-OCT-1999
                                                                                           Lund AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ71352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                         (LUND/)
(LOVM/)
(JORG/)
(DUCH/)
            (PEDE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ71352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ7740 represent amplification brimers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the pharmaceutical efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment.

N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and present invention
                                                                                                                                                                                                                                                                                                                           Novel biallelic markers used to construct a high density disequilibrium map of the human genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ65654 to AAZ69578 represent human biallelic markers from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human biallelic marker downstream amplification primer SEQ ID NO:9959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.2%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 2.6e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 BP; 3 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chumakov I;
                                                                                                                                                                                                      Chumakov I;
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 1448; 2745pp; English.
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                                                     98US-0082614P:
98US-0109732P.
99WO-IB000822.
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                                                                                                                                                                                                      Cohen D, Blumenfeld M,
                                                                                                                                                                                                                                                                  WPI; 2000-013267/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sest Local Similarity
                                                                                                                                             (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEST ) GENSET
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21-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-NOV-1998;
                                                        21-APR-1998;
                                                                                     23-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ75603;
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Seguence 18 BP; 2 A; 8 C; 0 G; 8 T; 0 U; 0 Other;
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AAZ65654 to AAZ68578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ65959 to AAZ7440 represent amplification primers for the biallelic markers. The biallelic markers of the invention primers for the biallelic markers. The biallelic markers of the invention primers for the biallelic markers of the invention composition sendies and haplotyping studies which are useful in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from of the differential efficacious responses to and side effects from fine SEQ ID NOS 2852, 2913, 2914, 3035, 3056, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the
                                                                                                           Novel biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                        Claim 8; Page 2354; 2745pp; English.
                                                                                                                                                                                             map of the human genome
WPI; 2000-013267/01
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Score 13.2; DB 1; Length 18; Pred. No. 2.6e+02;
                           Indels
                            0; Mismatches
                                                    209 ATCCCCCATTTCATTGCC 226
                                                                             18
    1.2%;
                                                                              1 Arccccrrrrrcarrrcc
    Query Match
Best Local Similarity 83.3
Matches 15; Conservative
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Gaps ; 0

> TM7XN1 cDNA antisense PCR primer. AAA91755 standard; DNA; 18 BP. (first entry) 02-JAN-2001 RESULT 517

Tumour; TM7XN1; metastatis; melanoma; seven transmembrane protein; secretin family; G-protein-coupled peptide hormone receptor; cancer; chromosome 16q13; tumour supressor; cyld1; cylindromatosis; PCR primer; human; se.

Homo sapiens

AU200013568-A.

03-AUG-2000

99EP-00101925 29-JAN-1999;

25-JAN-2000; 2000AU-00013568

(HOFF ) HOFFMANN LA ROCHE & CO AG

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F Hoffmann- La Roche Ag;

WPI; 2000-572508/54.

Nucleic acid molecule down-regulated during tumor progression and/or metastasis as prognostic markers in diagnosis of metastatic and progression potential of tumor cells, and for treating cancer.

Disclosure; Page 17; 48pp; English

The present invention relates to a novel human integral seven

ö transmembrane protein with a long N-terminal extracellular domain: TMYXNI (see AAA91751 and AAB31700). Based on homology comparison, TMYXNI can be placed in the secretin family of G-protein-coupled peptide hormone receptors. TMYXNI gene expression is down-regulated in metastatic human melanoma cells, and is down-regulated during tumour progression and/or metastasis. Therefore, TMYXNI may be involved in metastasis due to its down-regulation in melanoma cells. The TMYXNI gene is localised on chromosome 16q13, and is therefore a candidate gene for the tumour supressor gene cyldl, which is involved in cylindromatosis. The present sequence is a PCR primer for the coding sequence of TMYXNI. This sequence was used during the study of mRNA expression of TMYXNI in various human New polynucleotide encoding prolactin regulatory element binding protein useful for treating osteoporosis, cancer and autoimmune diseases. Prolactin regulatory element binding protein; PREB protein; kinase-mediated hormonal regulator; transcription factor; 1P element; prolactin promoter; osteoporosis; cancer; autoimmune disease; graft-versus-host disease; trisomy 2p; probe; PCR primer; ds. Gaps ö 1.2%; Score 13.2; DB 1; Length 18; ilarity 83.3%; Pred. No. 2.6e+02; Conservative 0; Mismatches 3; Indels PCR primer used to amplify a human PREB gene fragment. Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 U; 0 Other; (MOUN ) MOUNT SINAI SCHOOL MEDICINE. Clelland CL; Example; Page 57; 87pp; English. 349 GATCAAATGGGGAGCCTG 366 1 GAGCTGATGGGGAGCCTG 18 99US-0125728P. 23-MAR-2000; 2000WO-US007642 AAA75986/c ID AAA75986 standard; DNA; 18 (first entry) Fliss M, WPI; 2000-638247/61. Local Similarity nes 15; Conserv WO200056756-A2. 23-MAR-1999; Bancroft CF, Homo sapiens 08-FEB-2001 28-SEP-2000. AAA75986; Query Match RESULT 518 cell **Matches** 88888888888888888 ð g

The specification describes a prolactin regulatory element binding (PREB) protein. The protein is a kinase-mediated hormonal regulator of prolactin gene expression, i.e. a transcription factor. The protein binds to the 1P element pf the prolactin pronoter. PREB proteins are useful for treating osteoporosis. PREB modulators are useful for treating cancer, autoimmune sequences by inhibiting the expression of prolactin. PREB antisens of prolactin gene expression is useful for treating a development defect. Inhibition of prolactin gene expression is useful for inhibiting graft.versus-host flaseases in transplantations. PREB polymucleotides are useful as a probe for diagnosing trisomy 2p in a subject. PCR primers AAA75984-87 were useful to amplify a human PREB gene fragment

Sequence 18 BP; 8 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Fri Aug 19 11:00:00 2005

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13,
                              19-APR-2001 (first entry)
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nes 15, Conservative
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                                                                                                                                                                                                                  (UYMC-) UNIV MCGILL.
                                                                                                                                 WO200105963-A2.
                                                                                                                                                                                             15-JUL-1999;
                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                      Pundytus ME,
                                                                                                                                                      25-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to an oligonucleotide array comprising orligonucleotide tags fixed to a solid substrate. The oligonucleotide array is useful for genotyping a nucleic acid sample at one or more loci via single base extension (SBE) reactions. A pair of primers is used to amplify a polymorphic locus in a sample e.g. a single nucleotide polymorphism (SNP). The present sequence is one of the primers used in the method of the present invention to amplify a polymorphic sample. The amplified nucleic acid product is then used as a template in a SBE reaction with an extension primer. The SBE reaction products are used to
                                                                                                                                                                                                      Oligonucleotide array; genotyping; single base extension reaction; SBE; PCR primer; polymorphic locus; single nucleotide polymorphism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Universal array of oligonucleotides tags attached to a solid substrate along with locus-specific tagged oligonucleotides useful in genotyping using single base extension reactions.
                              Gaps
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Pred. No. 2.6e+02;
0; Mismatches 3; Indels
         Length 18;
 Score 13.2; DB 1; Dens-Pred. No. 2.66+02;
                                                                                                                                                                                                                                                                                                                                                                                  Lander ES,
                                                                                                                                                                                  Reverse primer #96 used in multiplexing PCR/SBE assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 BP; 6 A; 4 C; 7 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                  Kaplan P,
                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                   (WHED ) WHITEHEAD INST BIOMEDICAL RES. (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 7; Page 58; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  Huang X,
                                                 279 CATATTTCTTCACTACTG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGCATTATCCTTCAGTG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            form the oligonucleotide array
                                                                     Н
                                                                                                                     AAC73454 standard; DNA; 18 BP
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        1.2%;
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99US-0140359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.2%;
                                                                    18 CACATTTCTTCTCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recerrerecercagne
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Best Local Similarity 83.33,
Best Local 15; Conservative
                                                                                                                                                              (first entry)
                            15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  Hirschhorn JN,
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-656171/63
        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             Sklar P;
                                                                                                                                                                                                                                                         WO200058516-A2
                                                                                                                                                                                                                                                                                                                     26-MAR-1999;
23-JUN-1999;
                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                              02-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                             Ryder T,
                                                                                                                                           AAC73454;
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                                                                                                   519
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                           Matches
                                                                                                 AAF56336/
ID AAF5
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New antisense oligonucleotides to metabotropic glutamate receptor type 1 gene, which specifically hybridize to mRNA expressed from the gene useful for treating disorders related to elevated glutamate level such as pain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to an antisense oligonucleotide derived from the sequence of metabotropic glutamate receptor type 1 (mGluKl) gene. The antisense oligonucleotide binds to a portion of mRNA expressed from the gene or its splice variant. The binding of the oligonucleotide host cell expressing the gene. The oligonucleotides are useful for treating chronic pain caused by injury or inflammation of a nerve caused by arthritis. The oligonucleotides may be used with an opioid analgesic. They are also useful for minimizing glutamate enurotoxicity and/or excitotoxicity associated with stroke, isohemia, CNS trauma, neurodegenerative disorders, gastrointestinal disorders or to inhibit
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                                                                                   Antisense; metabotropic glutamate receptor type 1; mGluR1; pain; inflammation; arthritis; opioid analgesic; glutamate; neurotoxicity; tumour; human; ss.
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Human mGluRlbeta GB-PR2:HUMMGLUB antisense oligonucleotide #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.2%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 2.6e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vainio A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 5 A; 3 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Henry JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human HCN1 DNA amplifying antisense primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cohen SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 19; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     901 CAAGAGCCICAACATITC 918
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RESULT 523
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                                                                                                                                                                                                                                                                             The invention relates to new uses of human hyperpolarisation-activated, cyclic nucleotide-gated (HCN) channel polypeptides and their polymucleotides. The HCM channel polypeptides and polymucleotides can be polymucleotides. The HCM channel polypeptides and polymucleotides can be used in the manufacture of medicaments to treat stroke, ischaemia, head injury, epilepsy, Alzheimer's disease, Parkinson's disease, learning or memory and attention disorders. These compounds may also be used in treating pain, gut disorders, in particular Irritable bowel syndrome (IBS) or sleep disorders. HCM polymucleotides and polypeptides may also be employed as diagnostic reagents for detection of mutations in the above stated diseases. The present sequence is a reverse transcription (RT)-PCR primer used to amplify human HCN1 channel DNA and it is used in the tissue localisation of HCN1 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; glial cell derived neurotrophic factor; GDNF; PCR; primer; 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human glial cell derived neurotrophic factor (GDNF) PCR primer #30.
                                                                                                                                                                                                    New HCN channel polypeptides and polynucleotides which encode the polypeptides, for the manufacture of compositions to treat stroke, ischemia, head injury, epilepsy, Alzheimer's disease, Parkinson's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 BP; 2 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                          Davies C;
                                                                                                                                                            Gloger I,
                                                                                                                                                                                                                                                             Example 1; Page 21; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 GIGCCITAGAGGATTATG 161
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                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM PLC.
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                                                                                                                03-NOV-2000; 2000GB-00026946.
                                                                               03-JUL-2001; 2001WO-GB002959.
                                                                                                      2000GB-00016360.
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                                                                                                                                                             Strijbos PJLM, Bates S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nervous system disease.
                                                                                                                                                                                 WPI; 2002-188422/24.
                                    WO200202630-A2
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               Номо варіепв
                                                                                                      03-JUL-2000;
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                                                          10-JAN-2002
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The invention relates to the human glial cell derived neurotrophic factor (GDNF) and its derivatives and use. The invention also relates to a method of obtaining DNA encoding human glial cell derived neurotrophic factor or its active segments and a method of purifying and fining coarse GDNF. A composition comprising human glial cell derived neurotrophic factor and a medicinal acceptable carrier can be used in the treatment of nervous system diseases. Sequences ACA96807-ACA96859 represent PCR primers used to amplify human GDNF CDNA
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                                                                                               Human glial cell derived neurotrophic factor and its derivatives and use.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent the distinguishes between methylated and non-methylated CpG dinucleotides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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G, Lesche R, Leu E;
Mueller V, Otto T, E
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P, Grabs C
Model F, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                Claim 6; Page 3 (Claims); 28pp; Chinese.
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Lipscher E, Maier S,
I, Ziebarth H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         645 GACCTGTCAAATTTAGAT 662
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Best Local Similarity 83.3
Matches 15, Conservative
  Feng
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                                               WPI; 2003-000523/01
Zheng Z,
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Lewin A, Lij
Schwope I,
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  Zhou S,
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biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. AB209861 to AB211118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells, for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the maplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between the languages, diagnosis, presement and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative
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P, Grabs G, Lesche R, Leu E;
Model F, Mueller V, Otto T, Pelet C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                           sorders allowing for improved and informed treatment of patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; probe; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1.2%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 2.6e+02; ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 2 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
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Olek A, Piepenbrock C, Adorjan
Lewin A, Lipscher E, Maier S,
Schwope I, Ziebarth H;
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les 15; Conservative
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subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. AB209861 to AB21118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention calls for differentiating between acute invention. Oligonucleotic cells, for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the Cycosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the application of haematopoietic cell proliferation between sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferation of patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine, attenuated virus; recombinant virus; cancer; neoplasm; tumour; replication-competent virus; carcinoma; viral infection; HIV; rotavirus; respiratory syncytial virus (RSV); Hepatitis A virus; politovirus; prapilloma virus; measles virus; influenza virus; bacterial disease; PCR; Vibrio cholerae; enterotoxigenic Escherichia coli; Shigella; Listeria; Streptococcus; Salmonella; parasite; Plasmodium falciparum; trypanosome;
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Best Local Similarity 83.3
Matches 15, Conservative
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The invention relates to a population of live attenuated recombinant replication-competent viruses, which comprise at least two member viruses. Bach of the member viruses comprises a nucleotide sequence encoding a different antiganic polypeptide from a pathogenic organism other than a parent virus from which the recombinant virus was derived, and which is capable of being expressed in a eukaryotic cell. The replication-competent virus population is useful in a method of inducing an immune response in a subject. This comprises administering a first population of replication-competent viruses; and after a time, administering a second population in a second strain of the replication-competent viruses. The second strain is a different strain from the first strain. The population of ilve attenuated recombinant replication-competent viruses is useful as a varying a varying an immune rearrier is a subject of a subject of a varying an immune reasons. a vaccine, particularly for eliciting an immune response in a subject. In particular, the population of live attenuated recombinant replication-competent viruses is useful for treating or inhibiting cancer, neoplasm, tumour or carcinoma. Also for preventing, reducing, treating, inhibiting viral infection such as HIV, rotavirus, respiratory syncytial virus (RSV), Hepatitis A virus, poliovirus, papilloma virus, measles virus and influenza virus; bacterial diseases caused by e.g. Vibrio cholerae, enterotoxigenic Escherichia coli, see plasmodium falciparum, trypanosomes. The present sequence represents the DNA fragment B amplification primer Bl Novel mutant DNA sequence encoding peroxisome proliferator-activated receptor coactivator useful for identifying subjects who are at increased risk of developing type 2 diabetes. The invention relates to an isolated polynucleotide molecule comprising nucleotide sequence encoding peroxisome proliferator-activated receptor-Peroxisome proliferator-activated receptor-gamma coactivator-1; PGC-1; type 2 diabetes; antidiabetic; enzyme; PCR; primer; ss. Gaps ; 0 Query Match 1.2%; Score 13.2; DB 1; Length 18; Best Local Similarity 83.3%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatches 3; Indels Sequence 18 BP; 6 A; 3 C; 3 G; 6 T; 0 U; 0 Other; Pedersen OB; PGC-1 mutational analysis PCR primer #8. Example 1; Page 26; 44pp; English. 650 GTCAAATTTAGATTATGT 667 Ek J, Hansen T, AAL55147 standard; DNA; 18 BP 06-JUN-2002; 2002WO-DK000382 08-JUN-2001; 2001EP-00610061 10-JUL-2001; 2001DK-00001080 18 Grcaaarcrcaarargr 24-APR-2003 (first entry) (NOVO ) NOVO NORDISK AS. NPI; 2003-156949/15. WO2002100894-A2 Unidentified Andersen G, 19-DEC-2002 AAL55147; RESULT 526 AAL55147 ઠે 셤 

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cc diabetes of at least one nucleotide, or comprising a fragment of the uncleotide sequence including the mutation. The isolated polynucleotide is useful for detecting the presence of a mutation in the gene encoding CC is useful for detecting the presence of a mutation in the gene encoding PGC-1, by obtaining a biological sample from a subject and analyaing the sample for a mutation associated with type 2 diabetes of the nucleotides in PGC-1, by obtaining a biological sample is obtained from a subject, DNA is isolated polynucleotide which contains a mutation associated with type 2 diabetes of at least one nucleotide or comprising a fragment of the concleotide sequence including the mutation to be detected, and hybridisation of the labelled polynucleotide to the DNA is determined. The amplified DNA is hybridised to a second labelled polynucleotide comprising a DNA sequence corresponding to a part of the wild-type gene corresponding polynucleotide carrying the mutation is labelled polynucleotide to the amplified DNA is determined. The substance with which the second labelled polynucleotide carrying the mutation is labelled in the labelled corresponding to a part of the wild-type DNA is labelled. This method is corresponding to a part of the wild-type DNA is labelled. This method is corresponding to a part of the wild-type DNA is labelled. This method is useful for determining predisposition to type 2 diabetes and to determining predisposition to type 2 diabetes and to determining predisposition to type 2 diabetes and to determining the polynucleotide sequence anticy at the perceptor-gamma and for tailoring antidiabetic medication. This polynucleotide sequence represents a perimer used for mutational analysis of the peroxisome proliferator-gamma coactivator-I (PGC-1) of the invention ö Amplifying nùcleic acid in animal cells, useful e.g. for gene therapy or vaccination, uses an RNA-dependent, RNA-polymerase of a plant virus. RNA-dependent RNA polymerase; RdRP; plant virus; amplification system; Gaps ; 0 DB 1; Length 18; Indels Sequence 18 BP; 6 A; 6 C; 2 G; 4 T; 0 U; 0 Other; / Match 1.2%; Score 13.2; DB 1; Local Similarity 83.3%; Pred. No. 2.6e+02; tes 15; Conservative 0; Mismatches 3 TCV RdRP mutagenic PCR primer i120. 443 GATTTTAGCTGGGAGCAG 460 н ADA41736 standard; DNA; 18 BP 29-JUL-2002; 2002WO-DE002863. 30-JUL-2001; 2001DE-01037444. 18 GATTTTGGCTTGAAGCAG 20-NOV-2003 (first entry) Turnip crinkle virus. (PROB-) PROBIOGEN AG. Jordan I; WPI; 2003-248302/24. ss; primer; PCR. WO2003014366-A2. 20-FEB-2003. Sandig V, Synthetic ADA41736; Query Match RESULT 527 Matches ADA41736/ ઠ d

Example 1; Page 17; 39pp; German.

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This invention describes a novel method for amplifying nucleic acid in animal cells by introducing an RNA-dependent RNA polymerase (RARP) and it's associated promoters and cis-acting signals from a plant virus into the cells. RARP is normally active in plant cells and the gene that encodes it can be recovered from such cells. Both the RARP and the promoter are from plant viruses, particularly turnip crinkle virus and the amplified RNA is a modified satellite or genomic RNA of this virus. The method is particularly used for amplification of RNA (which may be remany for protein synthesis; an effector, e.g. antisense RNA or ribozyme, cor genomic RNA) in animal cells, for (i) control of gene expression or (ii) for gene therapy or vaccination. When the system includes an inducible promoter, it permits strong and rapid expression or conscious in response to a test substance, especially where the promoter capponds to the human immune deficiency virus or heavy metals, to produce a diagnostic system or biosensor, respectively. The method of the cinvention provides an inducible or constitutive, autonomous RNA-dependent CNA amplification system for animal cells that requires only one convention and does not use any viral structural genes or helper viruses. Amplification takes place in the cytoplasm without using any components octonically infectious for the host cells. Human 23 cells were constituting, iii) plu0-39, expressing a turnip crinkle virus 88 kD protein; iii) plu0-60, expressing a turnip crinkle virus 88 kD concent protein in the antisense orientation, and (iii) an expression concent protein in the antisense orientation, and (iii) an expression concent protein in the antisense orientation, and fill an expression concent protein of the reporter gene was detected by fluorescence promoter. Expression of the reporter gene was detected by fluorescence concent turnip crinkle virus (TCV) RARP gene into plu0-39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wnt-1 induced secreted protein; WISP; Wnt-1 induced gene; WIG; WISP-1; WISP-2; WISP-3; connective tissue growth factor; CTGP; tumour cell; cell death; atherosclerosis; malignant disorder; breast cancer; ovarian cancer; colon cancer; melanoma; antiarteriosclerotic; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.2%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 2.6e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 CCGCAAGCAGCCGCGCC 56
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98US-0073612P.
98US-0081695P.
98US-00182145.
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Best Local Similarity 83.3
Matches 15; Conservative
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29-OCT-1998;
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Levine AJ, Pennica D;

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                                                   New nucleic acid encoding Wnt-1-Induced Secreted Protein, useful for preparing a composition for treating a WISP-related disorder in a mammal comprising atherosclerosis or malignant disorder, e.g., breast, ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining predisposition to inverted nipples useful e.g. for selecting breeding animals comprises detecting specific microsatellite markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to the use of a nucleic acid to determine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 83.3%; Score 13.2; DB 1; Length 18; Best Local Similarity 83.3%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatchen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inverted nipple; microsatellite; PCR; primer; 88; pig.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in the examples of the present invention.
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                                                                                                                                                     Example 11; Page 39; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 23; 63pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  897 AGACCAAGAGCCTCAACA 914
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                                                                                                                  colon cancer.
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Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel human polymuclectide and the encoded polypeptide. A polymuclectide of the invention May have a use in gene therapy. An oligomuclectide of the invention ADM65202-M006773 is useful detecting the polymuclectide. The polymuclectide or as a probe for useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polymuclectides are useful as pharmaccutical agents. The present sequence represents an oligonuclectide used in the invention.
   S0200, SW2443, S0097, S0007, SW1301 or S0164 on chromosomes 6, 2, 4, 14, 1 and 3, respectively, in pigs, or homologous positions in the genomes of other mammals. The nucleic acids can be used to select pets, breeding or farm animals that lack inverted nipples, particularly by genomic screening of many related mammals in a population. The present sequence is a PCR primer used in the exemplification of the invention to identify microsatellite markers associated with the inverted nipple phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; gene therapy; diagnostic marker; pharmaceutical; ss; PCR; primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides and polypeptides are useful in gene therapy, developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.
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1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PCR primer SEQ ID NO:4925.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Seki N, Yoshikawa T,
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The invention relates to a method of inducing cellular apoptosis

comprising administering to a cell an effective amount of an antisense

compound targeted to a nucleic acid molecule encoding human cellular

inhibited and apoptosis 1 (GIAP-1), so that expression of GIAP-1 is

inhibited and apoptosis is induced. The cell used in the method is a

confort cell. The antisense compound is an antisense oligonucleotide that

comprises at least one modification of the internucleoside linkage, wherein the modification is a phosphorothioate

moiety or nucleobase, wherein the modification is a phosphorothioate

confortsosine nucleobase. The antisense oligonucleotide is a chimeric

coligonucleotide. The methods and compositions are useful for the

prevention and/or treatment of diseases or conditions associated with

coligonucleotides and virial infections. This sequence represents a

cautoimmune disorders and virial infections. This sequence represents a

chuman cIAP-1 DNA antisense oligonucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inducing cellular apoptosis by administering an antisense modulating the human Cellular Inhibitor of Apoptosis-1, useful in preventing or treating cancer, autoimmune disorders and viral infections.
                                                                                                                                                                                                                                                 cancer; antisense oligonucleotide; phosphorothioate internucleoside linkage; 2'-0-methoxyethyl sugar molety; 5-methylcytosine; autoimmune disorder; viral infection; cytostatic;
                                                                                                                                                                                                                                 cellular inhibitor of apoptosis-1; cIAP-1; ss; cellular apoptosis;
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Pred. No. 2.6e+02;
                                                                                                                                                                                                    Human cIAP-1 DNA antisense oligonucleotide #30
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24-SEP-2001; 2001US-00857278
immunosuppressive; virucide.
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                                                                                                   ADM96453 standard; DNA; 18
                                                                                                                                                                      (first entry)
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Matches
                                                                                       ADM96453,
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Gaps

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1.2%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 2.6e+02; ive 0; Mismatches 3; Indels

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Query Match Best Local Similarity 83.3 Matches 15; Conservative

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Unidentified
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                                                                                                                                                                                                                                                                                                            The invention relates to compounds, compositions and methods for modulating the expression of MD-1 RP105-associated (also called as MD-1 and MD1) DNA. The composition comprise antisense oligonucleotides targeted to MD-1 RP105-associated DNA. The compound is useful for preparing a composition for treating autoimmune disorder. It is also useful in gene therapy. The present sequence is a PCR primer used for amplifying human MD-1 RP105-associated DNA. This sequence is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                        New oligonucleotide compound that inhibits expression of MD-1 RP105-associated, useful for preparing a composition for treating autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic, Gene therapy; breast cancer; human, DLG1, KIAA0783, DPF3, CENPC1, SNP, single nucleotide polymorphism; centromere protein C1, Centromere autoantigen C1; chromosome 4q12-q13.3; extend; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                 MD-1 RP105-associated; MD-1; MD1; autoimmune disorder; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                               Human MD-1 RP105-associated DNA amplifying reverse PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                             1.2%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 2.6e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 BP; 1 A; 3 C; 8 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                            Claim 21; SEQ ID NO 6; 63pp; English.
883 AAAGTGTGGCCCACAGAC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 AAAGCCTGGCCCACACAC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADO80001 standard; DNA; 18 BP
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUN-2004
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The present invention relates to a method for identifying a subject at risk of breast cancer. The method comprising detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a subject. The nucleic acid sample comprises the DLG1 region (AD079402), KIAA0783 region (AD079403), DPF3 region (AD079404) or CEMPC1 region (AD079405). The gene DLG1 (discs, large homolog 1 (Drosophila)) is also known as synapse-associated protein 97, hdlg or SAP97. DLG1 has been mapped to chromosomal position 7p21.3. The KIAA0783 protein is an overland protein or protein the comprises with unknown function, however, being a zinc finger protein, cancer gene WIAA0783 protein is a novel gene with unknown function, however, being a zinc finger protein, can be been mapped to chromosomal position 14q44.3.q11.1. The cator. DPF3 has been mapped to chromosomal position 14q44.3.q11.1. The cator. DPF3 has been mapped to chromosomal position 4q12-q10.3.3. CENPC1 (centromere protein C1) is also known as Centromere catoantigen and a component of the inner kinetochore plate. The CENPC1 protein is required for maintaining proper kinetochore plate. The CENPC1 protein is required for maintaining proper kinetochore size and a timely translition to anaphase. The method is useful for identifying a subject at risk of breast cancer, to analyze and candidangosis, prevention and treatment of breast cancer, to analyze and predict a response to a breast cancer treatment, and in clinical drug crials. The present sequence was used in an example from the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying a subject at risk of breast cancer by detecting the presence of polymorphic variations in the DLG1, KIAA0783, DPF3 or CENPC1 regions which are associated with breast cancer in a nucleic acid sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gape
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                                                                                                                                                                                                                                                                                               Reneland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 2.6e+02;
0; Mismatches 3
                                                                                                                                                                                                                                                                                           Kammerer SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Page 91; 227pp; English.
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                                                                                                                                                                                                                                                                                               Braun A,
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25-NOV-2003; 2003WO-US037943.
                                                                              25-NOV-2002; 2002US-0429136P.
24-JUL-2003; 2003US-0490234P.
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                                                                                                                                                                                                                                                                                               Nelson MR,
                                                                                                                                                                                                            (SEQU-) SEQUENOM INC
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-441037/41.
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Local Similarity
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                                                                                                                                                                                                                                                                   Unidentified
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invention.
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                                                                                                                                                                         ADQ80462;
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                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to novel Pseudonocardia thermophila nitrile hydratase (I) sequences. (I) efficiently converts a nitrile compound into its corresponding amide compound and is useful for producing biocatalyst substances. The present sequence is a PCR primer used to illustrate the
                                                                                                                                                                        The present invention relates to novel Pseudonocardia thermophila nitrile dyfartase (I) sequences. (I) efficiently converts a nitrile compound into its corresponding amide compound and is useful for producing biocatalyst substances. The present sequence is a PCR primer used to illustrate the
                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                     Novel nitrile hydratase, useful for producing nitrile and amide compounds, comprises alpha and beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nitrile hydratase, useful for producing nitrile and amide compounds, comprises alpha and beta subunit.
                                                                     Tanaka
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Pred. No. 2.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nitrile hydratase; enzyme; biocatalyst; PCR; primer; ss.
                                                                    Matoishi K, Ito K, Kobayashi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kobayashi H,
                                                                                                                                                                                                                                      Sequence 18 BP; 3 A; 8 C; 6 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nitrile hydratase related PCR primer, SEQ ID 62
                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                   Disclosure; SEQ ID NO 32; 345pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ito K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matoishi K,
                                                                                                                                                                                                                                                                                                  17 CTGCCCGGGCCGTGGCAG 34
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10-NOV-2003; 2003JP-00379280.
15-DEC-2003; 2003WO-JP016014.
                   19-DEC-2002; 2002JP-00368360.
10-NOV-2003; 2003JP-00379280.
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                                                 (MITA ) MITSUI CHEM INC
                                                                     Banba S,
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                                                                                                  WPI; 2004-517682/49.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamaki T,
Oikawa T;
                                                                    Yamaki T,
Oikawa T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to treating abnormal cells in a mammal comprises treating the mammal with an echovirus or its modified forms of combinations, which recognize & &ggr; 2 &gbg: i for infectivity of the inoculant for generating echovirus is useful in the manufacture of medicament for inducing an immune response against cancer cells in a mammal. The present sequence represents a MGB probe to determine EVI viral RNA levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     echovirus; &agr2; &bgr1; Cytostatic; Immunostimulant; immune response; cancer; ss; probe.
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Pred. No. 2.6e+02;
0; Mismatches 3; Indels
                                                Length 18;
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G; 0 T; 0 U; 0 Other;
                                              Score 13.2; DB 1;
Pred. No. 2.6e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGB-probe to determine EV1 viral RNA levels.
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Local Similarity 83.3%;
les 15; Conservative (
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Sequence 18 BP; 1 A; 8 C; 9
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The present invention relates to murine oligonucleotides (ACC62754-ACC68806), which are associated with tumour suppression, tumour reversion, apoptosis and virus resistance. The oligonucleotides are useful as (1) as probes and primers for detecting, identifying, quantifying and/or amplifying nucleic acid, e.g. as one component of gene chip; in vitro as (anti) sense reagents; and (2) for production of recombinant polypeptides. The oligonucleotides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
                                                                                   Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine; tumour suppression; tumour reversion; apoptosis; virus resistance; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; ss.
                                                    Murine oligonucleotide associated with tumour supression, SEQ ID 4476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.1%; Score 12; DB 1; Length 17; 100.0%; Pred. No. 3.9e+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                  Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR ENGINES LAB.
                                                                                                                                                                                                                                                                                                  17-SEP-2002; 2002WO-IB004210.
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                 (first entry)
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1es 12; Conservative
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                 01-JUL-2003
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